The Arabidopsis MYB96 Transcription Factor Is a Positive Regulator of ABSCISIC ACID-INSSENSITIVE4 in the Control of Seed Germination

Kyounghee Lee2, Hong Gil Lee2, Seongmun Yoon, Hyun Uk Kim, and Pil Joon Seo*

Department of Bioactive Material Sciences and Research Center of Bioactive Materials (K.L., H.G.L., P.J.S.) and Department of Chemistry and Research Institute of Physics and Chemistry (P.J.S.), Chonbuk National University, Jeonju 561–756, Republic of Korea; and Department of Agricultural Biotechnology, National Academy of Agricultural Science, Rural Development Administration, Jeonju 560–500, Republic of Korea (S.Y., H.U.K.)

ORCID ID: 0000-0001-7263-8036 (S.Y.).

Seed germination is a key developmental transition that initiates the plant life cycle. The timing of germination is determined by the coordinated action of two phytohormones, gibberellin and abscisic acid (ABA). In particular, ABA plays a key role in integrating environmental information and inhibiting the germination process. The utilization of embryonic lipid reserves contributes to seed germination by acting as an energy source, and ABA suppresses lipid degradation to modulate the germination process. Here, we report that the ABA-responsive R2R3-type MYB transcription factor MYB96, which is highly expressed in embryo, regulates seed germination by controlling the expression of ABSCISIC ACID-INSSENSITIVE4 (ABI4) in Arabidopsis (Arabidopsis thaliana). In the presence of ABA, germination was accelerated in MYB96-deficient myb96-1 seeds, whereas the process was significantly delayed in MYB96-overexpressing activation-tagging myb96-ox seeds. Consistently, myb96-1 seeds degraded a larger extent of lipid reserves even in the presence of ABA, while reduced lipid mobilization was observed in myb96-ox seeds. MYB96 directly regulates ABI4, which acts as a repressor of lipid breakdown, to define its spatial and temporal expression. Genetic analysis further demonstrated that ABI4 is epistatic to MYB96 in the control of seed germination. Taken together, the MYB96-ABI4 module regulates lipid mobilization specifically in the embryo to ensure proper seed germination under suboptimal conditions.

1 This work was supported by the Basic Science Research (grant no. NRF–2013R1A1A1004831) and Global Research Network (grant no. NRF–2014S1A2A2028392) programs of the National Research Foundation of Korea and by the Cooperative Research Program for Agriculture Science & Technology Development (SSAC, project no. PJ01108101) of the Rural Development Administration (to H.U.K.) as well as by the BK21 PLUS program in the Department of Bioactive Material Sciences (to K.L. and H.G.L.).

2 These authors contributed equally to the article.

* Address correspondence to pjseo1@jbnu.ac.kr.

The author responsible for distribution of materials integral to the findings presented in this article in accordance with the policy described in the Instructions for Authors (www.plantphysiol.org) is: Pil Joon Seo (pjseo1@jbnu.ac.kr).

P.J.S. conceived and designed the experiments; P.J.S. and H.U.K. wrote the article; K.L., H.G.L., S.Y., and H.U.K. conducted the experiments and contributed to the study design.

www.plantphysiol.org/cgi/doi/10.1104/pp.15.00162

Seeds are products of plant sexual reproduction and facilitate the spread of offspring. Since plants are sessile organisms with a limited ability to seek favorable growth conditions, seed dispersal is an evolutionarily adaptive trait to disseminate their offspring to optimal locations (Bewley, 1997; Nonogaki, 2014). Thus, seeds enable plants to endure environmental disadvantages and confine growth until they encounter favorable environmental conditions (Bewley, 1997).

Seed embryogenesis is initiated by double fertilization (Gehring et al., 2004; Berger et al., 2008). While the zygote divides asymmetrically to form the diploid embryo, the triploid endosperm constantly proliferates inside the maternal ovule (Natesh and Rau, 1984; West and Harada, 1993). At the end of the embryonic growth phase, cell cycle activities in the embryo are arrested (Raz et al., 2001), and storage molecules, such as proteins, carbohydrates, and lipids, accumulate particularly in the cotyledons (Goldberg et al., 1989; Raz et al., 2001). This phase is referred to as seed maturation. Mature seeds become dehydrated and enter a quiescent state that is tolerant to desiccation (Crouch, 1987; Harada et al., 1988; Kermode, 1990; McCarty and Carson, 1991), establishing primary dormancy.

Seed dormancy can be broken when seeds experience stratification and/or after-ripening (Vleeshouwers et al., 1995; Bewley, 1997; Nonogaki, 2014). Germination is a key developmental transition to determine when to initiate the plant life cycle. Since it is an irreversible transition, seeds have to precisely monitor external environmental factors, such as light, temperature, water and nutrient availability, and high salinity (Huang et al., 2003; Qu et al., 2008; Joosen et al., 2013; Lim et al., 2013).
These environmental signals are integrated into internal developmental programs in seeds, which are operated primarily by antagonistic actions of two phytohormones: abscisic acid (ABA) and GA (Holdsworth et al., 1999; Finch-Savage and Leubner-Metzger, 2006; Seo et al., 2006). GA promotes germination, whereas ABA suppresses completion of the developmental transition (Garcia-Rubio et al., 1997; Debeaujon and Koornneef, 2000; Finkelstein et al., 2002; Peng and Harberd, 2002; Ogawa et al., 2003; Lau and Deng, 2010).

Transcriptional regulation is a fundamental regulation scheme for the seed germination process (Thomas, 1993; Nakabayashi et al., 2005). The GA function in promoting seed germination is accomplished partly through the action of central GA signaling repressors, DELLA-domain proteins, including GIBBERELLIN INSENSITIVE (GAI), REPRESSOR OF GIBBERELLIN1-3 (RGA), RGA-LIKE1 (RGL1), RGL2, and RGL3, all of which act as transcriptional regulators (Hussain and Peng, 2003; Tyler et al., 2004; Cao et al., 2006; Park et al., 2013). They interact with transcription factors to allow DELLAs to regulate gene expression by targeting specific gene promoters (de Lucas et al., 2008; Peng et al., 2008; Arnaud et al., 2010; Gallego-Bartolomé et al., 2010; Hong et al., 2012). Indeed, DELLAs bind to promoters of GIBBERELLIN INSENSITIVE DWARF1, WRKY27, and SCARECROW-LIKE3 to control seed germination (Zentella et al., 2007; Gallego-Bartolomé et al., 2011; Zhang et al., 2011; Stamml et al., 2012). The DELLA proteins are rapidly degraded in response to GA and are thus considered as repressors of seed germination in the absence of GA (Dill et al., 2001; Tyler et al., 2004).

ABA regulation of seed germination also requires ABA-responsive transcription factors. ABSCISIC ACID INSENSITIVE3 (ABI3), ABI4, and ABI5, which encode transcription factors with the B3 domain, APETAL2 domain, and basic Leu zipper domain, respectively, are expressed highly in seeds and are involved in regulating sensitivity to ABA (Giraudat et al., 1992; Finkelstein et al., 1998; Finkelstein and Lynch, 2000). Indeed, genetic mutants at these loci exhibit reduced ABA sensitivity as well as accelerated seed germination in the presence of exogenous ABA (Finkelstein and Somerville, 1990). They act in concert with each other and form combinatorial networks to determine the proper time to germinate (Söderman et al., 2000; Nakamura et al., 2001).

In addition to their overlapping roles in ABA-dependent seed germination, ABI3, ABI4, and ABI5 have their own unique functions. ABI4 is particularly interesting in that it plays a unique role in embryonic lipid catabolism during the germination process (Penfield et al., 2006). Seeds utilize lipid reserves to fuel post-germinative seedling growth (Penfield et al., 2005; Quettier and Eastmond, 2009), but the lipid catabolic process is inhibited in the presence of ABA in order to delay seed germination, thereby minimizing environmental damage to early seedlings. Notably, ABA specifically represses embryonic lipid breakdown (Penfield et al., 2006). The differential responses of embryo and endosperm to ABA are accomplished by the confined expression of ABI4 in the embryo (Penfield et al., 2006). However, the mechanisms by which ABI4 is expressed specifically in the embryo and by which specific regulator(s) participate in defining its spatial and temporal expression remain unknown.

We previously showed that the MYB96 transcription factor mediates a variety of plant responses to ABA, including drought resistance, stomatal conductance, lateral root development, anthocyanin accumulation, and cuticular wax biosynthesis (Seo et al., 2009, 2011; Seo and Park, 2010, 2011). The expression of MYB96 is considerably induced by drought stress and ABA (Seo et al., 2009), and it activates the expression of many ABA-responsive genes through direct binding to gene promoters to optimize plant growth and fitness under environmentally unfavorable conditions (Seo et al., 2009, 2011; Seo and Park, 2010).

Here, we report that MYB96 also plays a key role in the ABA control of seed germination in Arabidopsis (Arabidopsis thaliana). The MYB96 gene was significantly expressed in the embryo and conferred embryonic ABA sensitivity in seed germination as well as triacylglycerol (TAG) breakdown. In the presence of ABA, MYB96-overexpressing myb96-ox seeds exhibited delayed germination with reduced lipid breakdown, whereas myb96-1 seeds showed accelerated seed germination and lipid breakdown. The MYB96 regulation of seed germination was largely dependent on ABI4, a key repressor of embryonic lipid mobilization during the germination process. Together, our findings provide evidence that MYB96 is an unequivocal transcriptional regulator of ABI4 and defines the spatial and temporal specificity of its expression to fine-tune seed germination under unfavorable environmental conditions.

RESULTS

MYB96 Is Expressed in Embryos

MYB96 mediates ABA signal transduction in a variety of physiological processes, such as drought response, lateral root development, and cuticular wax accumulation (Seo et al., 2009, 2011). Since seed germination is also a key developmental transition governed by ABA (Bewley, 1997; Nakashima and Yamaguchi-Shinozaki, 2013), it was highly plausible that MYB96 may also regulate seed germination in an ABA-dependent manner.

To explore the role of MYB96 in seed germination, we first determined its expression patterns in seeds. Quantitative reverse transcription (qRT)-PCR analysis revealed that MYB96 transcripts accumulated at high levels in dry seeds (Fig. 1A), and its transcript accumulation was drastically reduced after cold stratification and imbibition. The transcript levels of MYB96 were reduced by 98% after stratification compared with those in dry seeds (Fig. 1A) and recovered at seedling stages (Supplemental Fig. S1), implying an inhibitory role of MYB96 in seed germination.

Spatial expression patterns of MYB96 were further examined using pMYB96:GUS transgenic seeds, in
MYB96 Regulates ABA-Dependent Seed Germination

Our observation that seed-expressed MYB96 was regulated by ABA suggested that it might have a physiological role in ABA-dependent seed germination. Therefore, we measured the germination rate of seeds expressing MYB96 in the absence of ABA (Fig. 2A). However, in the presence of ABA, the germination rate was substantially reduced in myb96-ox seeds but elevated in myb96-1 seeds compared with wild-type seeds (Fig. 2A). The differential ABA responses of myb96-ox and myb96-1 seeds were more evident at higher concentrations of ABA (Fig. 2A).

For ABA dose-response assays, seeds were germinated on MS medium plates supplemented with different concentrations of ABA, and germination percentages were scored 2 d after cold stratification. These assays clearly revealed that the myb96-ox seeds exhibited increased sensitivity to exogenous ABA and the myb96-1 seeds were hyposensitive to ABA relative to wild-type seeds (Fig. 2B). Cotyledon opening is also sensitive to exogenous ABA treatment in the association with seed germination. The cotyledon opening of myb96-ox and myb96-1 seeds was indistinguishable from that of wild-type seeds in the absence of ABA (Supplemental Fig. S5). However, in agreement with the seed germination rates, the cotyledon opening of myb96-ox was hypersensitive to ABA, whereas the myb96-1 mutants were hyposensitive (Supplemental Figs. S5 and S6). These observations indicate that MYB96 determines ABA sensitivity and regulates ABA-dependent seed germination.
ABI4 Is Up-Regulated in myb96-ox

To establish the molecular networks underlying the MYB96 regulation of seed germination, we monitored the expression patterns of genes associated with ABA-dependent seed germination, such as $ABI1$, $ABI2$, $ABI3$, $ABI4$, $ABI5$, ACYL-COENZYME A-BINDING PROTEIN1 (ACBP1), ARABIDOPSIS HISTIDINE KINASE1 (AHK1), BEL1-LIKE HOMEODOMAIN1 (BLH1), FLOWERING LOCUS Y (FY), RING-H2 FINGER A2A (RHA2a), SNF1-RELATED PROTEIN KINASE2.2 (SnRK2.2), and SnRK2.3 (Finkelstein and Somerville, 1990; Söderman et al., 2000; Carles et al., 2002; Fujii et al., 2007; Tran et al., 2007; Moes et al., 2008; Li et al., 2011; Jiang et al., 2012; Du et al., 2013; Kim et al., 2013), in the wild type, myb96-ox, and myb96-1, in the absence of ABA. In seeds, many genes were differentially expressed in myb96-ox and myb96-1, but MYB96 regulation of $ABI4$ was most likely relevant (Fig. 3A). The expression of $ABI4$ was reduced in myb96-1 seeds, whereas myb96-ox increased $ABI4$ expression. To further support this observation, we also analyzed the expression of these genes in wild-type, myb96-ox, and myb96-1 seedlings. Most of the genes examined were transcriptionally unchanged in the mutants, but the expression of $ABI4$ was elevated approximately 12-fold in the myb96-ox mutant (Fig. 3B). The $ABI3$ and $ABI5$ genes were also slightly up-regulated in myb96-ox (Fig. 3B). However, their expression was not down-regulated in myb96-1, possibly due to extremely low expression levels of the genes in wild-type seedlings under normal growth conditions.

Transcript levels of the same set of genes were analyzed in myb96-1 seeds in the presence of ABA. Most of the genes, except for AHK1, FY, and RHA2a, were induced by ABA. Notably, the ABA induction of $ABI4$ and $BLH1$ genes was significantly reduced in the myb96-1 seeds compared with wild-type seeds (Fig. 4), while the ABA induction of the others was not influenced. The expression of two genes was also analyzed in germinating myb96-ox seeds in the presence of ABA. Accordingly, their ABA induction was slightly hypersensitive in myb96-ox seeds in the presence of ABA. The expression of $BLH1$ seems to be dependent upon MYB96, based on the close correlation between $ABI4$ expression and MYB96 activity (Figs. 3 and 4), we hypothesized that MYB96 is intimately required for the proper expression of $ABI4$ in the control of percentages of the indicated genotypes grown on different concentrations of ABA were quantified after the end of stratification. Radicle emergence was used as a morphological marker for germination. At least 40 seeds per genotype were measured in each replicate. Biological triplicates were averaged. Error bars indicate SE. Statistically significant differences between wild-type Columbia-0 (Col-0) and mutants are indicated by asterisks (Student’s t test, *P < 0.05). B, ABA dose-response assay. Wild-type, myb96-ox, and myb96-1 seeds were germinated on an increasing concentration of ABA. Germination percentages were scored 2 d after cold stratification. Biological triplicates were averaged. Error bars indicate SE. Statistically significant differences between the wild type and mutants are indicated by asterisks (Student’s t test, *P < 0.05).
ABA-mediated seed germination. Consistent with this, the expression patterns of *ABI4* in seeds were similar to those of *MYB96*. The *ABI4* gene was highly expressed in dry seeds, particularly embryo (Söderman et al., 2000; Penfield et al., 2006; Bossi et al., 2009), and its expression was reduced after stratification and imbibition, like the transcript accumulation patterns of *MYB96* (Supplemental Fig. S8). Their spatial expression patterns were also similar (Supplemental Fig. S9), further supporting the positive regulation of *ABI4* by MYB96.

**MYB96 Binds Directly to the *ABI4* Promoter**

MYB96 is an R2R3-type MYB transcription factor (Seo et al., 2009). Plant R2R3 MYB-DNA-binding domain-containing proteins are known to bind directly to consensus DNA elements that are enriched in A and C residues (Seo et al., 2011; Prouse and Campbell, 2013). Therefore, we asked whether MYB96 binds directly to the consensus motifs on the *ABI4* promoter. Sequence analysis revealed that the *ABI4* promoter contains five conserved sequence motifs that are analogous to the R2R3-type MYB-binding consensus sequences (Fig. 5A). The presence of MYB-binding cis-elements led us to examine whether MYB96 is targeted to the *ABI4* promoter.

To perform chromatin immunoprecipitation (ChIP) assays, we generated pMYB96:MYB96-MYC transgenic plants. Total protein extracts from control pBA002 and pMYB96:MYB96-MYC transgenic seeds were immunoprecipitated with anti-MYC-antibody. DNA bound to epitope-tagged MYB96 proteins was analyzed by quantitative PCR assays. The ChIP analysis showed that the...
A region of the ABI4 promoter was enriched by MYB96 (Fig. 5B). In contrast, two other genomic fragments containing MYB-binding cis-elements, B and C, were not enriched (Fig. 5B), supporting the specific interaction of MYB96 with the A region of the ABI4 promoter. In addition, control ChIP with resin alone did not enrich the A fragment (Fig. 5B). To confirm the direct binding of MYB96 to the ABI4 promoter, we also generated transgenic plants expressing the R2R3-MYB DNA-binding domain (BD) of MYB96 fused with the MYC-coding sequences (35S:96BD-MYC). ChIP analysis revealed that the MYB DNA-binding domain was sufficient to bind to the ABI4 promoter (Supplemental Fig. S10).

To confirm the MYB96 binding to core sequences of the ABI4 promoter, we performed transient expression analysis using Arabidopsis protoplasts. Two core elements on the ABI4 promoter, A-1 (−264; CAAGTAACCTATGA) and A-2 (−335; GCTATAGTTACCCA), were fused to the 35S minimal promoter. A recombinant reporter plasmid and an effector plasmid, p35S:MYB96, were cotransformed into Arabidopsis protoplasts. Cotransformation with the reporter A-1 increased the GUS activity by 2- to 3-fold, but cotransformation with A-2 did not affect reporter gene expression (Fig. 5C). These results indicate that MYB96 specifically targets proximal sequences upstream of the ABI4 gene to activate its expression.

MYB96 Contributes to Inhibiting TAG Degradation during Germination

Seed germination is elaborately regulated by discrete actions of the embryo and endosperm (Lafon-Placette and Köhler, 2014). An intriguing example is ABA-controlled lipid breakdown and mobilization in the embryo under suboptimal growth conditions (Penfield et al., 2006). Seed TAG degradation is triggered to fuel embryonic growth during germination but is antagonized by ABA specifically in the embryo (Penfield et al., 2006). It is noteworthy that the ABI4 transcription factor is a well-known regulator of this process, which confers differential sensitivity of lipid catabolism to ABA in the embryo and endosperm (Penfield et al., 2006).

Since ABI4 is a major regulatory target of the MYB96 transcription factor, we hypothesized that MYB96 may also be responsible for the ABA regulation of lipid breakdown during seed germination, similar to the action of ABI4 (Penfield et al., 2006; Wind et al., 2013). To examine this hypothesis, we measured the levels of total fatty acid and eicosenoic acid (20:1) in wild-type, myb96-ox, and myb96-1 seeds for 3 d after cold imbibition in the absence or presence of exogenous ABA. In the absence of ABA, the levels of total fatty acid and eicosenoic acid were largely indistinguishable in myb96-ox and myb96-1 compared with wild-type seeds.
However, in the presence of ABA, the levels of total fatty acid and eicosenoic acid were noticeably altered in myb96-ox and myb96-1. Total fatty acid levels were reduced by approximately 30% to 35% 3 d after cold imbibition in wild-type seeds. However, TAG breakdown was largely repressed in the myb96-ox seeds, whereas 43% of total TAG was catabolized in the myb96-1 seeds (Fig. 6A). The levels of eicosenoic acid displayed similar degradation kinetics to total fatty acid (Fig. 6B). These observations demonstrate that MYB96 plays a role in regulating lipid breakdown during seed germination.

**ABI4 Is Epistatic to MYB96**

Our results indicated that the MYB96-ABI4 transcriptional cascade is crucial for the ABA regulation of seed germination, probably through lipid mobilization. To confirm the genetic relationship between MYB96 and ABI4, we genetically crossed myb96-ox to the abi4-1 mutant.

We investigated the ABA sensitivity of myb96-ox/abi4-1 seeds during germination. Delayed germination was observed in myb96-ox seeds, whereas the abi4-1 mutation led to accelerated seed germination, in the presence of ABA (Fig. 7A). The germination rate of myb96-ox/abi4-1 seeds was comparable to that of abi4-1 (Fig. 7A), indicating that MYB96 is an upstream regulator of ABI4 and that both genes act in the same pathway.

In agreement with the seed germination rate, the eicosenoic acid catabolism of myb96-ox/abi4-1 was also indistinguishable from that of abi4-1 (Fig. 7B). A significant amount of the stored TAG was degraded in both genotypes, even in the presence of ABA. Therefore, we conclude that ABI4 is genetically epistatic to MYB96 with respect to the control of ABA-dependent seed germination as well as TAG catabolism.

Taken together, our observations demonstrate that the MYB96 transcription factor serves as an ABA signaling mediator in modulating seed germination through ABI4-dependent embryonic lipid breakdown (Fig. 7C). MYB96 directly regulates ABI4, a key regulator of embryonic lipid mobilization during seed germination, by binding to its gene promoter. Genetic analyses further bolster this genetic hierarchy in the control of seed germination.

**DISCUSSION**

**MYB96 Regulation of ABI4**

ABA is perceived by receptor protein complexes that are composed of PYRABACTIN RESISTANCE
Seeds were germinated on MS plates supplemented with 1 μM ABA. Biological triplicates were averaged. Error bars indicate SE. At least 30 seeds per genotype were measured in each replicate.

Lipid breakdown in wild-type Columbia-0 (Col-0), myb96-ox, and myb96-1 seeds during seed germination in the presence of ABA. Seeds were germinated on MS plates supplemented with 1 μM ABA and incubated at 23°C under long-day conditions for 3 d. Lipid breakdown was determined by measuring the abundance of total fatty acid (FA; A) and eicosanoic acid (20:1; B). Fatty acid content was expressed as the percentage of the amount present in dry seeds of the indicated genotypes. At least 30 seeds per genotype were measured in each replicate. Biological triplicates were averaged. Error bars indicate se.

**Figure 6.** Lipid breakdown in wild-type Columbia-0 (Col-0), myb96-ox, and myb96-1 seeds during seed germination in the presence of ABA. Seeds were germinated on MS plates supplemented with 1 μM ABA and incubated at 23°C under long-day conditions for 3 d. Lipid breakdown was determined by measuring the abundance of total fatty acid (FA; A) and eicosanoic acid (20:1; B). Fatty acid content was expressed as the percentage of the amount present in dry seeds of the indicated genotypes. At least 30 seeds per genotype were measured in each replicate. Biological triplicates were averaged. Error bars indicate se.

(PYR)/PYR1-LIKE (PYL)/REGULATORY COMPONENT OF ABSCISIC ACID RECEPTOR (RCAR), type 2C protein phosphatases (PP2Cs), and SnRK2s (Raghavendra et al., 2010; Weiner et al., 2010). In the presence of ABA, PYR/PYL/RCAR proteins lead to the suppression of PP2C activities, derepressing SnRK2 protein kinases to activate ABA-responsive binding factors/ABA-responsive element-binding proteins (Fujii et al., 2009; Nishimura et al., 2010; Gonzalez-Guzman et al., 2012). Subsequent ABA responses are mediated by a large number of transcription factors, indicating that transcriptional cascades are a fundamental framework in ABA signal transduction (Giraudat et al., 1992; Busk and Pages, 1998; Finkelstein et al., 1998; Finkelstein and Lynch, 2000; Abe et al., 2003; Pandey et al., 2005; Seo et al., 2009).

In particular, the ABI3, ABI4, and ABI5 transcription factors all play a common role in the ABA regulation of seed germination by constituting combinatorial networks (Söderman et al., 2000; Nakamura et al., 2001). However, despite their functional similarities, the regulatory mechanisms of ABI3, ABI4, and ABI5 differ markedly. The ABI3 protein is proteolytically degraded by a RING E3 ligase, ABI3-INTERACTING PROTEIN2, a negative regulator of ABA signaling (Zhang et al., 2005). Controlled protein degradation also underlies ABI5 activity regulation. The KEEP ON GOING (KEG) E3 ligase executes ABI5 degradation under normal growth conditions (Stone et al., 2006; Liu and Stone, 2010). In the presence of ABA, KEG is rapidly degraded, promoting the accumulation of high levels of ABI5. Additional E3 ligases, such as DWD HYPERSENSITIVE TO ABSCISIC ACID1 (DWA1), DWA2, and SIZ1 (for SAP scaffold attachment factor, acinus, protein inhibitor of activated signal transducer and activator of transcription) and Miz1 [Msx2-interacting zinc finger], further fine-tune the protein accumulation of ABI5 (Miura et al., 2009; Lee et al., 2010).

Compared with ABI3 and ABI5, relatively less is known regarding how ABI4 activity is regulated at the molecular level. This study demonstrates that the MYB96 transcription factor regulates ABI4 expression by binding directly to the gene promoter and defines its spatial and temporal expression. Both MYB96 and ABI4 genes are strongly expressed in the embryo and are responsive to exogenous ABA (Penfield et al., 2006). Furthermore, the promotive effect of ABA on ABI4 expression is largely impaired in the myb96-1 mutant, indicating that MYB96 is an unequivocal transcriptional regulator required for the proper expression of ABI4 in an ABA signaling pathway.

The question, then, is how MYB96 activity is regulated by ABA. Given the myriad targets of MYB96, it is likely that MYB96 acts upstream of ABA signaling pathways. It is probable that controlled protein turnover and/or posttranslational modifications mediated by ABA receptor-like complex might underlie the ABA regulation of MYB96 activity, and the ABA induction of MYB96 transcription may be a result of feedback regulation. Further work is required to get a comprehensive view of the signaling network built up from MYB96.

**TAG Degradation during Seed Germination**

The utilization of seed storage reserves, such as carbohydrates, proteins, and lipids, is crucial to drive germination and postgerminative seedling growth (Penfield et al., 2004, 2006; Quettier and Eastmond, 2009), albeit controversial (Pritchard et al., 2002; Kelly et al., 2011). Arabidopsis seeds mainly store TAG as the major carbon reserve, which accumulate at the later stages of seed maturation (Lu and Hills, 2002; Maeh et al., 2009). Following seed imbibition, fatty acids are degraded through β-oxidation (Footitt et al., 2002) and primarily consumed as a form of soluble carbohydrates that are converted by the glyoxylate cycle and gluconeogenesis (Penfield et al., 2005; Pracharoenwattana et al., 2010). In agreement with this, mutants with defective TAG hydrolysis exhibit delayed germination and perturbed postgerminative
seedling growth (Penfield et al., 2005, 2006; Quettier and Eastmond, 2009; Kelly et al., 2011).

Exogenous ABA provokes delayed germination in part by reducing lipid breakdown (Penfield et al., 2006). Genes involved in the conversion of TAG into soluble sugars are down-regulated in response to ABA (Pritchard et al., 2002); thus, the levels of fatty acid-derived sugars in ABA-treated seeds are markedly decreased (Pritchard et al., 2002). Notably, the ABA regulation of lipid breakdown is relevant particularly in embryos (Penfield et al., 2006), indicating the differential sensitivity of embryo and endosperm to ABA. The ABI4 transcription factor is a major regulator in this process. Embryo-expressed ABI4 negatively regulates lipid mobilization and thus seed germination in the presence of ABA (Penfield et al., 2006).

In this study, we discovered the MYB96-ABI4 signaling module that regulates the ABA-dependent seed germination process, possibly through the control of lipid mobilization. MYB96 not only confers ABA sensitivity to embryos but also participates in embryonic lipid mobilization to properly regulate seed germination, similar to the role of ABI4 in seed germination (Penfield et al., 2006). The myb96-1 seeds degrade a significant content of TAG even in the presence of ABA, whereas TAG breakdown is largely impaired in myb96-ox seeds. Given that the MYB96-mediated physiological responses in seeds largely depend on ABI4, MYB96 appears to be an explicit transcriptional regulator of ABI4 to define its expression pattern in seeds and to ensure proper seed germination.

**Importance of MYB96-ABI4 Transcriptional Cascades in Seed Germination**

The MYB96 transcription factor modulates a variety of plant developmental processes in response to ABA, including shoot development, root architecture remodeling, stomatal closure, cuticular wax accumulation, and hormone biosynthesis (Seo et al., 2009, 2011; Seo and Park, 2010). Based on this study, MYB96 also appears to play a role in ABA-dependent seed germination.

Multiple functions of MYB96 are achieved by regulating myriad transcriptional target genes that underlie a variety of signaling pathways. For example, ABA-induced cuticular wax biosynthesis is mediated by MYB96 regulation of 3-KETOACYL-COENZYME A SYNTHASE genes encoding rate-limiting enzymes of the very-long-chain fatty acid elongation process (Seo et al., 2011). MYB96-GRETCHEN HAGEN3 transcriptional cascades regulate lateral root development under water-deficient conditions by reestablishing auxin homeostasis (Seo et al., 2009). The RESPONSIVE TO DESSICATION22 gene is probably one of the regulatory targets of MYB96 that functions in the control of drought tolerance (Seo et al., 2009). LIPID TRANSFER PROTEIN3 is responsible in part for the MYB96 regulation of freezing and drought tolerance (Guo et al., 2013). In addition, the MYB96-ABI4 transcriptional module is crucial for ABA-dependent seed germination. Genetic analysis reveals that delayed germination...
of myb96-ox is fully suppressed by the abi4 mutation, indicating that ABI4 is the principal target of MYB96 in the control of seed germination. Collectively, MYB96 is an important ABA signaling mediator that globally links multiple signaling pathways and thus helps plants to trigger efficient physiological and cellular reprogramming for environmental adaptation.

Meanwhile, ABI4 integrates a variety of external and internal signals, such as light, ABA, reactive oxygen species, and soluble sugars (Pesaresi et al., 2007; Shkolnik-Inbar and Bar-Zvi, 2010; Kerchev et al., 2011; Yang et al., 2011b; Foyer et al., 2012), and regulates hormone biosynthesis and sugar and lipid metabolism (Kerchev et al., 2011; Shu et al., 2013; Wind et al., 2013). Thus, ABI4 coordinates developmental programs with environmental signals to optimize plant growth and development processes. MYB96 is particularly relevant in ABA signal transduction to ABI4, and other signaling regulators are likely responsible for the transcriptional regulation of ABI4 with respect to other input signals.

Taken together, the MYB96-ABI4 signaling module is important for the control of ABA-dependent seed germination. MYB96 precisely conveys ABA signaling to ABI4 in embryos during seed germination, and ABI4 in turn integrates multitude environmental and developmental information to determine the proper timing for germination. Multiple transcriptional cascades not only allow for signal amplification but also enable plants to make integrative decisions.

**MATERIALS AND METHODS**

**Plant Materials and Growth Conditions**

*Arabidopsis (Arabidopsis thaliana)* Columbia-0 ecotype was used for all experiments described, unless specified otherwise. Plants were grown under long-day conditions (16-h-light/8-h-dark cycle) with cool-white fluorescent light (100 μmol photons m−2 s−1) at 23°C. The myb96-ox and myb96-1 mutants (GABI 120B05) were reported previously (Seo et al., 2009). The abi4-1 mutant (CS8104) was obtained from the Arabidopsis Biological Resource Center (http://abrc.osu.edu/). The myb96-ox/abi4-1 double mutant was generated by genetic cross of myb96-ox and abi4-1 mutants. Identification of abi4-1 was performed as described previously (Finkelstein et al., 1998).

**qRT-PCR Analysis**

Total RNA was extracted using TRI agent (Takara Bio) according to the manufacturer’s recommendations. Reverse transcription was performed using Moloney murine leukemia virus reverse transcriptase (Dr. Protein) with oligo(dT)18 to synthesize first-strand complementary DNA (cDNA) from 2 μg of total RNA. Total RNA samples were pretreated with an RNase-free DNase. cDNAs were diluted to 100 μL with Tris-EDTA buffer, and 1 μL of diluted cDNA was used for PCR amplification.

qRT-PCR was performed in 96-well blocks using the Step-One Plus Real-Time PCR System (Applied Biosystems). The PCR primers used are listed in Supplemental Table S1. The value for each of primers was normalized relative to eIF4a (At3g13920). All qRT-PCRs were performed in triplicate using total RNA samples extracted from three independent biological replicates. The comparative ΔΔCt method, which is a calculation for the relative quantification of target DNA, was employed to evaluate relative quantities of each amplified product in the samples. The threshold cycle was automatically determined for each reaction by the instrument software using default parameters. The specificity of the qRT-PCR was determined by melt curve analysis of the amplified products using the standard method installed in the system.

**Measurement of GUS Activity**

Seeds were dissected into embryo and endosperm surrounded with seed coat. For histochemical staining of GUS activity, plant materials were fixed by immersing in 90% (v/v) acetone for 20 min on ice, washed twice with rinsing solution [50 mM sodium phosphate, pH 7, 0.5 mM K3Fe(CN)6, and 0.5 mm K3[Fe(CN)6]3] and subsequently incubated in staining solution containing 1 mM 5-bromo-4-chloro-3-indolyl-β-D-glucoronic acid (Duchefa) at 37°C for 18 to 24 h, depending on staining intensity (Padmanaban et al., 2007).

**Seed Germination Assays**

All genotypes were grown at 23°C under long-day conditions, and seeds were collected at the same time. Harvested seeds were dried at room temperature at least 1 month before germination assays. For seed germination assays, 40 to 50 seeds for each line were sterilized and plated on MS medium (one-half-strength MS salts, 0.05% [w/v] MES, pH 5.7, and 0.7% [w/v] agar) supplemented with various concentrations of ABA (0, 0.5, 1, and 3 μM). Plates were stratified in darkness for 3 d at 4°C and transferred to a culture room set at 23°C with a 16-h-light/8-h-dark cycle. Germination was scored at the indicated time points by counting the frequency of radicle emergence from the seed coat and endosperm. For each germination assay, biological triplicates were performed. To investigate the effects of ABA on cotyledon greening, the percentage of cotyledon greening was scored after the end of stratification. Cotyledon greening was defined as complete expansion of the cotyledon and greening.

**ChIP Assays**

ChIP assays were performed as described previously (Yang et al., 2011a). pMYB96::MYC-MYC::MYB96 transgenic plants, anti-MYC antibodies (Millipore), and salmon sperm DNA/protein A agarose beads (Millipore) were used for ChIP. DNA was purified using phenol/chloroform/isoamyl alcohol and sodium acetate (pH 5.2). The level of precipitated DNA fragments was quantified by quantitative real-time PCR using specific primer sets (Supplemental Table S2). Values were normalized with the level of input DNA. The value in pBA002 control plants was set to 1 after normalization against elf4a for quantitative PCR analysis.

**Transient Gene Expression Assays**

For transient expression assays using Arabidopsis protoplasts, reporter and effector plasmids were constructed. The reporter plasmid contains a minimal 35S promoter sequence and the GUS gene. The core elements on the ABI4 promoter were inserted into the reporter plasmid. To construct the p35S:MYB96 effector plasmid, the MYB96 CDNA was inserted into the effector vector containing the cauliflower mosaic virus 35S promoter. Recombinant reporter and effector plasmids were cotransformed into Arabidopsis protoplasts by polyethylene glycol-mediated transformation (Yoo et al., 2007). GUS activities were measured by a fluorometric method. A cauliflower mosaic virus 35S promoter-luciferase construct was also cotransformed as an internal control. The luciferase assay was performed using the Luciferase Assay System kit (Promega).

**Fatty Acid Determinations**

The total fatty acid content and amount of eicosanoic acid (20:1 n-9) in seeds were measured by gas chromatographic analysis with a known amount of 15:0 fatty acid as an internal standard. The total fatty acid content and amount of eicosanoic acid (20:1 n-9) in seeds were measured by gas chromatographic analysis with a known amount of 15:0 fatty acid as an internal standard. The total fatty acid content and amount of eicosanoic acid (20:1 n-9) in seeds were measured by gas chromatographic analysis with a known amount of 15:0 fatty acid as an internal standard. Samples were transmethylated at 90°C for 90 min in 0.3 mL of toluene and 1 mL of 5% (v/v) H2SO4 (in methanol). After transmethylation, 1.5 mL of 0.9% (w/v) NaCl solution was added, and the fatty acid methyl esters were transferred to a new tube for three sequential extractions with 1.5 mL of n-hexane. Fatty acid methyl esters were analyzed by gas chromatography using a GC-2010 Plus instrument (Shimadzu) with a 30-m × 0.25-mm (i.d.) HP-FFAP column (Agilent), during which the oven temperature was increased from 170°C to 180°C at 1°C min⁻¹.

Sequence data from this article can be found in the Arabidopsis Genome Initiative or GenBank/EMBL databases under the following accession numbers: ABI1 (At4g26080), ABI2 (At5g7050), ABI3 (At3g24650), ABI4 (At2g40220), ABI5 (At3g36270), MYB96 (At5g65240), ACBP1 (At5g53470), AHH1 (At2g17820), BLH1 (At2g35940), FTY (At1g513480), and others.
Role of MYB96 in Seed Germination

Supplemental Data

The following materials are available in the online version of this article.

Supplemental Figure S1. Temporal expression of MYB96.

Supplemental Figure S2. Expression of MYB96 in embryo after cold imbibition.

Supplemental Figure S3. ABA induction of MYB96 in embryo.

Supplemental Figure S4. Expression of MYB96 in quadruple-DELLA and GA-deficient mutants.

Supplemental Figure S5. Cotyledon opening of myb96-ax and myb96-1 in the presence of ABA.

Supplemental Figure S6. ABA dose-response assays.

Supplemental Figure S7. Expression of AB14 and BLH1 in the myb96-ax mutant in the presence of ABA.

Supplemental Figure S8. AB14 expression in dry seeds and during seed germination.

Supplemental Figure S9. Spatial expression of MYB96 and AB14.

Supplemental Figure S10. ChiP using 35S:MYC2 transgenic plants.

Supplemental Figure S11. Lipid breakdown in wild-type, myb96-ax, and myb96-1 seeds during seed germination in the absence of ABA.

Supplemental Table S1. Primers used in qRT-PCR.

Supplemental Table S2. Primers used in ChiP assays.

Received February 2, 2015; accepted April 10, 2015; published April 13, 2015.

LITERATURE CITED

HaraDAJJ, Baden CS, Comai L (1988) Spatially regulated genes expressed during seed germination and postgerminative development are activated during embryogenesis. Mol Gen Genet 212: 466–473
Kelly AA, Quettier AL, Shaw E, Eastmond PJ (2011) Seed storage oil mobilization is important but not essential for germination or seedling establishment in Arabidopsis. Plant Physiol 157: 866–875
Qu Xu, Huang ZY, Baskin JM, Baskin CC (2008) Effect of temperature, light and salinity on seed germination and radicle growth of the geographically widespread halophyte shrub Halocnemum strobilaceum. Ann Bot (Lond) 101: 293–299


