Arabidopsis Duodecuple Mutant of PYL ABA Receptors Reveals PYL Repression of ABA-Independent SnRK2 Activity

Yang Zhao1,7,*, Zhengjing Zhang1,2,7, Jinghui Gao3,4,7, Pengcheng Wang1,3,7, Tao Hu1,5,7, Zegang Wang3, Yueh-Ju Hou3, Yizhen Wan3, Wenshan Liu3, Shaojun Xie3, Tianjiao Lu1,2, Liang Xue6, Yajie Liu1,2, Alberto P. Macho1, W. Andy Tao6, Ray A. Bressan3, and Jian-Kang Zhu1,3,8,*

1Shanghai Center for Plant Stress Biology, and CAS Center of Excellence in Molecular Plant Sciences, Chinese Academy of Sciences, Shanghai 200032, China
2University of Chinese Academy of Sciences, Beijing 100049, China
3Department of Horticulture and Landscape Architecture, Purdue University, West Lafayette, IN 47907, USA
4College of Animal Science and Technology, Northwest A&F University, Yangling, Shaan’xi 712100, China
5Key Laboratory of Plant Germplasm Enhancement and Specialty Agriculture, Wuhan Botanical Garden, Chinese Academy of Science, Wuhan 430074, Hubei, China
6Department of Biochemistry, Purdue University, West Lafayette, IN 47907, USA

SUMMARY

Abscisic acid (ABA) is an important phytohormone controlling responses to abiotic stresses and is sensed by proteins from the PYR/PYL/RCAR family. To explore the genetic contribution of PYLs toward ABA-dependent and ABA-independent processes, we generated and characterized high-order Arabidopsis mutants with mutations in the PYL family. We obtained a pyl quattuordecuple mutant and found that it was severely impaired in growth and failed to produce seeds. Thus, we carried out a detailed characterization of a pyl duodecuple mutant, pyr1pyl1/2/3/4/5/7/8/9/10/11/12. The duo-decuple mutant was extremely insensitive to ABA effects on seed germination, seedling growth, stomatal closure, leaf senescence, and gene expression. The activation of SnRK2 protein kinases by ABA was blocked in the duodecuple

This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).
*Correspondence: zhaoyang@sibs.ac.cn (Y.Z.), jkzhu@purdue.edu (J.-K.Z.).
7These authors contributed equally
8Lead Contact

AUTHOR CONTRIBUTIONS


DECLARATION OF INTERESTS

The authors declare no competing interests.

SUPPLEMENTAL INFORMATION

Supplemental Information includes three figures and three tables and can be found with this article online at https://doi.org/10.1016/j.celrep.2018.05.044.
mutant, but, unexpectedly, osmotic stress activation of SnRK2s was enhanced. Our results demonstrate an important role of basal ABA signaling in growth, senescence, and abscission and reveal that PYLs antagonize ABA-independent activation of SnRK2s by osmotic stress.

In Brief
Zhao et al. generated duodecuple and quattuordecuple Arabidopsis PYL ABA receptor mutants. Characterization of the mutants revealed that the ABA receptors are critical for plant growth and development and negatively regulate ABA-independent SnRK2 activity by interacting with and inhibiting osmotic stress-activated SnRK2 protein kinases.

INTRODUCTION

The plant hormone abscisic acid (ABA) regulates plant growth, seed dormancy, leaf senescence, and responses to abiotic stresses (Cutler et al., 2010; Fujii and Zhu, 2009; Gonzalez-Guzman et al., 2012; Munemasa et al., 2015; Zhao et al., 2016). ABA is perceived by the intracellular pyrabactin resistance 1 (PYR1) and PYR1-like (PYL)/regulatory component of ABA receptor (RCAR) proteins (hereafter referred to as PYLs) (Ma et al., 2009; Park et al., 2009). All of the 14-members of PYLs, with the exception of PYL13, are able to respond to ABA and inhibit clade A PP2Cs in an ABA-dependent or -enhanced manner, resulting in the activation of sucrose non-fermenting 1-related protein kinase 2 s (SnRK2s) (Fujii et al., 2009; Fujii and Zhu, 2009; He et al., 2014; Li et al., 2013; Zhao et al., 2013). ABA-activated SnRK2s regulate the expression of ABA-responsive genes through phosphorylation of transcription factors, such as ABA-responsive element-binding factors (ABFs) (Furihata et al., 2006) and phosphorylate other substrates related to many processes. In unstressed plants, the target of Rapamycin (TOR) kinase phosphorylates PYLs to prevent activation of stress responses (Wang et al., 2018).

PYLs represent the largest family of hormone receptors in plants and function diversely and redundantly in ABA signaling (Ma et al., 2009; Park et al., 2009). PYLs selectively interact
with PP2Cs and selectively inhibit the phosphatase activity of the nine clade A PP2Cs (Antoni et al., 2012; Bhaskara et al., 2012; Tischer et al., 2017; Zhao et al., 2016). PYR1 and PYL1-2 are dimers in solution, while PYL4-6 and PYL8-10 are monomers (Dupeux et al., 2011; Hao et al., 2011). Generally, monomeric PYLs have higher binding affinities for ABA than dimeric PYLs in the absence of PP2Cs, and these monomeric PYLs can partially inhibit PP2Cs in the absence of ABA (Dupeux et al., 2011; Hao et al., 2011). PYL13 inhibits PP2CA in an ABA-independent manner but cannot inhibit ABI1, HAB1, and AHG1 even in the presence of ABA (Li et al., 2013; Tischer et al., 2017; Zhao et al., 2013). The diversity in these biochemical properties of PYLs is associated with natural variations of PYLs.

Saturated mutations of PYR1 on residues that contact ABA or PP2Cs have been screened for the interaction of PYR1 and HAB1. Twenty-nine mutated PYR1 that have mutations located in 10 different residues (H60, V83, I84, L87, A89, M158, F159, T162, L166, and K170) interact with HAB1 without ABA (Mosquina et al., 2011). Among these mutations, V83L and I84K double mutations enable PYL2 to be a monomeric PYL with partially ABA-independent activity (Hao et al., 2011). Natural variations of H60P and I84K can be found in PYL7-9; three variations including H60P, V83L, and I84K can be found in PYL10; L166F can be found in PYL11; and moreover, four variations including H60R, V83L, L87F, and L166Y can be found in PYL13. The overlap of these mutations with natural variations partially explains the higher basic activities of monomeric PYLs and PYL13 in the absence of ABA and also explains the oligomeric status of these PYLs.

Based on the diversity of their expression patterns and biochemical properties, PYLs are expected to have functional diversity. The pyr1 single mutant is resistant to pyrabactin, which led to the identification of PYL ABA receptors (Park et al., 2009). The pyl8 single mutants are less sensitive to ABA-induced growth inhibition of primary roots compared with the wild-type (WT), whereas ABA-induced inhibition of lateral root elongation is enhanced in pyl8 mutants (Antoni et al., 2013; Zhao et al., 2014). PYL8 promotes auxin responses by directly interacting with and enhancing the activities of MYB77 and its paralogs (Zhao et al., 2014). The pyl9 single mutant shows a reduced ABA-induced leaf senescence under low light (Zhao et al., 2016). PYL9 promotes ABA-induced leaf senescence by activating ABFs through core ABA signaling in an ethylene-independent manner (Zhao et al., 2016).

AtPYL13 and its rice ortholog OsPYL12 inhibit the phosphatase activity of some PP2Cs in the absence of ABA, and OsPYL12 is unable to bind to ABA (He et al., 2014; Li et al., 2013).

Osmotic stress inhibits plant growth and affects development. In response to osmotic stress, plants accumulate ABA, which subsequently induces ABA-dependent responses. Osmotic stress also activates ABA-independent responses through SnRK2s (Fujii et al., 2011). In Arabidopsis, the ten members of the SnRK2 family function redundantly in osmotic stress responses (Boudsocq et al., 2004; Fujii et al., 2011). Five SnRK2s including SnRK2.2, −2.3, −2.6, −2.7, and −2.8 are activated by ABA (Furihata et al., 2006). Understanding how PYLs affect ABA-dependent responses and ABA-independent osmotic stress responses requires genetic impairment of PYLs to block ABA signaling. The pyr1 pyl1 pyl2 pyl4 pyl5 pyl8 T-DNA sextuple mutant (abbreviated as 112458) and the CRISPR/Cas9-generated pyl sextuple mutant (abbreviated as 112458-C) show strong ABA insensitivity in seed germination and seedling establishment, plant growth, stomatal movement, and expression of specific genes.
Since the mutation in PYL8 is in the 5′ untranslated region, the root length and fresh weight of 112458-C mutant are lower than that of the 112458 T-DNA sextuple mutant under high concentration of ABA (Zhang et al., 2016). The 112458 mutant is also impaired in vegetative and reproductive growth (Gonzalez-Guzman et al., 2012), supporting that ABA signaling is required for plant growth and development. However, the growth of 112458 is still more robust than snrk2.2/3/6, and stomatal aperture of 112458 is smaller than that of snrk2.2/3/6 (Gonzalez-Guzman et al., 2012). This suggests that other PYLs are still capable of activating some ABA signaling.

Indeed, a pyl9 single mutant shows reduced ABA-induced leaf yellowing under low light (Zhao et al., 2016). In this study, we generated a pyl quattuordecuple mutant and a pyl pyl1/2/3/4/5/6/7/8/9/10/11/12 (abbreviated as 112458 379101112) duodecuple mutant using a CRISPR/Cas9 gene editing system. Our characterization of these high-order phytohormone receptor mutants provides important insights into the physiological function of PYLs in not only ABA-dependent plant processes but also ABA-independent osmotic stress responses.

RESULTS

Generation of pyl Duodecuple and Quattuordecuple Mutants

Using a multiplex CRISPR/Cas9 system described previously (Zhang et al., 2016), we generated two CRISPR/Cas9 constructs containing eight single guide RNAs (sgRNAs) and co-transformed these two constructs into the 112458 pyl T-DNA sextuple mutant (Figures 1A and S1A; Table S1). One of these two constructs contained six sgRNAs, targeting six PYLs (PYL3, PYL6, PYL7, PYL9, PYL11, and PYL12), and the other construct contained two sgRNAs, targeting PYL10 and PYL13. We were able to mutate six of these eight PYLs, generating the 112458 379101112 pyl duodecuple mutant (Figure 1A). We then generated a pyl pyl13 mutant in the 112458 background using CRISPR/Cas9 and crossed it with the 112458 pyl duodecuple mutant. We screened thousands of F2 seedlings and identified pyl quattuordecuple mutant plants with all 14 PYLs mutated (Figures 1B and 1C). In the pyl quattuordecuple mutants, PYL3-179insA resulted in a frameshift at codon 60; PYL6-140insT resulted in a frameshift at codon 47; PYL7-93insA resulted in a nonsense mutation at codon 30; PYL9-60insC resulted in a frameshift at codon 21; PYL10-Del225-263 resulted in a deletion from codon 75 to 87, which falls into the switch loop region for PP2C binding (Yin et al., 2009); PYL11-73insT resulted in a frameshift at codon 25; PYL12-Del67-71 resulted in a frame-shift at codon 23; and PYL13-Del391-394 resulted in a frameshift at codon 131 (Figures 1C and S1B). The pyl quattuordecuple mutant plants were severely impaired in growth in soil (Figure 1B). Although the pyl quattuordecuple mutants produced a few seeds on occasions, these seeds were all heterozygous, likely due to pollen pollution from adjacent plants, suggesting that the mutants were male sterile. Thus, we were only able to carry out further analysis on the 112458 379101112 mutant.

We also transformed the construct containing the six sgRNAs into Col-0 and generated the pyl3/7/9/11/12 (abbreviated as 3791112) quintuple mutant. In the 3791112 mutant, PYL3-179insT resulted in a frameshift at codon 60; PYL7-93insA resulted in a nonsense mutation at codon 30; PYL9-Del59-63 resulted in a frameshift at codon 20; PYL11-
Del71-78 resulted in a frameshift at codon 25; and PYL12-Del46-75 resulted in a deletion from codon 16 to 25 (Figure S1C).

**Growth Defects of the 112458 379101112 Mutant**

Similar to the snrk2.2/3/6 mutant (Fujii and Zhu, 2009), the 112458 379101112 mutant showed severely impaired growth in soil and could hardly survive under low humidity conditions (Figure 2). In contrast, the 3791112 mutant showed no obvious difference compared with Col-0 WT. Although most of the 112458 379101112 mutant seedling could grow under our growth room conditions (60%–65% relative humidity, 16 hr light/8 hr dark), they were very small, hardly survived after bolting, and failed to produce seeds (Figure 2A, left). The 112458 379101112 mutant seedlings were dwarf plants with small rosettes, short roots, and very reduced biomass (Figures 2B–2G). Their inflorescences frequently wilted and dried, and sometimes quick dehydration happened to whole seedlings (Figure S1D). Although short-day conditions improved the plant height and rosette width of 112458 379101112 and snrk2.2/3/6 mutants, their total biomass did not increase, since they showed fewer axillary branches under short-day conditions compared to long-day conditions (Figures 2A–2E). When a plastic cover was used to maintain a near dew point humidity, the 112458 379101112 mutant plants grew better and occasionally produced a few seeds. The seedlings and seeds of the 112458 379101112 and snrk2.2/3/6 mutants were very susceptible to fungal infection under high humidity. When the humidity was reduced to 80%–90% by removing part of the plastic cover, a small amount of seeds could be obtained occasionally (Figures 2A, right, 2H, and S1E). Furthermore, some batches of the 112458 379101112 seeds did not germinate, and the germinated batch did not have the same seed vigor as WT seeds (Figure 2I). Thus, it was extremely difficult to maintain the 112458 379101112 mutant.

**Extreme ABA-Insensitive Phenotypes of the 112458 379101112 Mutant**

Elegant work of Gonzalez-Guzman et al. showed that the 112458 mutant plants are insensitive to ABA-induced stomatal closure (Gonzalez-Guzman et al., 2012). We noticed that 112458 379101112 mutant plants lost water very quickly when transferred to environments with lower humidity. To avoid the growth retardation of 112458 379101112 plants in soil, we performed water loss and stomatal assays using 25-day-old seedlings grown on agar plates. The excised 3791112 mutant showed similar water loss compared with WT plants, whereas an enhanced water loss was found in the 112458, 112458 379101112, and snrk2.2/3/6 mutants (Figure 3A, upper panel and Figure 3B). By growing the plants in the presence of 200 μM ABA, the shrinking and water loss were obviously reduced in the 112458 mutant, but not in the 112458 379101112 and snrk2.2/3/6 mutants (Figure 3A, lower panel and Figure 3C). Consistent with the water loss results, stomata of 112458 plants were closed by growing the plants on 200 μM ABA, whereas stomata of 112458 379101112 and snrk2.2/3/6 plants grown on 200 μM ABA were still widely open (Figures 3D and 3E).

We also analyzed the ABA-induced inhibition of seed germination and seedling growth. The seed germination and root and shoot growth of the 112458, 112458 379101112, and snrk2.2/3/6 mutants were resistant to 100 μM ABA (Figures 3F–3K). Radicle emergence and seedling growth of 112458 plants were slightly reduced by 100 μM ABA. In contrast,
the seed germination of 112458 379101112 and snrk2.2/3/6 plants was not reduced even under treatment with 100 μM ABA (Figures 3F and 3G). Interestingly, the role of ABA in promoting root growth and total biomass was obvious in 112458 379101112 seedlings (Figures 3H, 3J, and 3K). Although ABA also promoted the root growth of the 112458 mutant, the total biomass of these mutants was not obviously improved by ABA. Consistent with a previous study (Zhao et al., 2016), ABA dramatically reduced the osmotic potential in both Col-0 and 3791112 mutant, but this effect was nearly blocked in the 112458, 379101112, and snrk2.2/3/6 mutants (Figure 3L).

Senescence and Abscission Defects of the 112458 379101112 Mutant

Consistent with our previous findings (Zhao et al., 2016), the 112458, 112458 379101112, and snrk2.2/3/6 mutants were highly insensitive to ABA-induced leaf senescence (Figure 4A). The 112458 379101112 and snrk2.2/3/6 mutants had an extremely low seed yield (Figure 2H). A very low level of fertilization was observed in these two mutants even when stems and flowers did not wilt (Figure 4B), which could have been caused by male infertility. Similar to the anthers of the snrk2.2/3/6 mutants, nearly no pollen was released from anthers in most 112458 379101112 mutant flowers (Figure 4C). We also noticed that the abscission of flower organs was delayed in 112458 379101112 and snrk2.2/3/6 plants (Figure 4D). In contrast, stigma abscission was not abolished in pistils of 112458 plants, whereas the anther dehiscence and the flower organ abscission were also delayed in 112458 flowers (Figures 4B–4D). The 3791112 mutant did not show any difference from WT plants in either ABA-induced senescence or anther dehiscence (Figure 4).

Gene Expression Responses to ABA and to Osmotic Stress in the 112458 379101112 Mutant

The 112458 379101112 mutant is the most relevant mutant to analyze ABA-dependent and ABA-independent osmotic stress responses at the present time, because the snrk2.2/3/6 triple and snrk2 decuple mutants are affected in both ABA-dependent and -independent pathways (Fujii et al., 2011). When seedlings were treated with 100 μM ABA for 24 hr, 3,024 genes showed altered transcript levels (2-fold or greater, false discovery rate, p < 0.05) compared with that of control conditions in WT seedlings, whereas only 356 showed altered expression in the 112458 379101112 mutant after ABA treatment compared with that of control conditions (Figure 5A; Table S2). Among these genes, only 211 genes overlapped between WT seedlings and the 112458 379101112 mutant, indicating that the ABA-induced regulation of the expression of 93% of the genes altered in WT plants was impaired in the 112458 379101112 mutant (Figure 5A). Heatmaps clearly show that nearly all of the transcript level responses to ABA in WT seedlings were diminished in the 112458 379101112 mutant (Figure 5B).

In contrast, transcript level responses to osmotic stress were readily detectable in the 112458 379101112 mutant (Figures 5C and 5D). When seedlings were treated with 300 mM mannitol for 24 hr, 4,609 genes showed altered expression (2-fold or greater, false discovery rate, p < 0.05) in WT seedlings, and 3,407 genes were altered in 112458 379101112 plants.
compared with that of control conditions (Figure 5C). Among them, 2,132 genes overlapped between WT seedlings and the 112458 379101112 mutant. This indicates that the mannitol-induced regulation of the expression of ~54% of the genes altered in WT plants was impaired in the 112458 379101112 mutant and suggests that these genes must be regulated by osmotic stress in an ABA-dependent manner, since their regulation requires the presence of the ABA receptors (Figure 5C). Osmotic stress may regulate gene expression directly through an ABA-independent activation of SnRK2s, and/or indirectly through the regulation of ABA accumulation and the subsequent ABA signaling. Among the 1,865 genes co-regulated by ABA and mannitol in WT seedlings, 1,036 overlapped with mannitol-regulated genes in the 112458 379101112 mutant (Figure S2). Among those 2,744 genes exclusively regulated by mannitol treatment in WT seedlings, 1,096 overlapped with mannitol-regulated genes in the 112458 379101112 mutant. Among those 1,275 genes regulated by osmotic stress in 112458 379101112 mutant but not in WT plants, 555 were upregulated, indicating that PYLs negatively regulate these genes under osmotic stress (Figure 5C). Gene ontology (GO) analysis showed that biological processes associated with responses to fungus, bacterium, wounding, organic substance, oxidative stress, and jasmonic acid were enriched in the osmotic stress upregulated genes exclusive in the 112458 379101112 mutant (Figure S3). Heatmaps clearly show that only a relatively small percentage of the transcript level responses to osmotic stress was abolished in the 112458 379101112 mutant, and the majority of the responses was maintained, although the levels of up- or downregulation of many of the transcripts were reduced in the mutant (Figure 5D).

In the 112458 379101112 duodecuple mutant, only PYL6 and PYL13 are WT alleles. Moreover, PYL13 cannot respond to ABA in inhibiting PP2Cs (Li et al., 2013; Zhao et al., 2013). We found that the expression of PYL6 was higher in the 112458 379101112 mutant than in WT seedlings, and the downregulation of PYL6 by ABA was abolished in the 112458 379101112 mutant (Figure 5E). In the 112458 379101112 and snrk2.2/3/6 mutants, both ABA and osmotic stress failed to induce a group of ABA-dependent responsive genes, including desiccation/dehydration (RD) genes such as RD29B, several responsive to ABA (RAB) genes, such as RAB18 and KIN1, and even the sucrose efflux transporter SWEET15 (Figures 5E and 5F). In contrast, another group of genes could be substantially induced by osmotic stress but not ABA in the 112458 379101112 and snrk2.2/3/6 mutants, including the proline biosynthesis gene P5CS1, several senescence-associated genes (SAGs), such as SAG13 and AtNAP, RD genes, such as RD20 and RD22, and ABFs, such as ABI5 (Figures 5G and 5H). We also found that a group of genes that are known as positive regulators of osmotic stress responses were mainly induced by osmotic stress but not ABA, including the plant natriuretic peptide (PNP) gene PNP-A, the NAC transcription factor gene NAC096, and also several WRKY transcription factor genes, such as WRKY46 and ABOJ (Ding et al., 2014; Ren et al., 2010; Wang et al., 2011; Xu et al., 2013). These genes were upregulated in 112458 379101112 and snrk2.2/3/6 mutant plants under osmotic stress (Figures 5I and 5J). Consistent with these expression profiles, ABA and proline levels increased in the 112458 379101112 mutant after mannitol treatment, and the osmotic potential and seed germination of the 112458 379101112 mutant was reduced after treatment with mannitol but not with ABA (Figures 5K–5N).
Activation of SnRK2s by Osmotic Stress Is Inhibited by PYLs

In order to evaluate the activation of SnRK2s, we performed in-gel kinase assays (Fujii et al., 2011) with proteins extracted from ABA-insensitive mutants upon treatments with ABA and mannitol. The activation of SnRK2s by ABA was abolished in the 112458, 112458 379101112, and snrk2.2/3/6 mutants but not in the 3791112 mutant (Figure 6A). Interestingly, the activation of SnRK2s by osmotic stress (mannitol treatment) was dramatically enhanced in the 112458 379101112 mutant (Figure 6A, lane 14). The enhancement of SnRK2 activation could also be observed in the 112458 mutant under mannitol treatment (Figure 6A, lane 13). To confirm this result and to investigate SnRK2 activation in more pyl mutants, we generated antibodies for phosphorylated Ser175 in the activation loop of SnRK2.6 using the peptide SVLHSQPK-pS-TVGTP as antigen. Ser175 phosphorylation is essential for the activation of SnRK2s (Belin et al., 2006; Vlad et al., 2010). The anti-phosphorylation antibodies recognized ABA- and osmotic stress-activated SnRK2s, since the activation loop is conserved among these proteins (Figure 6B). The phosphorylation of this conserved Ser in the activation loop of SnRK2s was induced by ABA in Col-0 and the 3791112 mutant, but not in the 112458, 112458 379101112, and snrk2.2/3/6 mutants (Figure 6B, left panel). Osmotic stress-induced phosphorylation of Ser175 was dramatically enhanced in 112458 and 112458 379101112 mutants (Figure 6B, right panel). These results suggest that the PYLs negatively regulate osmotic-stress-induced activation of SnRK2s in vivo. To test whether recombinant PYLs inhibit osmotic-stress-activated SnRK2s, we performed immunoprecipitation-kinase assays using anti-GFP antibodies and osmotic-stress-treated plants expressing GFP-tagged SnRK2.6 (SnRK2.6-GFP). The immunoprecipitated SnRK2.6-GFP from osmotic stress-treated plants phosphorylated histones, and this phosphorylation was reduced by recombinant GST-fused PYL1 and PYL11 but not by recombinant UXS5, used as control (Figure 6C). Moreover, the inhibition of SnRK2.6-GFP activity by PYL1 and PYL11 was not relieved by addition of ABA (Figure 6C). These data show that PYLs can negatively regulate osmotic-stress-induced activation of SnRK2s. Interestingly, the kinase activity of recombinant SnRK2.6 purified from E. coli was not inhibited by PYL1 or PYL11 (Figure 6D). This observation suggests that the inhibition of SnRK2s by PYLs may depend on posttranslational modifications of SnRK2s induced by osmotic stress, or on an unidentified factor co-immunoprecipitated with osmotic stress-activated SnRK2s.

Interactions between PYLs and SnRK2s

To further investigate the relationship between PYLs and SnRK2s, we generated transgenic Arabidopsis plants expressing tagged PYL5 and PYL9 driven by their respective native promoters (ProPYLs:PYLs-HA-YFP). PYL5- and PYL9-associated proteins were isolated using tandem affinity purification (TAP) from extracts of 9-day-old seedlings with or without mannitol or ABA treatment and were identified by mass spectrometry (Table S3). PYL5-associated proteins included PYL4/6/9/10, SnRK2.6, and SnRK2.5 (Figure 7A). PYL9-associated proteins included PYL5/7/8/10, SnRK2.6, −2.5, −2.2, −2.3, −2.4, −2.9, and −2.10 (Figure 7B). Besides the PYLs and SnRK2s, PP2Cs were also co-purified with PYL9, and the association between PYL9 and PP2Cs was enhanced by mannitol and ABA treatment (Figure 7B). These data indicate that PYLs interact with SnRK2s in vivo, and their interaction is not altered upon ABA or mannitol treatment. To corroborate these interactions,
we performed split luciferase (LUC) complementation assays in *Nicotiana benthamiana* leaves. We fused PYLs to the N-terminal domain of firefly LUC (PYLs-nLUC) and SnRK2.6 to the C-terminal domain of LUC (SnRK2.6-cLUC), and co-transformed the two constructs using *Agrobacterium* infiltration. LUC activity was detected in leaves co-expressing SnRK2.6-cLUC with PYLs-nLUC or with the positive control ABI1-nLUC, but not with the negative control nLUC (Figures 7C and 7D). The results confirm that PYLs interact with SnRK2s. To further test the interaction between PYLs and SnRK2.6, we fused SnRK2.6 to the GAL4-activation domain (AD) and PYLs to the GAL4 DNA binding domain (BD) and performed yeast two-hybrid assays. We did not find obvious interactions between PYLs and SnRK2s (Figure 7E). These results suggest that PYLs indirectly interact with SnRK2.6, or that their interaction requires protein modifications of SnRK2.6 and/or PYLs in planta, or additional factors present in plant cells.

**DISCUSSION**

Osmotic stress or reduced water availability induce the accumulation of ABA, which is perceived by proteins from the PYL family, activating responses that are critical for plant adaptation to stress and other aspects of growth and development. The previously reported *pyl* 1124 (Park et al., 2009) and 112458 (Gonzalez-Guzman et al., 2012; Zhang et al., 2016) mutants have been instrumental to reach our current understanding of ABA receptor function in several aspects of plant growth and development, including stress responses. However, a deeper understanding of the physiological function of the PYL family of ABA receptors requires higher-order mutants defective in additional *PYL* genes. In this study, we generated *pyl* quattuordecuple mutants by mutating all 14 members of the *PYL* family. However, the *pyl* quattuordecuple mutants failed to produce seeds even under very high humidity conditions. We thus characterized in detail a 112458 379101112 duo-decuple mutant. In the 112458 379101112 duo-decuple mutant, *PYL13* remains as its WT allele but does not respond to ABA (Li et al., 2013; Zhao et al., 2013). Therefore, only one functional ABA receptor, *PYL6*, remains in the duodecuple mutant, where the *PYL6* gene is overexpressed in comparison with WT plants (Figure 5E). Approximately 7% of transcript level responses to 100 μM ABA treatment remained in the 112458 379101112 background, presumably due to the overexpression of the *PYL6* allele (Figures 5A and 5E). Although a *pyl6* single mutant does not show obvious differences compared with WT plants (Antoni et al., 2013; Fuchs et al., 2014), the *pyl6 pyl13* double mutant is less sensitive to ABA-induced inhibition of seed germination (Fuchs et al., 2014). Similar to the *snrk2.2/3/6* triple mutant (Fuji and Zhu, 2009), the 112458 379101112 mutant is defective in growth, flower development, and seed production (Figures 1, 2, and 4) and is extremely insensitive to ABA effects on seed germination, seedling growth, stomatal closure, osmotic regulation, leaf senescence, and global regulation of gene expression (Figures 3, 4, and 5). The growth defects of 112458 379101112 and *snrk2.2/3/6* mutants could be alleviated by keeping a near saturation humidity, suggesting that these two mutants suffered from excessive transpiration due to a severe defect in stomatal closure and the less developed roots in these mutants (Figures 2 and 3). The growth defects of these ABA-insensitive mutants could also be alleviated under short-day conditions (Figure 2). Interestingly, the growth of the 112458 379101112 mutant could be promoted by ABA supplementation (Figures 3H–3K), suggesting that *PYL6* is still
able to activate ABA signaling and promote plant growth. Compared with the 112458 sextuple mutant, the 112458 379101112 mutant is additionally impaired in growth and seed yield and vigor (Figure 2), and less sensitive to 200 μM ABA in germination, growth, stomatal closure, and water loss (Figure 3). However, the 3791112 quintuple mutant did not show obvious differences compared with WT plants in growth or ABA responses (Figures 2, 3, and 4). These results suggest that PYL3/7/9/10/11/12 are functional, but redundant with PYR1/PYL1/2/4/5/8 in the regulation of these processes. A previous study reported a reduced ABA-induction of leaf yellowing in the pyl9 single mutant under low light (Zhao et al., 2016), suggesting that PYL9 plays an important role in this response. Taken together, these results suggest that PYL3, PYL7, PYL11, and PYL12 play a minor role in these ABA responses, which is consistent with the extremely low expression of these genes (Gonzalez-Guzman et al., 2012). Overall, our results and results from previous studies (Gonzalez-Guzman et al., 2012; Park et al., 2009) reinforce the notion that PYLs are the major ABA receptors, if not the sole ABA receptors, in higher plants. Although we recovered only one allele of the pyl 112458 379101112 duodecuple mutant, and we were not able to do complementation experiments with the mutant due to its growth defects and extreme sensitivity to environmental perturbations, we believe that the above phenotypes observed in the 112458 379101112 mutant were caused by the pyl mutations, because similar phenotypes were also found in the snrk2.2/3/6 triple mutant, which is nearly completely insensitive to ABA (Fujii and Zhu, 2009). The results obtained using the pyl quattuordecuple and duodecuple mutants, together with those on snrk2.2/3/6 triple mutants, demonstrate that ABA signaling is critical for growth and development in plants.

Our RNA sequencing (RNA-seq) analysis revealed that ABA-dependent osmotic stress responses were nearly blocked in the 112458 379101112 mutant, whereas the majority of ABA-independent responses remained (Figure 5). This confirms the existence of ABA-independent osmotic stress responses (Fujii et al., 2011). SnRK2s are key components of both ABA-dependent and ABA-independent osmotic stress response pathways (Fujii et al., 2011; Fujii and Zhu, 2009). To our surprise, osmotic-stress-induced activation of SnRK2s was enhanced in 112458 379101112 and 112458 mutants, whereas ABA-induced activation of SnRK2s was blocked in these pyl mutants and in snrk2.2/3/6 mutants (Figure 6). These results reveal that PYLs play a role in antagonizing ABA-independent SnRK2 activity and gene expression and suggest a compensatory mechanism in the regulation of ABA-dependent and -independent osmotic stress responses. In such a case, PYLs could simultaneously promote ABA-dependent responses and repress ABA-independent responses to ensure signal specificity, and their mutation in 112458 379101112 and 112458 mutants would relieve this suppression. Genes related to proline biosynthesis (i.e., P5CS1), senescence (i.e., SAG13 and AtNAP), and osmotic responses (i.e., ABI5, RD20, and RD22) were induced by osmotic stress, but not ABA, in 112458 379101112 mutant plants (Figure 5F). This was also the case for other putative ABA-independent osmotic stress-responsive genes (i.e., NAC096) (Figure 5G). Osmotic stress may induce the expression of these genes through an ABA-independent pathway, involving the activation of SnRK2s or the accumulation of toxic hydrogen peroxide. These genes are associated with osmotic stress responses: NAC096 directly interacts with AFB2 and AFB4 and synergistically activates stress responsive genes (Xu et al., 2013), WRKY transcription factors, such as WRKY46
and ABO3, positively regulate genes involved in osmotic regulation and redox homeostasis (Ding et al., 2014; Ren et al., 2010), and PNP signaling may participate in regulating osmotic stress responses (Wang et al., 2011). Consistent with these results, ABA accumulation induced by osmotic stress is not affected in the snrk2.2/3/6 mutant, and proline accumulation is induced by osmotic stress, but not ABA, in the snrk2.2/3/6 mutant (Fujii et al., 2011). Although ABA-induced leaf senescence was blocked in 112458 379101112 and snrk2.2/3/6 mutants, age-dependent leaf senescence appeared accelerated in these mutants in soil after bolting (Figures 1B and 2A). Due to their constitutively open stomata, the extremely ABA-deficient or ABA-insensitive mutants (i.e., aba2-1, 112458 379101112, and snrk2.2/3/6) suffer from an inadequate water supply even in well-watered soil when the humidity is not near saturation. This appears to activate ABA-independent osmotic stress responses including leaf senescence in these mutants, but not in WT plants.

Osmotic stress, but not ABA, activates subclass I SnRK2s (SnRK2.1/2.4/2.5/2.9/2.10). These genes apparently evolved later than ABA-activated subclass III SnRK2s (SnRK2.2/2.3/2.6) (Lind et al., 2015). Although the activation of SnRK2s by osmotic stress was enhanced in 112458 and 112458 379101112 mutants (Figures 6A and 6B), we observed neither an induction of stomatal closure nor an induction of ABA-dependent osmotic-stress-responsive genes in 112458 379101112 under osmotic stress conditions (Figure 5E). These results indicate that the substrates of osmotic-stress-activated SnRK2s are quite different from those of the ABA-activated SnRK2s. Besides ABFs, other transcription factors such as ANAC096, WRKY6, WRKY57, and ABO3 also positively regulate osmotic stress responses (Huang et al., 2016; Jiang et al., 2012; Xu et al., 2013), but these other transcription factors may not be substrates of SnRK2s. Thus, the activation of SnRK2s is essential but may not be sufficient to initiate general osmotic stress responses.

We discovered that PYLs interact with SnRK2s in vivo and negatively regulate osmotic stress activation of SnRK2s (Figures 6A and 6B). We found that recombinant PYLs inhibit the activity of immunoprecipitated osmotic-stress-activated SnRK2.6-GFP, but do not inhibit the activity of recombinant SnRK2.6 from E. coli (Figures 6C and 6D). Among the ABA-deficient or insensitive mutants, pyl mutants, but not aba1-3, abi1-1, or snrk2.2/3/6, show an enhanced activation of SnRK2s by osmotic stress (Boudsocq et al., 2007; Fujii et al., 2011). This suggests that PYLs may inhibit osmotic stress activation of SnRK2s in a manner that is independent of the core ABA signaling. Further investigation indicated that the physical association with and inhibition of SnRK2s by PYLs may depend on protein modifications of SnRK2s in vivo (e.g., phosphorylation induced by osmotic stress), or unidentified components of osmotic stress signaling (Figures 6 and 7). Recent studies suggest that, besides the clade A PP2Cs, members of other protein phosphatase families also regulate the activity of SnRK2s (Hou et al., 2016; Waadt et al., 2015), supporting the notion that a complex network exists for the regulation of SnRK2 activities.
**STAR+METHODS**

**KEY RESOURCES TABLE**

<table>
<thead>
<tr>
<th>REAGENT or RESOURCE</th>
<th>SOURCE</th>
<th>IDENTIFIER</th>
</tr>
</thead>
<tbody>
<tr>
<td>Antibodies</td>
<td>Yun-de-ZymTM antibodies, LLC (South San Francisco, CA)</td>
<td>Antigen: SVLHSQPK-pS-TVGTP</td>
</tr>
<tr>
<td>Mouse monoclonal anti-GFP</td>
<td>Sigma-Aldrich</td>
<td>Cat#11814460001</td>
</tr>
<tr>
<td>Rabbit polyclonal anti-Actin</td>
<td>Abcam</td>
<td>Cat#ab197345</td>
</tr>
<tr>
<td>Goat Anti-Mouse IgG (H+L)-HRP Conjugate</td>
<td>Bio-rad</td>
<td>Cat#172-1011</td>
</tr>
<tr>
<td>Goat Anti-rabbit IgG (H+L)-HRP Conjugate</td>
<td>Bio-rad</td>
<td>Cat#172-1019</td>
</tr>
<tr>
<td>Abscisic Acid</td>
<td>Sigma-Aldrich</td>
<td>Cat#A1049</td>
</tr>
<tr>
<td>D-Mannitol</td>
<td>Sigma-Aldrich</td>
<td>Cat#M4125</td>
</tr>
<tr>
<td>Leupeptin</td>
<td>Sigma-Aldrich</td>
<td>Cat#11017101001</td>
</tr>
<tr>
<td>Aprotinin</td>
<td>Sigma-Aldrich</td>
<td>Cat#10236624001</td>
</tr>
<tr>
<td>Antipain</td>
<td>Sigma-Aldrich</td>
<td>Cat#10791</td>
</tr>
<tr>
<td>cOmplete, EDTA-free Protease Inhibitor Cocktail</td>
<td>Roche</td>
<td>Cat#04693132001</td>
</tr>
<tr>
<td>HA peptide</td>
<td>Abcam</td>
<td>Cat#ab13835</td>
</tr>
<tr>
<td>ATP, [γ-32P]-6000Ci/mmol</td>
<td>PerkinElmer</td>
<td>NEG502Z500UC</td>
</tr>
<tr>
<td>Firefly D-luciferin</td>
<td>NanoLight</td>
<td>CAS#2591-17-5</td>
</tr>
<tr>
<td>Critical Commercial Assays</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ECL Prime Western Blotting System</td>
<td>GE</td>
<td>Cat#RPN2232</td>
</tr>
<tr>
<td>Monoclonal anti-HA agarose with antibody produced in mouse</td>
<td>Sigma-Aldrich</td>
<td>Cat#A2095</td>
</tr>
<tr>
<td>GFP-Trap Agarose</td>
<td>Chromotek</td>
<td>Cat#gta-20</td>
</tr>
<tr>
<td>Micro Bio-Spin Columns with Bio-Spin® Gel P-6</td>
<td>Bio-rad</td>
<td>Cat#732-6221</td>
</tr>
<tr>
<td>Trizol reagent</td>
<td>ThermoFisher Scientific</td>
<td>Cat#15596026</td>
</tr>
<tr>
<td>TURBO DNA-free Kit</td>
<td>Ambion</td>
<td>Cat#AM1907</td>
</tr>
<tr>
<td>M-MLV Reverse Transcriptase</td>
<td>Promega</td>
<td>Cat#M1705</td>
</tr>
<tr>
<td>Ni-NTA Agarose</td>
<td>QIAGEN</td>
<td>Cat#30210</td>
</tr>
<tr>
<td>Glutathione Sepharose 4B</td>
<td>GE Healthcare</td>
<td>Cat#17-0756-01</td>
</tr>
<tr>
<td>Deposited Data</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Raw and processed RNA sequencing data</td>
<td>GEO (Gene Expression Omnibus) <a href="https://www.ncbi.nlm.nih.gov/geo/">GEO: GSE114379</a></td>
<td></td>
</tr>
</tbody>
</table>

**Experimental Models: Organisms/Strains**

<table>
<thead>
<tr>
<th>Organism</th>
<th>N/A</th>
<th>N/A</th>
</tr>
</thead>
<tbody>
<tr>
<td>E. coli BL21</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>Agrobacterium tumefaciens (strain GV3101)</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>Yeast strain AH109</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>Arabidopsis WT Col-0</td>
<td>N/A</td>
<td>N/A</td>
</tr>
</tbody>
</table>

*Cell Rep. Author manuscript; available in PMC 2018 August 09.*
<table>
<thead>
<tr>
<th>REAGENT or RESOURCE</th>
<th>SOURCE</th>
<th>IDENTIFIER</th>
</tr>
</thead>
<tbody>
<tr>
<td>Arabidopsis: pyl quattuordecuple</td>
<td>This study</td>
<td>N/A</td>
</tr>
<tr>
<td>Arabidopsis: pyl1124583791112</td>
<td>This study</td>
<td>N/A</td>
</tr>
<tr>
<td>Arabidopsis: pyl3791112 quintuple</td>
<td>This study</td>
<td>N/A</td>
</tr>
<tr>
<td>Arabidopsis: pyl124583791112</td>
<td>Gonzalez-Guzman et al., 2012</td>
<td>N/A</td>
</tr>
<tr>
<td>Arabidopsis: snRK2.2/2.3/2.6</td>
<td>Fujii and Zhu, 2009</td>
<td>N/A</td>
</tr>
<tr>
<td>Arabidopsis: SnRK2.6-GFP</td>
<td>Wang et al., 2015</td>
<td>N/A</td>
</tr>
<tr>
<td>Arabidopsis: ProPYL5:PYL5-HA-YFP</td>
<td>This study</td>
<td>N/A</td>
</tr>
<tr>
<td>Arabidopsis: ProPYL9:PYL9-HA-YFP</td>
<td>This study</td>
<td>N/A</td>
</tr>
</tbody>
</table>

**Oligonucleotides**

- Primers used in this study: This study; Table S1 N/A
- Recombinant DNA
  - Vector A-6 × sgR-PYL3,6,7,9,11,12-Cas9 | This study | N/A |
  - Vector B-2 × sgR-PYL10,13-Cas9 | This study | N/A |
  - Vector C-2 × sgR-PYL6,13-Cas9 | This study | N/A |
- ProPYL5:PYL5-HA-YFP | This study | N/A |
- ProPYL9:PYL9-HA-YFP | This study | N/A |
- pmal-c2X-SnRK2.6 | Fujii et al., 2009 | N/A |
- GST-ABF | Fujii et al., 2009 | Gly 73 to Gln 119 |
- pGEX-4T1-PYL1 | This study | N/A |
- pGEX-6P1-PYL11 | Hou et al., 2016 | N/A |
- pGEX-6P1-UXS5 | This study | N/A |
- pET28a-PYL1 | This study | N/A |
- pET28a-PYL11 | Hou et al., 2016 | N/A |
- PYR1-nLUC | This study | N/A |
- PYL1-nLUC | This study | N/A |
- PYL2-nLUC | This study | N/A |
- PYL3-nLUC | This study | N/A |
- PYL4-nLUC | This study | N/A |
- PYL5-nLUC | This study | N/A |
- PYL6-nLUC | This study | N/A |
- PYL7-nLUC | This study | N/A |
- PYL8-nLUC | Zhao et al., 2014 | N/A |
- PYL9-nLUC | This study | N/A |
- PYL10-nLUC | This study | N/A |
- PYL11-nLUC | Hou et al., 2016 | N/A |
- PYL12-nLUC | This study | N/A |
- PYL13-nLUC | This study | N/A |
- SnRK2.6-cLUC | Yan et al., 2017 | N/A |

*Cell Rep. Author manuscript; available in PMC 2018 August 09.*
CONTACT FOR REAGENT AND RESOURCE SHARING

Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Jian-Kang Zhu (jkzhu@purdue.edu).

EXPERIMENTAL MODEL AND SUBJECT DETAILS

All plants are in the Col-0 background. Plants were grown at 23°C under a 16/8 hr light/dark photoperiod with 60%–70% relative humidity unless indicated.

METHOD DETAILS

Generation of the 112458 379101112 Mutant—The constructs for CRISPR were designed according to the protocol described previously (Zhang et al., 2016). We constructed two CRISPR/Cas9 vectors to edit the remaining PYLs in the 112458 sextuple mutant background (Gonzalez-Guzman et al., 2012). Vector A targets PYL3/6/7/9/11/12 genes with six sgRNAs and a hygromycin resistance gene. Vector B targets PYL10/13 with two sgRNAs and a kanamycin resistance gene. The arrangement of these sgRNAs in these two CRISPR/Cas9 constructs is shown in Figure S1A. The sequences of the synthesized guide oligos are shown in Table S1.

Vector A and vector B were co-transformed into the 112458 pyl-T-DNA mutant using agrobacterium-mediated co-transformation. All transgenic plants were screened for hygromycin and kanamycin resistance with 30 mg/L hygromycin and 50 mg/L kanamycin.
plus 50 mg/L carbenicillin. The surviving T1 plants were transplanted to soil after growing under long-day conditions (16 h light/8 h dark) at 22°C for 2 weeks.

Thirty individual T1 transformants were analyzed by sequencing their PYL target regions, which were amplified by PCR using primer pairs listed in Table S1. Mutations on targeted genes were detected by aligning the sequencing chromatograms of these PCR products with the WT controls. We detected mutations in seven PYLs including PYL3/7/10/11/12/13 in line #20. Then we used 48 individuals from T2 segregation of line #20 and generated the homozygous pyr1pyl1/2/4/5/8/3/7/11/12 decuple mutant (line #20-43), in which PYL9 and PYL10 are heterozygous. We then used 12 individuals from the T3 segregation of line #20-43 and generated the homozygous pyr1pyl1/2/4/5/8/3/7/11/12 hendecuple mutant, in which PYL9 is heterozygous. Finally, we generated the 112458 379101112 duodecuple mutant in the T4 generation (Figure S1B).

**Generation of pyl Quattuordecuple Mutants**—We constructed vector C to edit PYL6 and PYL13 in the 112458 sextuple mutant background. Vector C targets PYL6/13 with two sgRNAs and a hygromycin resistance gene. The gRNA oligo “GCTGATGTGCCGGAGCACGTGG” was selected for PYL6 and the gRNA oligo “CGTGGTGGATGTGCCGGAAGG” was selected for PYL13 (Figure S1B). Vector C was transformed into the 112458 pyl T-DNA mutant using Agrobacterium-mediated transformation. All transgenic plants were screened for hygromycin resistance with 30 mg/L hygromycin plus 50 mg/L carbenicillin. The surviving T1 plants were transplanted to soil after growing under long-day conditions (16 h light/8 h dark) at 22°C for 2 weeks.

Twenty individual T1 transformants were analyzed by sequencing their PYL6 and PYL13 target regions, which were amplified by PCR using primer pairs listed in Table S1. We detected mutation in PYL13 in four lines, but no PYL6 mutation was detected in T1 lines. From 37 individual T2 segregations of these four lines, we detected mutation in PYL6. Then we generated the homozygous pyr1pyl1/2/4/5/8/6/13 octuple mutant.

We crossed pyr1pyl1/2/4/5/8/6/13 octuple mutant with the 112458 379101112 duodecuple mutant. We screened thousands of F2 seedlings and finally obtained the pyl quattuordecuple mutants.

**Plant Growth Conditions**—Seeds were sterilized for 10 min in 20% bleach and then rinsed four times in sterile-deionized water. Sterilized seeds were grown horizontally on 0.3% Phytagel (Sigma) or vertically on 0.6% Phytagel medium containing 1/2 MS nutrients (PhytoTech), 1% sucrose, pH5.7, and kept at 4–8°C for 3 days. For ABA related analysis, 1 g/L MES buffer anhydrous (Amresco, E183) was added before autoclaving to prevent acidification of ABA. ABA (Sigma, A1049) was added to the cooled, autoclaved medium prior to pouring plates. Seedlings were grown in a Percival CU36L5 incubator at 23°C under a 16-h light/8-h dark photoperiod. Seedlings were grown vertically for 4 d before transfer to medium with or without the indicated concentrations of ABA or mannitol. *Arabidopsis* plants were grown in soil (Fafard Super Fine Germination Mix) in a growth room at 22°C.
under a 60%–65% relative humidity and a 16-h light/8-h dark photoperiod. For ppy decuple, hendecuple, duodecuple mutants and snrk2.2/3/6 triple mutant, seedlings were partially covered with stackable plastic covers to maintain 80%–90% humidity (Figure S1E) and were watered every two days.

**Measurement of Water Loss and Stomatal Assay**—We used 25-d-old seedlings grown on 1/2 MS plates to avoid the serious growth retardation of extreme ABA-insensitive mutants. These seedlings were grown on 1/2 MS plates for 5-days. And then transferred to 1/2 MS plates (0.3% Phytagel) with or without 200 μM ABA and grown horizontally for 20 days. Seedlings were spaced 3 cm apart. Whole rosettes of 25-d-old plants were cut from the base and weighed at indicated time points. Stomatal apertures were measured in rosette leaves of 25-d-old plants using a ZEISS AX10 microscope.

**Osmotic Potential Measurements**—Osmotic potential was measured as previously reported (Zhao et al., 2016). For Figure 3L, osmotic potentials were analyzed 11 d after the 4-d-old seedlings were transferred to medium with indicated concentrations of ABA. For Figure 5H, osmotic potentials were analyzed after 24 h treatment with 30 μM ABA or 400 mM mannitol.

**Measurement of ABA and Proline Assay**—For quantification of ABA and proline, tissues were ground in liquid nitrogen. ABA concentration was measured with by UPLC-MS/MS method (Balcke et al., 2012). ABA level was analyzed 12 hour after the 9-d-old seedlings were transferred to medium with 200 mM mannitol. Proline was assayed using the ninhydrin-based colorimetric assay as reported (Bates et al., 1973). Proline level were analyzed 24 hour after the 9-d-old seedlings were transferred to filter papers with 400 mM mannitol or 30 μM ABA.

**RNA Sequencing and Real-Time PCR**—Seedlings were grown vertically for 9 days before treatment. These seedlings (0.05 ~0.1 g) were mock treated, or treated with 100 μM ABA or 300 mM mannitol for 24 hours on filter papers. Total RNA was extracted with Trizol reagent (ThermoFisher Scientific, 15596026). The library construction and sequencing were performed in the Genomics Core Facilities of the Shanghai Center for Plant Stress Biology, CAS (Shanghai, China) with Illumina HiSeq2500. The expression data of genes analyzed is listed in Table S2. Real-time PCR was performed as previously reported (Zhao et al., 2016).

Reads of RNA-seq data were mapped to *Arabidopsis* reference genome (TAIR10) using TopHat (Trapnell et al., 2012). Differentially expressed genes (DEG) were identified using cuffdiff in Cufflinks. We define a gene as DEG by requiring q-value < 0.05 and at least 2 fold change of expression level.

**In-gel Kinase Assay**—The in-gel kinase assay were performed as previously described (Wang et al., 2018). We used 20-μg total proteins for each sample and histone as substrate. Ten-day-old seedlings grown on 1/2 MS medium with 1% sucrose were transferred into liquid MS medium, or medium with 50 μM ABA, and 0.5 M mannitol for 30 min. After electrophoresis, the gel was dried under vacuum at 80°C for 1.5 hour on filter paper and
exposed to a phosphor imager for 3 days. Radioactivity was detected with a Personal Molecular Imager (Bio-Rad, Hercules, CA).

**Generation of Anti-phosphorylation Antibodies and Immunoblotting**—The generation of anti-phosphorylation rabbit antibody was performed in the Yun-de-ZymTM antibodies, LLC (South San Francisco, CA). The HPLC high purity modified peptide CSVLHSQPK-pS-TVGTP-amide was used as antigen to generate polyclonal anti-phosphorylation antibody for Ser175 in SnRK2.6. The antibody was purified using modified-peptide conjugated affinity matrix. The phosphorylation-site-specific antibody was purified using non-modified peptide CSVLHSQPKSTVGTP-amide, which absorbs the phosphorylation-site-nonspecific antibody.

For extraction of total protein from plants, we used an extraction buffer containing 100 mM HEPES, pH 7.8, 5 mM EDTA, 5 mM EGTA, 10 mM Na$_3$VO$_4$, 10 mM NaF, 50 mM Glycero-P, 10 mM DTT, 10 μg/ml Leupeptin, 10 μg/ml Antipain, 10 μg/ml Aprotinin, 1 mM PMSF, and 5% Glycerol. Samples were ground in extraction buffer and centrifuged at 4°C for 40 min at 13,500 rpm. The total protein in supernatants was determined with the Bradford method. We used 20-μg total proteins for each sample for in-gel assay and 40-μg total proteins for western blots.

Western blots were performed as described (Zhao et al., 2013). We incubated the membranes at 4°C overnight in PBS-T with 1% skim milk containing 1:1000 diluted anti-phosphorylation antibodies for Ser175 in SnRK2.6. After they were washed five times (5 min each) with PBST, membranes were incubated for 1 h at room temperature in PBS-T with 1% skim milk containing 1:2000 diluted goat anti-rabbit HRP-conjugated antibodies (Pierce, 32460), and then washed and detected using Lumi-Light Western Blotting Substrate (Roche) with 10–60 min exposure.

**Immunoprecipitation (IP) Kinase Assay**—The immunoprecipitation kinase assays of SnRK2.6-GFP kinase were performed as previously described with some modification (Boudsocq et al., 2004). Ten-day-old ostl/SnRK2.6-GFP seedlings were treated with or without 0.5 M mannitol for 30 min. Samples (1 g) were collected and grounded in liquid nitrogen. Total protein was extracted in 4 mL IP-buffer (10 mM Tris-HCl, pH 7.5, 150 mM NaCl, 0.5 mM EDTA, 1 mM NaF, 1 mM Na$_4$VO$_3$, 10 mM β-glycerophosphate, 0.5% NP-40, with protease inhibitor). After centrifuged at 20,000 g for 20 min, the supernatants were incubated with 20 μL GFP-trap for 4 hours at 4°C. After incubation, the beads were washed with IP-buffer for 2 times, washing buffer (10 mM Tris-HCl, pH 7.5, 300 mM NaCl, 0.5 mM EDTA, 1 mM NaF, 1 mM Na$_4$VO$_3$, 10 mM β-glycerophosphate, 0.5% NP-40, with protease inhibitor) for 2 times, and kinase buffer (25 mM Tris-HCl, pH 7.5, 10 mM MgCl$_2$, 0.25 mM DTT) for 1 time. Two μL aliquot of GFP-trap was incubated with 0.2 μg of GST-PYL1, GST-PYL11, GST-UXS5 or GST elution buffer (25 mM Tris-HCl, pH 7.5, 10 mM GSH) for 20 min at room temperature. After incubation, 2 μg histone and hot ATP were added to the reaction and incubated for additional 90 min at room temperature. The proteins were separated by SDS-PAGE. After electrophoresis, the gel was dried under vacuum at 80°C for 1.5 hour on filter paper and exposed to a phosphor imager for 10 h.
**In vitro Kinase Assay**—His tagged PYL proteins were desalted using Micro Bio-Spin Columns with Bio-Spin® Gel P-6 (Catalog #732-6221). MBP-SnRK2.6 (0.5 μg) was incubated with HIS tagged PYL proteins (0.5–1.5 μg) with or without 5 μM ABA in 20 μL reaction buffer (50 mM Tris-HCl pH 7.0, 20 mM MgCl2, 0.1 mM EGTA and 0.1% β-mercaptoethanol) at room temperature. After incubated for 30 min, 1 μM ATP, 4 μg GST-ABF2 and 5 μCi[γ-32P]ATP were added to the reaction. After incubated at room temperature for 30 min, proteins were separated by SDS-PAGE. After electrophoresis, the gel was dried under vacuum at 80°C for 1.5 hour on filter paper and exposed to a phosphor imager for 2 h. Radioactivity was detected with a Personal Molecular Imager (Bio-Rad, Hercules, CA).

**Tandem affinity purification**—To generate the ProPYLs:PYLs-HA-YFP constructs, the promoter fragments of PYLs was cloned into the SalI and BamHI sites of the modified pSAT vector with YFP and 3HA tags at the C terminus. The coding region of PYLs was cloned between the PYL promoter and the YFP sequence. The whole insertion cassette was digested with PI-Psp1 and inserted into pRCS2-htp binary plasmids. These plasmids were transformed into pyr1pyl1/2/3. Transgenic plants were verified by western blot assay.

The tandem affinity purification was performed as previously described (Zhao et al., 2016). The transgenic *Arabidopsis* plants expressing ProPYLs:PYLs-HA-YFP were used for tandem affinity purification (TAP). Ten-day-old seedlings (3–4 g fresh weight) were soaked for 30 min with or without 0.8 M mannitol. Generally, proteins were pre-purified with monoclonal anti-HA agarose with antibody produced in mouse (A2095, Sigma) in IP buffer (50 mM Tris-HCl, pH 7.5, 150 mM NaCl, 1 mM EDTA, 0.1% NP-40, 1 x protease cocktail, Roche), and eluted by HA peptide (Abcam, ab13835) with a concentration of 0.5 μg/μL in 200 μL IP buffer. PYLs-HA-YFP and their interacting proteins were then affinity purified with GFP-Trap Agarose (Chromotek, gta-20) and identified by mass spectrometric (MS) analyses. All steps were performed at 4°C.

The sequence of the peptides is listed in Table S3.

**Split luciferase (LUC) complementation assay**—The coding sequence of PYLs was amplified by PCR, cloned into pENTR vectors and transferred to pEarley-nLUC/cLUC vectors through LR reactions. Split-LUC complementation assay was performed by transient expression in tobacco leaves through agrobacterium-mediated infiltration as previously described (Hou et al., 2016). Two days after infiltration, luciferase activity was detected with a CCD camera by applying firefly D-luciferin (NanoLight).

**Yeast Two Hybrid Assay**—pBD-GAL4-PYLs were as reported (Park et al., 2009). *Saccharomyces cerevisiae* AH109 cells were transformed with pGADT7-SnRK2.6 and pBD-GAL4-PYLs plasmids. Colonies were identified on yeast SD medium lacking Leu and Trp and transferred to selective SD medium lacking Leu, Trp and His. To determine the interaction intensity, dilutions of saturated yeast cultures (10⁻¹, 10⁻² and 10⁻³) were spotted onto selection medium. Photographs were taken after 5 days incubation at 28°C.
QUANTIFICATION AND STATISTICAL ANALYSIS

Radioactivity quantification of bands in in-gel and immunoprecipitation kinase assays was performed using ImageJ. Student’s t test was used to determine the statistical significance between wild-type and mutants in assays related to germination, rosette width, root length, fresh weight, osmotic potential, and relative intensity (*p < 0.05).

DATA AND SOFTWARE AVAILABILITY

The accession number for the raw and processed RNA sequencing data reported in this paper is GEO: GSE114379.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

This work was supported by the Chinese Academy of Sciences and by NIH grant R01GM059138 (to J.-K.Z.). We are grateful to Prof. Pedro Rodriguez of Universidad Politecnica de Valenci, Spain, for kindly providing the pyr1pyl12458 mutant seeds.

References


Highlights

- High-order quattuordecuple Arabidopsis PYL ABA receptor mutants were generated
- PYL-mediated signaling is critical for plant growth and development
- PYL-mediated ABA signaling antagonizes ABA-independent SnRK2 activity
- PYLs interact with and inhibit osmotic stress-activated SnRK2 protein kinases
Figure 1. Generation of pyl Quattuordecuple Mutants
(A) Generation of pyl quattuordecuple mutants. To generate pyl duodecuple mutants, we co-transferred vector A and vector B into 112458 T-DNA sextuple mutant. To generate the pyl112458 613 mutant, we transferred vector C into 112458 T-DNA sextuple mutant. To generate pyl quattuordecuple mutants, we crossed the pyl duodecuple mutant with the pyl112458 613 mutant.

(B) Growth defects of the pyl quattuordecuple mutant. Images of representative seedlings of the pyl quattuordecuple mutant, pyl duodecuple mutant, pyl112458 mutant, snrk2.2/3/6 mutant, aba2-1 mutant, and WT. Shown are 50-day-old plants under long-day conditions grown with a plastic cover.

(C) Mutations in the pyl quattuordecuple mutant. Mutations in PYL3/6/7/9/10/11/12/13 genes in the pyl quattuordecuple mutant. ins, insertion; Del, deletion.

See also Figure S1 and Table S1.
Figure 2. Growth Defects of the 112458 379101112 Mutant

(A) Images of representative seedlings of ABA-insensitive mutants in soil. Image of 50-day-old plants under long-day conditions (left panel), 130-day-old plants under short-day conditions (middle panel), and 100-day-old plants under long-day conditions with a plastic cover (right panel).

(B) Plant height of 50-day-old plants under long-day conditions and 130-day-old plants under short-day conditions. Error bars indicate SEM (n ≥ 25 seedlings).

(C) Rosette width of 50-day-old plants under long-day or short-day conditions. Error bars indicate SEM (n ≥ 25 seedlings).

(D and E) Fresh weight (D) and dry weight (E) of shoots of 50-day-old plants under long-day conditions and 130-day-old plants under short-day conditions. Error bars indicate SEM (n ≥ 15 seedlings).

(F) Root length of 50-day-old plants under long-day conditions. Error bars indicate SEM (n ≥ 15 seedlings).

(G) Fresh weight of roots of 50-day-old plants under long-day conditions. Error bars indicate SEM (n ≥ 15 seedlings).

(H) Seed production of 100-day-old plants under long-day conditions. Error bars indicate SEM (n ≥ 16 seedlings).

(I) Seed germination of ABA-insensitive mutants on MS plates. Error bars indicate SEM (n ≥ 4 different batches).
Figure 3. Extreme ABA-Insensitive Phenotypes of the 112458 379101112 Mutant

(A–C) Water loss from detached rosette of 25-day-old ABA-insensitive mutants grown on plates. Representative images show rosettes 1 hr after detached (A). Cumulative transpirational water loss from plants grown without ABA (B) or with 200 μM ABA (C). Error bars indicate SEM (n ≥ 3).

(D and E) Constitutively open stomata of the 112458 379101112 and snrk2.2/3/6 mutants. Representative images (D) and aperture (E) of stomata in each genotype grown with or without 200 μM ABA. Error bars indicate SEM (n ≥ 90).

(F and G) Germination and growth of ABA-insensitive mutants. Representative images (F) and germination rate (G) of each genotype with or without ABA. Error bars indicate SEM (n ≥ 7). *p < 0.05, Student’s t test.

(H–L) Growth of ABA-insensitive mutants were analyzed 11 days after the seedling were transferred to medium with or without ABA. Representative images (H), rosette width (I), root length (J), fresh weight (K), and osmotic potential (L) were documented. Error bars indicate SEM (n ≥ 15 seedlings) in (I–K), and SEM (n ≥ 3) in (L). *p < 0.05, Student’s t test.
Figure 4. Senescence and Abscission Phenotypes of the 112458 379101112 Mutant
(A) ABA-induced leaf senescence in 40-day-old plants under long-day conditions.
(B) Inflorescence of 130-day-old plants under short-day conditions.
(C) Anther dehiscence in 50-day-old plants under long-day conditions.
(D) Siliques of 50-day-old plants under long-day conditions.
Figure 5. Gene Expression Responses to ABA and to Osmotic Stress in the \textit{112458 379101112} Mutant

(A–D) Gene expression responses to ABA (A and B) and to osmotic stress (C and D) in the \textit{112458 379101112} mutant. The venn diagram (A and C) and heatmap (B and D) represent genes with changed expression (2-fold or greater, false discovery rate, \( p < 0.05 \)) in seedlings with ABA or osmotic stress treatment compared with that of control conditions.

(E–H) Relative expression of selected genes responsive to osmotic stress in an ABA-dependent manner (E and F) or ABA-independent manner (G and H). Expression of genes were assayed by quantitative RT-PCR. Error bars indicate SEM (\( n \geq 3 \)).

(I and J) Relative expression of selected genes mainly responsive to osmotic stress but not ABA. Expression of genes were assayed by quantitative RT-PCR in \textit{112458379101112} (I) and \textit{snrk2.2/3/6} seedlings (J). Error bars indicate SEM (\( n \geq 3 \)).

(K) ABA level was documented after 12 hr treatment with mannitol. Error bars indicate SD (\( n = 3 \)).

(L) Germination was scored for radicle emergence after 24 hr with treatments of ABA and mannitol. Error bars indicate SEM (\( n \geq 4 \)).

(M) Osmotic potential was documented after 48 hr treatment with ABA or mannitol. Error bars indicate SD (\( n \geq 4 \)). \( \ast p < 0.05 \), Student’s t test.
(N) Proline accumulation was documented after 24 hr with treatments of ABA and mannitol. Error bars indicate SD (n = 3). See also Figures S2 and S3 and Table S2.
Figure 6. The Activation of SnRK2s by Osmotic Stresses Was Enhanced in pyl Mutants

(A) In-gel kinase assay with proteins extracted from ABA-insensitive mutants upon treatments with ABA and mannitol. Histones were used as the phosphorylation substrate. The expected position of SnRK2s was indicated by arrowheads. Radioactivity of the band was normalized with respect to the radioactivity of the band in the mannitol treated Col-0. Error bars indicate SEM (n ≥ 4). *p < 0.05, Student’s t test.

(B) ABA and mannitol induced auto-phosphorylation of SnRK2s in 8-day-old ABA-insensitive mutants. Anti-phospho-S175-SnRK2s antibody was used to detect auto-phosphorylation of SnRK2s. Actin was used as a loading control.

(C) Phosphorylation activity of GFP-tagged SnRK2.6 extracted from transgenic plants with mannitol treatment. SnRK2.6-GFP pre-incubated with recombinant GST-fused PYL1, PYL11, and UXS5 was incubated with histones in the presence of radioactive ATP. Phosphorylation activity of SnRK2.6-GFP was detected by autoradiography (upper panel). Radioactivity of the band was normalized with respect to the radioactivity of the band in SnRK2.6 without PYLs and UXS5 (lane 3). The input proteins of histone substrate and SnRK2.6-GFP were detected by Coomassie staining (middle panel) and western blotting with anti-GFP antibodies (lower panel). Error bars indicate SEM (n ≥ 3). *p < 0.05, Student’s t test.

(D) Phosphorylation activity of recombinant SnRK2.6. SnRK2.6 pre-incubated with recombinant PYL1 and PYL11 was incubated with ABF in the presence of radioactive ATP. Phosphorylation activity of SnRK2.6 was detected by autoradiography (left panel). The input proteins of ABF2 and PYLs were detected by Coomassie staining (right panel).
Figure 7. PYLs Interact with SnRK2s In Vivo

(A and B) ABA signaling core components co-immunoprecipitated with PYL5-HA-YFP (A) and PYL9-HA-YFP (B) from PropYLs:PYLs-HA-YFP transgenic plants with and without mannitol or ABA treatment.

(C and D) PYLs interact with SnRK2.6 in split LUC complementation assays in Nicotiana benthamiana leaves. The SnRK2.6-cLUC and ABI1-nLUC combination was used as a positive control, and combinations of SnRK2.6-cLUC/nLUC and PYR1-nLUC/cLUC were used as negative controls (C). LUC signal intensity was normalized with respect to the signal intensity of the combination of cLUC/nLUC (D). Error bars indicate SD (n = 3).

(E) PYLs do not interact with SnRK2.6 in yeast two-hybrid assays. Interactions was determined by yeast growth in media lacking His with dilutions (10^{-1}, 10^{-2}, and 10^{-3}) of saturated cultures. Combination of AD-SnRK2.6 and BD was used as negative control. See also Table S3.