Omics Approaches Toward Defining the Comprehensive Abscisic Acid Signaling Network in Plants

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ABBA is a plant hormone that plays crucial roles in controlling cellular and physiological responses to osmotic stress and in developmental processes. Endogenous ABA levels are increased in response to a decrease in water availability in cells, and ABA sensing and signaling are thought to be mediated according to the current model established in Arabidopsis thaliana, which involves pyrabactin resistance 1 (PYR)/PYR1-like (PYL)/regulatory components of ABA receptor (RCAR), protein phosphatase 2C (PP2C) and sucrose non-fermenting-1 (SNF1)-related protein kinase 2 (SnRK2). These core components of ABA signaling have a pivotal role in stress-responsive gene expression and stomatal regulation. However, because a limited number of their upstream and downstream factors have been characterized, it is still difficult to define the comprehensive network of ABA signaling in plants. This review focuses on current progress in the study of PYR/PYL/RCARs, PP2Cs and SnRK2s, with particular emphasis on omics approaches, such as interactome and phosphoproteome studies. Moreover, the role of ABA in plant growth and development is discussed based on recent metabolomic profiling studies.

Keywords: Abscisic acid • Arabidopsis • Omics studies • Protein phosphatase 2C (PP2C) • Pyrabactin resistance 1 (PYR)/PYR1-like (PYL)/Regulatory components of ABA receptor (RCAR) • Sucrose non-fermenting-1 (SNF1)-related protein kinase 2 (SnRK2).

Abbreviations: ABC transporter, ATP-binding cassette transporter; AB1/2/5, ABA insensitive 1/2/5; ABRE, ABA-responsive element; AHG3, ABA-hypersensitive germination 3; AIB1, ABA-induced basic helix–loop–helix 1; AKS1, ABA-responsive kinase substrate 1; AREB/ABF, ABRE-binding protein/ABRE-binding factor; bHLH, basic helix–loop–helix; BIN2, brassinosteroid-insensitive 2; CAR, C2-domain ABA-related; CBL, calcineurin B-like; CIPK, CBL-interacting protein kinase; CO, CONSTANS; CPK, calcium-dependent protein kinase; EEL, enhanced Em level; FBH3, flowering bHLH 3; FRET, fluorescence resonance energy transfer; GHR1, guard cell hydrogen peroxide-resistance 1; GSK3, glycogen synthase kinase 3; HAB1, hypersensitive to ABA 1; HA1/1, highly ABA-induced PP2C gene 1; ICE1, inducer of CBF expression 1; KAT1, potassium channel in Arabidopsis thaliana 1; MAP3K, mitogen-activated protein kinase kinase kinase; MAPK, mitogen-activated protein kinase; MOS3, modifier of snc1; 3; MPK, mitogen-activated protein kinase; PP2C, protein phosphatase 2C; PYR/PYL/RCAR, pyrabactin resistance 1/PYR1-like/regulatory components of ABA receptors; SLAC1, slow anion channel-associated 1; SLAH3, SLAC1 homolog 3; SnRK2, sucrose non-fermenting-1 (SNF1)-related protein kinase 2; SNS1, SnRK2-substrate 1; START domain, steroidogenic acute regulatory protein-related lipid transfer domain; TAF5, TATA-binding protein-associated factor 5; XRN3, exoribonuclease 3.

Introduction

ABA is a plant hormone that regulates diverse processes, including seed maturation and germination, stomatal closure and osmotic stress-responsive gene expression. In the current model established in Arabidopsis thaliana, ABA sensing and signaling are mediated by three classes of proteins: pyrabactin resistance 1 (PYR)/PYR1-like (PYL)/regulatory components of ABA receptor (RCAR), protein phosphatase 2C (PP2C) and sucrose non-fermenting-1 (SNF1)-related protein kinase 2 (SnRK2). Under normal growth conditions, in which cellular ABA levels are low, group-A PP2Cs interact with subclass III SnRK2s and inhibit their kinase activities. When ABA accumulates in cells under osmotic stress conditions, such as drought and high salinity, ABA is perceived by PYR/PYL/RCAR receptors that inhibit the phosphatase activities of PP2Cs. Ternary complexes composed of ABA–PYR/PYL/RCAR–PP2C enable the activation of SnRK2s, resulting in the phosphorylation of downstream substrates, such as transcription factors and membrane channel proteins (Fig. 1). Thus, major advances have been made toward understanding the molecular basis of the core components of ABA signaling in plants. However, due to the lack of knowledge regarding their upstream and downstream factors, it is still challenging to obtain a comprehensive picture of the ABA signaling network. In this review, we highlight recent progress in the study of PYR/PYL/RCARs, group-A PP2Cs and subclass III SnRK2s in ABA signaling, with particular emphasis on global analyses, including interactome and phosphoproteome profiling. Moreover, the role of ABA in plant growth and development is discussed based on recent studies of metabolomic profiling.

PYR/PYL/RCARs Have Overlapping but Distinct Roles as ABA Receptors

A group of steroidogenic acute regulatory protein-related lipid transfer (START) domain proteins, termed PYR/PYL/RCARs,
has been demonstrated to act as functional ABA receptors in plants (for reviews, see Cutler et al. 2010, Hubbard et al. 2010, Raghavendra et al. 2010, Weiner et al. 2010). Structural studies (Melcher et al. 2009, Miyazono et al. 2009, Yin et al. 2009) have revealed that PYR/PYL/RCARs harbor binding sites for group-A PP2Cs, which are the key negative regulators in ABA signaling, as well as for ABA. Currently, PYR/PYL/RCARs can be grouped into two subclasses according to their oligomeric states and appear to function via one of two different mechanisms (Miyakawa et al. 2013). For example, PYR1/RCAR11, PYL1/RCAR12, PYL2/RCAR14 and PYL3/RCAR13, which form homodimers in the absence of ABA, are released as monomers following ABA binding and subsequently interact with group-A PP2Cs. In contrast, PYL4/RCAR10, PYL5/RCAR8, PYL6/RCAR9, PYL8/RCAR3, PYL9/RCAR1 and PYL10/RCAR4 behave as monomers in both the presence and absence of ABA, and these monomers can inhibit group-A PP2Cs regardless of ABA binding. The inhibition of group-A PP2Cs by PYR/PYL/RCARs in the absence of ABA has been observed in vitro and in protoplasts (Fujii et al. 2009, Hao et al. 2011). In addition,
electropically expressed ABA insensitive 1 (ABI1) fused with yellow fluorescent protein has been shown to interact with PYR/PYL/RCARs in Arabidopsis with or without ABA application (Nishimura et al. 2010). Although it is still unclear whether structural differences among PYR/PYL/RCARs are reflected in variations in their biological functions, the roles of PYR/PYL/RCARs in plants have been extensively studied since they were first identified as ABA receptors.

Given that the protein sequences of 14 members of Arabidopsis PYR/PYL/RCARs are highly homologous, these proteins are thought to have redundant functions in ABA signaling. In fact, studies of multiple mutants of PYR/PYL/RCARs have demonstrated that PYR1/RCAR11, PYL1/RCAR12, PYL2/RCAR14, PYL4/RCAR10, PYL5/RCAR8 and PYL8/RCAR3 have overlapping roles in the regulation of seed germination, stomatal closure and gene expression in ABA signaling (Park et al. 2009, Gonzalez-Guzman et al. 2012). In contrast to the other 13 PYR/PYL/RCARs, PYL13/RCAR7 has three variant amino acid residues in a conserved ABA-binding pocket; therefore, its roles in ABA sensing have remained obscure. Although two prior studies have claimed that PYL13/RCAR7 selectively inhibits PP2Cs in an ABA-independent manner and does not bind ABA (Li et al. 2013, Zhao et al. 2013), a recent study has revealed that it inhibits the phosphatase activities of ABI1, ABI2 and PP2CA/ABA-hypersensitive germination 3 (AHG3), but not that of hypersensitive to ABA 1 (HAB1), at nanomolar ABA levels (Fuchs et al. 2014). Moreover, Arabidopsis plants ectopically expressing PYL13/RCAR7 exhibit increased sensitivity to ABA during seed germination and stomatal closure. Although the ABA sensitivity of the rcar7 mutant during seed germination is comparable with that of wild-type plants, the rcar7 rcar9 double mutant shows ABA insensitivity. Taken together, these findings suggest that PYL13/RCAR7 functions as an ABA co-receptor during early seedling development and partners with specific PP2Cs.

In addition, several recent studies have suggested that the role of PYL8/RCAR3 is overlapping with but distinct from that of other PYR/PYL/RCARs. Two large-scale protein–protein interaction studies have found that PYL8/RCAR3 interacts with transcription factors such as MYB77 (Arabidopsis Interactome Mapping Consortium 2011, Lumba et al. 2014). This finding has been further confirmed by a study showing that PYL8/RCAR3, but not other PYR/PYL/RCARs, interacts with MYB77 and its homologs (Zhao et al. 2014). The interaction between PYL8/RCAR3 and MYB77 promotes the DNA binding affinity and transcriptional activity of MYB77. Furthermore, the lateral root growth of the pyl8 and myb77 mutants is more strongly inhibited by ABA compared with that of wild-type plants. These data are probably in accordance with an observation that the pyl8 mutant displays decreased sensitivity to ABA during primary root growth compared with wild-type plants and other pyr/pyl single mutants (Antoni et al. 2013). Because MYB77 modulates auxin signaling during lateral root development together with auxin response factors (Shin et al. 2007), PYL8/RCAR3 that is expressed in roots might be involved in auxin signaling, as well as in ABA signaling, by binding to MYB transcription factors (Fig. 1).

The identification of proteins that interact with PYR/PYL/RCARs has provided new insight into the regulation of their subcellular localization. A yeast two-hybrid screening assay with PYL4/RCAR10 as bait identified a family of small proteins that contain a lipid-binding C2 domain. These proteins are referred to as C2-domain ABA-related (CAR) proteins (Rodriguez et al. 2014). C2 domains, which are found in myriad eukaryotic proteins, are part of various enzymes that harbor catalytic domains, and they serve as Ca2+-activated modules to promote targeting of catalytic activity to membranes. Although additional catalytic domains are absent in a number of small C2-domain proteins in plants, including CARs, these C2-domain proteins are thought to play roles as calcium sensors. Additionally, many C2-domain proteins exhibit Ca2+-dependent phospholipid binding; indeed, CAR1 and CAR4 bind phospholipid vesicles in response to calcium in vitro (Rodriguez et al. 2014). Moreover, CAR1 and CAR4 mediate phospholipid binding of PYL1/RCAR12, PYL4/RCAR10, PYL6/RCAR9 and PYL8/RCAR3 in a Ca2+-dependent manner. In plant cells, interactions between CARs and PYR/PYL/RCARs were observed in plasma membranes and in the nucleus. Additionally, car multiple mutants and Arabidopsis plants overexpressing CAR genes display reduced and increased sensitivity to ABA, respectively. Thus, CARs that mediate the interaction of PYR/PYL/RCARs with phospholipid vesicles in calcium signaling might be involved in the regulation of PYR/PYL/RCAR subcellular localization, which affects ABA signaling.

PP2C Phosphatases Form a Complex Network with a Variety of Proteins in ABA Signaling

Biological, molecular biological and structural analyses have shown that PYR/PYL/RCAR ABA receptors interact with and inhibit group-A PP2Cs. Consistently, previous genetic and molecular biological studies have revealed that group-A PP2Cs are key negative regulators in ABA signaling (Hirayama and Shinozaki 2007). In the Arabidopsis genome, there are 76 genes encoding PP2C-type serine/threonine phosphatases, nine of which are classified into group-A (Schweighofer et al. 2004). Considering the ABA sensitivities of their mutants and their expression patterns in response to ABA (Yoshida et al. 2006b, Fujita et al. 2009), 6–9 group-A PP2Cs are currently considered to be the core regulators of ABA signaling. As pivotal negative regulators of ABA signaling, group-A PP2Cs have been shown to interact with a variety of proteins, including kinases, transcription factors, metabolic enzymes and chromatin-remodeling complexes (Guo et al. 2002, Himmelbach et al. 2002, Ohta et al. 2003, Miao et al. 2006, Yoshida et al. 2006a, Saez et al. 2008). The signaling network including group-A PP2Cs has been further elucidated by the recent generation of a protein interaction map of ABA-responsive genes (Lumba et al. 2014). ABA-responsive genes identified by whole-genome transcript profiling of an ABA-deficient mutant, aba2, have been assessed in yeast two-hybrid assays, resulting in the identification of an interaction network consisting of 512 statistically significant protein–protein interactions.
interactions among 138 proteins. The interaction network, which includes three PYR/PYL/RCARs (PYR1/RCAR11, PYL4/RCAR10 and PYL8/RCAR3) and four group-A PP2Cs (ABI1, AHG3, HAB and highly ABA-induced PP2C gene 1 (HA11)), but no subclass III SnRK2s, has revealed new interactions as well as previously documented interactions. In agreement with the previous literature, PP2Cs have been found to interact with a variety of proteins, including kinases, phosphatases, transcription factors and metabolic enzymes. In addition to subclass III SnRK2s, SnRK3.15, SnRK3.22 and mitogen-activated protein kinase kinase kinase (MAP3Kδ4) have also been identified as kinases that interact with PP2Cs (Fig. 1). Among members of the SnRK3/calcineurin B-like (CBL)-interacting protein kinase (CIPK) families, which are composed of 26 members in Arabidopsis and mediate various signaling pathways through interactions with CBL proteins, SnRK3.15/CIPK14 and SnRK3.22/CIPK11 are close homologs, and their gain- and loss-of-function mutants exhibit decreased and increased ABA sensitivity during seed germination, respectively (Lumba et al. 2014). Moreover, transcriptome analysis has shown that SnRK3.15/CIPK14 induced by dexamethasone impairs the expression of ABA-inducible genes. In agreement with these results, it has been previously shown that ABI1 and AB1 interact with several SnRK3/CIPKs (Ohta et al. 2003) and that SnRK3.17/CIPK3 is involved in the induction of gene expression in response to ABA, cold and high salinity (Kim et al. 2003). Collectively, SnRK3/CIPKs might be involved in PP2C-mediated ABA signaling. Interestingly, a subgroup of SnRK3/CIPKs, including CIPK26, SnRK3.12/CIPK9, SnRK3.17/CIPK3 and SnRK3.23/CIPK23, has recently been shown to interact with subclass III SnRK2s (Mogami et al. 2015) (Fig. 1). Furthermore, multiple mutants of SnRK3/CIPKs, as well as the srk2dei and ab2 mutants, have exhibited increased susceptibility to high levels of exogenous Mg2+. Although ABA is a key plant hormone that functions under water deficit conditions, the observation that the hypersensitivity of the ab2 mutant is rescued by ABA application suggests that basal ABA signaling mediated by subclass III SnRK2s has an important role in Mg2+ homeostasis. Notably, the increased sensitivity of the cipk3 cipk9 cipk23 cipk26 quadruple mutant to high Mg conditions was concurrently reported by another group (Tang et al. 2015). Consistent with the interactions of these SnRK3/CIPKs with CBL2 and CBL3 at the vacuolar membrane, whole-vacuole Mg2+ currents are impaired in the cbl2 cbl3 double mutant, which is also hypersensitive to high Mg conditions. Although Mg2+ transporters functioning downstream of SnRK2s and SnRK3/CIPKs have not yet been determined, emerging evidence suggests that the phosphorylation network downstream of ABA and calcium signaling is essential for Mg2+ homeostasis. As demonstrated by multiple studies, several calcium signaling proteins, such as calcium-dependent protein kinases (CPKs), are involved in ABA signaling via SnRK2s and ABA-responsive element (ABRE)-binding proteins (AREBs)/ABRE-binding factors (ABFs) (for a review, see Fujita et al. 2013). Further studies are needed to reveal the functional significance of the association between core ABA signaling mediated by PP2Cs and SnRK2s and calcium signaling mediated by SnRK3/CIPKs and CPKs.

In addition to the crucial role of subclass III SnRK2s in ABA-dependent gene expression (Fujita et al. 2009), transcriptional regulation mediated by PP2Cs may also be important for ABA signaling. Indeed, an HD-Zip transcription factor, ATHB6, and bZIP transcription factors, such as AREB/ABFs, have been shown to function downstream of group-A PP2Cs (Himmelbach et al. 2002, Lynch et al. 2012). Moreover, HAB1 may be involved in ABA-inducible gene expression by interacting with SW1B, which is an Arabidopsis ortholog of the yeast SWI subunit of SW1/SNF chromatin-remodeling complexes (Saez et al. 2008). The interactome study has revealed that many transcription factors interact with group-A PP2Cs and that individual interaction partners can be altered in response to different abiotic stresses (Lumba et al. 2014). Each gene involved in the interaction map exhibits similar expression patterns in response to osmotic and salt stress. However, taking into account the co-expression data, several protein–protein interaction pairs are differentially expressed. For example, HAI1 and its interacting partners exhibit similar co-expression patterns under both osmotic and salt stress conditions, whereas MAP3Kδ4 and its interacting partners show highly correlated gene expression in response to osmotic stress, but not salt stress. Likewise, the expression of a basic helix–loop–helix (bHLH) transcription factor gene, ABA-induced basic helix–loop–helix 1 (AIB1), is highly correlated with the expression of its interacting proteins under salt stress. Given that transgenic seedlings expressing dexamethasone-inducible AIB1 show increased sensitivity to salt, but not to mannitol, the function of AIB1 and its interacting proteins may be more closely related to salt stress than osmotic stress. Thus, the integration of the protein–protein interaction map with transcriptomic data appears to be a novel approach to determining the factors that function in a stress-specific manner.

ABA has an essential role in stomatal regulation as well as stress-responsive gene expression. Several membrane proteins, including slow anion channel-associated 1 (SLAC1) and potassium channel in Arabidopsis thaliana 1 (KAT1), have been demonstrated to function in ABA signaling in guard cells (Joshi-Saha et al. 2011). Another interactome study further advanced the understanding of membrane proteins involved in ABA signaling (Jones et al. 2014b). A split-ubiquitin yeast two-hybrid screen of 3,286 Arabidopsis membrane and signaling proteins identified 12,102 protein interactions among 1,523 proteins. The further application of transcriptomic, genetic and other experimental data to the interaction network allowed for the generation of an ABA-related subnetwork as well as other plant hormone subnetworks. Notably, PYR1/RCAR11 and KAT1 have been found to interact with AP2C1 in the ABA signaling subnetwork (Fig. 1). AP2C1 is a member of group-B PP2Cs that has been shown to regulate negatively mitogen-activated protein kinase 4 (MPK4) and MPK6 in response to wounding and pathogens (Schweighofer et al. 2007). Moreover, the stomatal aperture of the ap2c1 mutant is slightly increased (Brock et al. 2010). Given that the channel activity of KAT1 is completely inhibited by the co-expression of AP2C1 in oocytes
In contrast to the key negative regulatory role of PP2Cs, subclass III SnRK2s are the pivotal activators of ABA signaling. Nine out of 10 Arabidopsis SnRK2 kinases are activated by osmotic stress, subclass III SnRK2s are the pivotal activators of ABA signaling. Nine out of 10 Arabidopsis SnRK2 kinases are activated by osmotic stress, subclass III SnRK2s, SRK2D/SnRK2.2, SRK2E/SnRK2.6/OST1 and SRK2I/SnRK2.3 are also strongly activated by ABA. SLAC1 is a slow anion channel that is activated by subclass III SnRK2s in an ABA-dependent manner. A recent study has identified a receptor-like kinase, guard cell hydrogen peroxide-resistant 1 (GHR1), that mediates the phosphorylation of SLAC1 (Hua et al. 2012). GHR1 is a receptor-like kinase localized to the plasma membrane that interacts with SLAC1 and ABI2, but not ABI1. Whereas SLAC1 activity is activated by GHR1 in oocytes, the co-expression of ABI2, but not ABI1, inhibits this activation. Taken together with the results of genetic studies of the ghr1 and ost1 mutants, it is likely that GHR1 phosphorylates SLAC1 independently of SRK2E/SnRK2.6/OST1 and is inhibited by ABI2. Moreover, it has been shown that ABI1 perturbs the interaction between SLAC1 homolog 3 (SLA3H) and CPK21 in the absence of ABA (Demir et al. 2013). SLA3H is inhibited by ABI1 and activated by CPK21 in ABA signaling mediated by PYL9/RCAR1 (Geiger et al. 2011). Thus, as key negative regulators, group-A PP2Cs might form a complex signaling network with a myriad of proteins to fine-tune ABA signaling.

**Phosphoproteomic Studies Have Identified Substrates of SnRK2 Kinases**

In contrast to the key negative regulatory role of PP2Cs, subclass III SnRK2s are the pivotal activators of ABA signaling. Nine out of 10 Arabidopsis SnRK2 kinases are activated by osmotic stress, and subclass III SnRK2s, SRK2D/SnRK2.2, SRK2E/SnRK2.6/OST1 and SRK2I/SnRK2.3 are also strongly activated by ABA (Boudsocq et al. 2004). Extensive analyses of SnRK2s have been performed, revealing that the srk2d/e/i triple mutant exhibits an extreme ABA-insensitive phenotype with regard to seed germination, seedling growth, stomatal regulation and osmotic stress-responsive gene expression (Fujii and Zhu 2009, Fujita et al. 2009, Nakashima et al. 2009). Nonetheless, a limited number of substrates of SnRK2s, such as AREB/ABF transcription factors and the SLAC1 anion channel, were characterized until phosphoproteome studies of the srk2d/e/i (alias snrk2.2/2.3/2.6) triple mutant were conducted (Umezawa et al. 2013, Wang et al. 2013). A comparison of the phosphoproteomic profile of the srk2d/e/i mutant after ABA and dehydration stress treatments with the profile of wild-type plants revealed 32 phosphopeptides that are possible substrates of SnRK2s, including AREB/ABF transcription factors, SnRK2-substrate 1 (SNS1), AtMPK1 and AtMPK2 (Umezawa et al. 2013) (Fig. 1). SNS1, the expression of which is constitutive in both the presence and absence of abiotic and biotic stresses, is a protein of unknown function that is conserved in higher plants. Whereas SNS1 phosphopeptides are increased in wild-type plants after ABA and dehydration stress treatments, SNS1 is not phosphorylated in the srk2d/e/i mutant. Moreover, the expression of ABA-responsive genes, such as RD29B and RAB18, is slightly enhanced under ABA treatment in the sns1 mutant, which displays increased sensitivity to ABA during the post-germination stages. These findings suggest that SNS1 is a negative regulator that acts downstream of subclass III SnRK2s in ABA signaling. Previous reports have shown that the subgroup C1 mitogen-activated protein kinases (MAPKs) AtMPK1 and AtMPK2 are activated by diverse stimuli, including ABA, jasmonic acid, wounding and high salinity stress (Ortiz-Masia et al. 2007, Hwa and Yang 2008). The peptide identified in the activation loop of AtMPK1 and AtMPK2 has also been demonstrated to be phosphorylated in response to ABA and dehydration; however, it is not phosphorylated in the srk2d/e/i mutant (Umezawa et al. 2013). Given that the phosphorylation of the minimal MAPK target motif, [-pS/pT-p]-P, is impaired in the srk2d/e/i mutant, subclass III SnRK2s may directly or indirectly activate the phosphorylation states of MAPK cascades, which include AtMPK1 and AtMPK2, in response to ABA and dehydration stress. Although further studies are needed, a growing body of evidence indicates that MAPK pathways play key roles in ABA signaling as well as subclass III SnRK2s (for reviews, see Danquah et al. 2014, Umezawa et al. 2014).

Another phosphoproteomic study of the srk2d/e/i triple mutant identified 84 phosphopeptides that are candidate substrates for SnRK2s, most of which have been classified into the nucleotide binding, transcriptional regulation, chloroplast processes and signal transduction categories by gene ontology analysis (Wang et al. 2013). The transcriptional regulators identified correspond to eight proteins, including AREB1/ABF2, AREB3, enhanced Em level (EEL), flowering bHLH 3 (FBH3) and TATA-binding protein-associated factor 5 (TAF5). Three bZIP transcription factors, AREG1/ABF2, AREG2/ABF4 and ABF3, have been well characterized as transcription factors functioning downstream of SnRK2s (Furihata et al. 2006, Fujita et al. 2009) and have been shown to play key roles in ABA-responsive gene expression (Yoshida et al. 2010). Moreover, it has been recently shown that ABF1 is a functional homolog of AREG1/ABF2, AREG2/ABF4 and ABF3, and that a large number of genes functioning downstream of SnRK2s are impaired in the areb1 areb2 abf3 abf1 quadruple mutant (Yoshida et al. 2015). In contrast to these AREB/ABFs, it has been found that AREB3, EEL, FBH3 and TAF5 are involved in developmental processes rather than osmotic stress-responsive gene expression (Ito et al. 2012, Mougiou et al. 2012, Fujita et al. 2013). Given that transcription factors other than AREB1/ABF2, AREG2/ABF4, ABF3 and ABF1 were not determined to be SnRK2 substrates in the aforementioned phosphoproteomic study (Umezawa et al. 2013), it is likely that osmotic stress-responsive gene expression downstream of SnRK2s is predominantly regulated by the four AREB/ABFs in ABA signaling during the vegetative stages (Fig. 1). Although the role of ABA has been well studied in osmotic stress signaling, ABA is also thought to play a role in cold stress signaling. A recent study suggests that SRK2E/SnRK2.6/OST1 is involved in cold signaling through its phosphorylation of...
ABA Signaling is Involved in Metabolic Regulation

In addition to its critical role in the stress response, ABA is also involved in growth and developmental processes, such as seed maturation and the regulation of seed germination. As evidenced by its increased levels in seeds, ABA is one of the key plant hormones in seed maturation, and the molecular mechanism underlying the mediation of ABA signaling by transcription factors such as ABI5 has been extensively studied (Finkelstein 2013). However, little is known about the manner by which ABA regulates plant growth and development in vegetative tissues. Integrated transcriptome and metabolome analyses have revealed the roles of ABA-dependent and ABA-independent signaling in the metabolic changes occurring under osmotic stress conditions in Arabidopsis and rice (Urano et al. 2009, Maruyama et al. 2014). Moreover, the growth phenotypes and gene expression patterns of six Arabidopsis accessions grown under mild drought stress conditions have been recently analyzed, and it has been shown that ABA signaling, proline metabolism and cell wall adjustments promote a robust response to drought stress that occurs in different genetic backgrounds (Clauw et al. 2015). Cytokinin signaling is reportedly down-regulated by dehydration stress in Arabidopsis and rice (Maruyama et al. 2014) and is suggested
to play a key role in osmotic stress signaling together with ABA (Ha et al. 2012). In addition, transcriptome and metabolome profiling of developing Arabidopsis leaves grown under mild osmotic stress conditions has shown that cell proliferation and expansion are mainly regulated by ethylene and gibberellin signaling in leaves (Skirycz et al. 2010). Thus, the cross-talk that occurs between ABA signaling and other plant hormone pathways could be exploited to control rigorously the tolerance and growth of plants exposed to osmotic stress conditions.

Recent studies have shown that the key regulators in ABA signaling are involved in metabolomic regulation in various plant species. Arabidopsis SnRK1 kinases are essential for energy and stress signaling (Baena-González and Sheen 2008). SnRK1.1 has recently been shown to interact with and be inhibited by group-A PP2Cs, such as ABI1 and PP2CA/AHG3 (Rodrigues et al. 2013). In addition to the finding that pp2c mutants and Arabidopsis overexpressing SnRK1.1 were hypersensitive to sugar, genes induced by SnRK1.1 activation were found to overlap with ABA-inducible genes. Thus, group-A PP2Cs might play a role in processes involved in both ABA and energy signaling. Moreover, a role for ABA in fruit development has been postulated by several research groups (Fig. 1). Consistent with ABA accumulation during tomato fruit ripening (Zhang et al. 2009), metabolomic profiling has shown that SIAREB1, which is a close ortholog of Arabidopsis AREB/ABFs that functions in ABA signaling, regulates primary metabolism in tomato fruit (Bastias et al. 2014). Similarly, a grape ortholog of Arabidopsis AREB/ABFs, VvABF2, which is highly expressed in the berry, has been shown to be involved in phenolic compound synthesis and cell wall softening, as determined by transcriptome analysis of cultured cells overexpressing VvABF2 (Nicolas et al. 2014). Additionally, strawberry orthologs of Arabidopsis PYR1/RCAR11, ABI1 and SRK2E/SnRK2.6/OST1 have been suggested to be involved in fruit ripening (Chai et al. 2011, Jia et al. 2013, Han et al. 2015). Although plant hormones such as ethylene, gibberellin and auxin have been extensively studied, these recent findings suggest that ABA signaling also has a substantial role in fruit development and ripening.

Conclusions and Future Perspectives

In this review, we focused on recent progress made toward greater understanding of the comprehensive ABA signaling network, in which PYR/PYL/RCARs, group-A PP2Cs and subclass III SnRK2s serve as the core components. Global analyses, such as interactome and phosphoproteome studies, have revealed that group-A PP2Cs and subclass III SnRK2s function as hubs in ABA signaling via a variety of substrates and interacting proteins (Fig. 1). In addition, metabolomic profiling has been performed to elucidate the manner in which ABA mediates plant growth and development. Our understanding of plant molecular biology is rapidly increasing due to technological advances that facilitate comprehensive analyses, including hormone analysis (Kojima et al. 2009), lipidomic profiling (Bromke et al. 2015) and the construction of an artificial microRNA library (Hauser et al. 2013). In fact, genome-wide genetic screening using this library was performed to identify functionally redundant genes involved in ABA signaling (Hauser et al. 2013). In addition to the identification of ABA signaling components, the identification of ABA transporters has broadened our knowledge of the manner by which ABA is transported in plants (Umezawa et al. 2010). Recently, a study of the ATP-binding cassette (ABC) transporter ABCG25, which is an ABA exporter, showed that ABA that is synthesized in specific cells, such as phloem companion cells in vascular tissues, can be transported to guard cells (Kuromori et al. 2014). Furthermore, the fluorescence resonance energy transfer (FRET)-based reporters that have been developed enable the monitoring of the distribution and dynamics of ABA in plants (Jones et al. 2014a, Waadt et al. 2014). Thus, the future application of these omics approaches and technologies to the study of various plants will enable a deeper understanding of the mechanisms of ABA synthesis, metabolism, transport and signaling. This knowledge may be useful for the manipulation of drought stress tolerance in crops. In addition to numerous attempts to engineer the genes involved in ABA synthesis and signaling, an important step toward the maintenance of crop growth and yield during drought stress has recently been achieved using an engineered PYR1/RCAR11 ABA receptor in combination with an agrochemical (Park et al. 2015). Expression of a modified form of PYR1/RCAR11 caused sensitivity to the agrochemical mandipropamid at nanomolar concentrations and altered stomatal responses and drought stress tolerance in transgenic Arabidopsis and tomato. A chemical screening approach has also proven to be useful for the identification of chemicals that manipulate ABA responses in plants (Okamoto et al. 2013). Although a sulfonamide ABA agonist, quinabactin, inhibits the activity of HAB1 specifically through dimeric PYR/PYL/RCARs, drought stress tolerance in Arabidopsis and soybean was efficiently enhanced by application of quinabactin as well as ABA. Based on these studies, promising combinations of PYR/PYL/RCARs and agrochemicals that can maintain crop growth and yield might be identified in further investigations. Despite the considerable gap between achievements under controlled conditions and the improvement of agronomic traits in the field, our knowledge of the nature of ABA in plants should be useful for increasing crop production, which is a global concern.

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