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Mechanisms of abscisic acid-mediated control of stomatal aperture

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Abstract

Drought stress triggers an increase in the level of the plant hormone abscisic acid (ABA), which initiates a signaling cascade to close stomata and reduce water loss. Recent studies have revealed that guard cells control cytosolic ABA concentration through the concerted actions of biosynthesis, catabolism as well as transport across membranes. Substantial progress has been made at understanding the molecular mechanisms of how the ABA signaling core module PYR/PYL/RCAR-PP2C-SnRK2 controls the activity of anion channels and thereby stomatal aperture. In this review, we focus on our current mechanistic understanding of ABA signaling in guard cells including the role of the second messenger Ca²⁺ as well as crosstalk with biotic stress responses.

Introduction

Guard cells form stomatal pores in the leaf epidermis, which enable plants to balance CO_2 uptake for photosynthesis and water loss via transpiration. Guard cells represent a powerful single-cell model system for understanding early signal transduction mechanisms in plants. They can sense and rapidly respond to a diverse set of environmental stimuli such as light, CO_2 , pathogen infection, and plant hormones in a cell-autonomous way [1,2]. In response to drought, plants synthesize the phytohormone abscisic acid (ABA) that induces stomatal closure, thereby reducing transpirational water loss. It has been shown that ABA is de-novo synthesized from C_{40} carotenoids and has also been proposed to be rapidly released from its

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inactive conjugate, ABA glucose ester (ABA-GE) [3,4]. Through complex signaling mechanisms ABA triggers efflux of anions and potassium via guard cell plasma membrane ion channels, resulting in decrease of turgor pressure in guard cells and stomatal closure (Figure 1). Recent *in vitro* and *in vivo* studies have revealed the molecular mechanisms of how ABA signaling is initiated and transduced into the turgor regulation response in guard cells. Here we review recent advances on ABA signaling in guard cells.

ABA biosynthesis, degradation, and transport in guard cells

A recent work showed that guard cells are capable of autonomously synthesizing ABA [5], providing evidence for classical observations [6]. The wilting phenotype of the Arabidopsis *aba3-1* mutant that lacks the final step of ABA biosynthesis (the conversion of ABA-aldehyde to ABA) [7] was complemented by guard cell-targeted expression of *ABA3* [5], suggesting that guard cell-autonomous ABA synthesis is sufficient for low humidity-induced stomatal closure. Hydrolysis of ABA-GE by β-glucosidase AtBG1 is a mechanism proposed for a rapid concentration increase of ABA [8]. Interestingly, the *aba3-1* mutant exhibited an induced expression of the ABA-GE-hydrolyzing enzyme AtBG1, indicating a putative but incomplete compensatory effect for the lack of *de-novo* ABA synthesis [5]. ABA is inactivated either through hydroxylation and subsequent catabolic degradation pathways or by conjugation with glucose. The hydroxylation of ABA in Arabidopsis guard cells is catalyzed by CYP707A1, which encodes the key ABA 8'-hydroxylase [9]. There are also indications for ABA-glucosylating enzyme activities in guard cells [10,11].

Transport of ABA across membranes can be passive as described by the 'ionic trap model' [12]. Active ABA uptake into Arabidopsis guard cells has been reported through the ABC transporter ABCG40 [13]. Another ABCG gene, ABCG22, which is also highly expressed in guard cells, is required for proper regulation of stomatal movements [14]. However, ABA transport activity of ABCG22 has not been proven yet. Four members of the NRT/PTR family have been characterized as ABA-IMPORTING TRANSPORTERS (AIT), of which AIT1 was implicated to mediate ABA uptake into guard cells of inflorescence stems [15]. The ABA efflux transporter DETOXIFICATION EFFLUX CARRIER 50 (DTX50) is expressed in guard cells and a T-DNA insertion mutant of the DTX50 gene exhibits a reduced water loss and ABA-hypersensitive stomatal closure [16]. FRET-based reporters for ABA (ABACUS, ABAleon) enable direct in vivo monitoring of ABA transport and the visualization of cytosolic ABA concentration ([ABA]_{cyt}) changes in real-time [17,18]. It was observed that guard cell [ABA]_{cvt} increases in response to NaCl treatment or a humidity drop, but not in response to sorbitol [17]. Compared to other cells or tissues, guard cells exhibit increased [ABA]_{cvt} [17]. Taken together with the guard cell autonomous ABA synthesis [5,6] and the expression of an ABA efflux transporter DTX50 [16] in guard cells, current data indicate that guard cells could also function as an ABA source.

Core ABA signal components in Guard Cells

The perception of ABA is achieved by members of the START protein family of ABA receptors, PYRABACTIN RESISTANCE 1 (PYR)/PYR1-LIKE (PYL)/REGULATORY COMPONENT OF ABA RECEPTOR (RCAR). In the presence of ABA, the PYR/PYL/

RCAR proteins bind to and inhibit clade A protein phosphatases type 2Cs (PP2Cs) [19,20], followed by activation of the Ca²⁺-independent protein kinases SNF1-RELATED KINASE 2s (SnRK2s), most importantly OPEN STOMATA 1 (OST1/SnRK2.6), which phosphorylate multiple downstream targets (reviewed in [21]). In guard cells, ABA causes activation of two types of plasma membrane anion channels, called slow-sustained (S-type) and rapid-transient (R-type) anion channels, which drives plasma membrane depolarization and subsequent K⁺ efflux through voltage-dependent K⁺ channels (reviewed in [22–24]) (Figure 1). The release of anions and K⁺ causes a reduction in the turgor pressure of guard cells, resulting in stomatal closure. In Arabidopsis guard cells, S-type and R-type anion channels are mainly encoded by SLOW ANION CHANNEL-ACCOCIATED 1 (SLAC1) [25,26] and ALUMINUM-ACTIVATED MALATE TRANSPORTER 12/QUICKLY ACTIVATING ANION CHANNEL 1 (ALMT12/OUAC1) [27,28], respectively. Several in vitro studies using Xenopus laevis oocytes show how the core ABA signaling module PYR/PYL/RCAR-PP2C-SnRK2 complex regulates SLAC1 and ALMT12/QUAC1 activity (Figure 1). In Arabidopsis guard cells, the GUARD CELL OUTWARD RECTIFYING K⁺ CHANNEL (GORK) accounts for the voltage-dependent K⁺ efflux channel (K⁺_{out}) activity [29,30]. Involvement of K⁺ UPTAKE TRANSPORTERs (KUPs) in guard cell K⁺ efflux during stomatal closure was also recently reported [31].

ABA regulation of Ca²⁺ Signaling in Guard Cells

It has been demonstrated in several plant species that cytosolic Ca^{2+} functions as a second messenger in guard cell ABA signaling. ABA-induced S-type anion channel activation and stomatal closure are suppressed by cytoplasmic loading of a Ca^{2+} chelator, 1,2-bis(2-aminophenoxy)ethane-N,N,N',N'-tetraacetic acid (BAPTA) in intact guard cells [32,33]. Interestingly, it has been also shown that guard cells exhibit spontaneous cytosolic free Ca^{2+} ([Ca^{2+}]_{cyt}) elevations and ABA does not cause [Ca^{2+}]_{cyt} elevations in all guard cells [34,35]. Furthermore, ABA enables [Ca^{2+}]_{cyt} activation of S-type anion channels [33]. These observations suggest that ABA turns on guard cell Ca^{2+} signaling by enhancing (priming) [Ca^{2+}]_{cyt} sensitivity of the downstream targets as well as by inducing [Ca^{2+}]_{cyt} elevations [22,34,35]. It has been reported that Ca^{2+} -DEPENDENT PROTEIN KINASES (CPKs) function as Ca^{2+} sensors that mediate the Ca^{2+} -dependent regulation of S-type anion channels [36–39]. Recent *in vitro* and *in vivo* studies identified a mechanism of how the Ca^{2+} -CPK-dependent pathway is integrated with PYR/PYL/RCAR-PP2C-SnRK2 in guard cells (Figure 1).

ABA causes guard cell $[Ca^{2+}]_{cyt}$ elevations through activation of plasma membrane Ca^{2+} permeable cation (I_{Ca}) channel and Ca^{2+} release from intracellular Ca^{2+} stores (reviewed in [22,35]). ABA activation of I_{Ca} channels requires PYR/PYL/RCAR ABA receptors [39,40], CPKs [36], and a receptor-like kinase GUARD CELL HYDROGEN PEROXIDE-RESISTANT1 (GHR1) [41]. The molecular mechanism of how ABA regulates Ca^{2+} release from intracellular Ca^{2+} stores remains to be clarified in detail.

Activation of S-type anion channel SLAC1 by protein kinases

Activation of S-type anion channels has been considered as a key step in stomatal closure. Several studies investigated the regulation of SLAC1 in Xenopus oocytes. When SLAC1 is expressed alone in *Xenopus* oocytes, no significant anion currents can be detected while coexpression of the Ca²⁺-independent OST1 or several CPKs evokes large anion currents [37,39,42–44]. The importance of this central drought stress signaling mechanism is highlighted by the conservation of the SLAC1 activation mechanism by OST1 in several land plant species [45,46]. OST1 and CPKs phosphorylate the N-terminus of SLAC1 [37,42–44]. Mass spectroscopy approaches revealed that OST1 could phosphorylate SLAC1 at Serine (S) 59, S86, S113, and S120 in vitro [47]. S59 is also phosphorylated by CPK6 [44]. When S120 of the SLAC1 N-terminus is mutated to non-phosphorylatable Alanine (A), SLAC1 cannot be activated by OST1 anymore, but activation by CPKs is still intact in Xenopus oocytes [37,39,43,44,48]. A second key amino acid for the SLAC1 activation in oocytes, S59, is required for the activation by CPK5, CPK6, and CPK23 but not OST1 [39,44,48]. Research in Arabidopsis guard cells showed that for in planta ABA activation of S-type anion channels, either S59 or S120 of SLAC1 is sufficient for complete guard cell ABA responses and only mutating both of the S59 and S120 impairs guard cell ABAresponses [39]. The SLAC1 S120F mutation impairs stomatal closing in response to ozone, elevated CO₂, and low humidity [47,49], which might be due to the effect of the bulky phenylalanine residue.

Although functional reconstitution of ABA activation of SLAC1 in *Xenopus* oocytes has been achieved by co-expression of either the Ca²⁺-dependent CPK6 or the Ca²⁺ independent OST1 protein kinase [44], it was recently found that disruption of either multiple CPKs or Ca²⁺-independent SnRK2s causes impairment of ABA activation of S-type anion channels. Use of these higher order *cpk* and *snrk2* mutants suggests that *in planta* both Ca²⁺-dependent and the Ca²⁺-independent branches are required for intact stomatal ABA responses [39]. The molecular mechanism of this interdependence is still unknown and subject of future research.

The role of the cytosolic C-terminal region of SLAC1 in the regulation of SLAC1 activity is still under investigation. Reports show that the SLAC1 C-terminus can be phosphorylated by OST1 [42,43], but not by CPK6 and CPK23 [37,44]. Replacement of Threonine (T) 513 in the SLAC1 C-terminus by Aspartate, which mimics phosphorylation, results in constitutive current activation, indicating a regulatory role of the SLAC1 C-terminus T513 [48]. A SLAC1 T513A mutant channel is still activated by OST1 and CPKs [48], which suggests that T513 is not strictly required for phosphorylation dependent activation of SLAC1. The Aspartate mutation of SLAC1 T513D may also have a structural impact on the channel rendering it constitutively active. The determination of the function of the SLAC1 C-terminus for SLAC1 regulation requires further research.

SLAC1 activation and phosphorylation by all of the above-mentioned protein kinases are inhibited by PP2Cs, for example by ABA-INSENSITIVE 1 (ABI1) and PROTEIN PHOSPHATASE 2CA (PP2CA) [37,42–44,48]. Recent research revealed the mechanism by which PP2Cs inhibit SLAC1 activation by protein kinases: While OST1 kinase activity is

directly regulated by PP2Cs [50,51], detailed biochemical analyses showed no evidence for a direct regulation of CPK protein kinase activity by ABI1 and PP2CA [39]. In vitro data showed that the PP2Cs could inhibit the activation of SLAC1 by CPKs via direct dephosphorylation of the channel [39,44]. It was initially reported that ABI1 is not able to dephosphorylate OST1-added phospho-groups at SLAC1 [43]. However, recent research shows that the OST1-phosphorylated SLAC1 N-terminus could be de-phosphorylated by PP2Cs [39,48]. The dual action of PP2Cs in directly down-regulating SnRK2.6/OST1 and SLAC1 ensures the tight and robust negative regulation of SLAC1 activity, a crucial mechanism ensuring plant stress adaption and resistance (Figure 1). In planta analyses revealed that GHR1, which encodes a receptor-like kinase localized on the plasma membrane, is involved in ABA- and hydrogen peroxide (H₂O₂)-induced stomatal closure [41]. GHR1 directly phosphorylates the SLAC1 N-terminus in vitro and activates the channel current in Xenopus oocytes. Although OST1, CPK6, and CPK23 activation of SLAC1 in *Xenopus* oocytes is inhibited by both PP2Cs, ABI1 and ABI2 [37,43,44], GHR1 activation of SLAC1 is inhibited by ABI2, but not ABI1 [41]. Together with a previous study [52], these results suggest different roles of each PP2C in guard cell ABA signaling. However, more detailed biochemical analyses are required to understand how PP2Cs downregulate GHR1 activation of the SLAC1 channel.

The CBL-INTERACTING PROTEIN KINASE 23 (CIPK23) was also reported to activate SLAC1 in oocytes when the Ca²⁺ sensing CALCINEURIN-B-LIKE 1 and 9 (CBL1 and CBL9) are co-expressed [48], but the role of CIPK23 in guard cell ABA signaling was not confirmed *in planta*.

PP2Cs-based Ca²⁺ sensitivity priming mechanism in guard cells

As intracellular Ca^{2+} represents a universal second messenger, a key question is how Ca^{2+} signaling specificity is achieved in plant cells. Stomatal closing stimuli, such as ABA and CO_2 prime $[Ca^{2+}]_{cyt}$ sensitivity in guard cells, thus enabling $[Ca^{2+}]_{cyt}$ activation of S-type anion channels [33,53,54]. A recent *in planta* electrophysiological study found that disruption of PP2Cs causes non-specific $[Ca^{2+}]_{cyt}$ activation of S-type anion channels [39]. These findings reveal a first mutant in guard cells that causes constitutively primed $[Ca^{2+}]_{cyt}$ signaling. Thus PP2Cs function as a master regulator that ensures Ca^{2+} signal specificity in guard cells. PP2Cs have also been shown to down-regulate ABA activation of I_{Ca} channels [52] (Figure 1).

Evolution and conservation of guard cell ABA signaling

Molecular biological and genomic analyses provide evidence that the core ABA signaling pathway consisting of PYR/PYL/RCAR, PP2Cs and OST1-like kinases and its target genes was established during the transition from an aquatic to a terrestrial environment over 400 million years ago [45,55,56]. Functional analysis in *Xenopus* oocytes using the homologs from organisms lacking stomata such as liverwort or alga supports this model [46]. An alternate view of ABA-mediated control of stomatal aperture has also been proposed [57–59]. This view is based on data obtained in evolutionary younger fern and lycophytes which show that stomata in these organisms respond poorly to endogenous ABA with the leaf

water potential being proposed as the major factor determining stomatal aperture in a passive-hydraulic mechanism [57,58]. Data on the functional role and evolution of stomata in bryophytes [60] appear to be more complex in particular since stomata are not present in all sub clades and current evolutionary models implicate the existence of three origins of stomatal emergence in tracheophytes [61]. Another layer of complexity is added by the dependence of ABA responsiveness on the developmental stage as stomata are relevant for desiccation of the spore capsule [62] and in hornworts stomata never close once they open [61]. CO₂ control of stomatal development has been observed in the fossil record and is considered to be an ancient trait in plants [63]. A recent study provides evidence that this CO₂ response requires intact ABA signaling, pointing to the hypothesis that ABA signaling itself evolved at the time of or before the developmental CO₂ response [63]. For stomatal closing responses, amplification of CO₂-induced stomatal closing by ABA was identified in classical studies [64] and studies have shown that partial CO₂ responses prevail in intact leaves of strongly ABA-insensitive mutants (e.g. [49]). The study of [63] also points to the open question whether or not CO₂ causes a rapid increase in the guard cell ABA concentration (within ca. 3 min of CO₂ exposure) or whether basal ABA signaling synergistically amplifies the CO₂ response as CO₂ and ABA target the same stomatal closing mechanisms. Further evidence for establishing the evolutionary timeline when functional ABA signaling gene expression appeared in guard cells could be helpful for further refinement of evolutionary models.

Regulation of stomatal movements by pathogens and interaction with ABA signaling

Open stomata represent main gateways for pathogen entry. Therefore, closing of stomata in response to pathogens and pathogen-associated molecular patterns (PAMPs) serves as the first line of defense against pathogen invasion [65]. Many studies have investigated the interplay of PAMP-mediated and ABA-mediated stomatal closure. Exposure of guard cells to pathogens and PAMPs activates S-type anion channels [66-69]. It has been shown that OST1 is required for stomatal closure induced by PAMPs including lipopolysaccharides [70], the flagellin peptide flg22 [69,70], and yeast elicitor (YEL) [68]. However it was also reported that flg22-induced stomatal closure is partially dependent on OST1 [71], and OST1 is not activated by flg22 [71] and YEL [68]. The ABA receptors PYL8/RCAR3 and PYL7/ RCAR2 and the PP2C PP2CA are not involved in Pseudomonas syringae pv tomato (Pst)and flg22-triggered stomata closing [72]. The PP2C ABI1 was reported as not involved in flg22-triggered stomatal closure [69], while an independent study shows ABI1 plays a role in YEL-mediated closure [68]. It is evident that further investigation is required for the role of early ABA signaling components including OST1 in biotic signaling in guard cells. The roles of CPKs in biotic signaling will also be of interest [67]. Roles of ABA biosynthesis in pathogen/MAMP-triggered stomatal closing are controversially discussed in Arabidopsis and tomato [69–71,73].

Reactive oxygen species (ROS) function as a second messenger in both guard cell ABA and biotic signaling. The NAD(P)H oxidases RESPIRATORY BURST OXIDASE HOMOLOG D (RBOHD) and RBOHF function in ABA-triggered ROS production and Ca²⁺ channel

activation in guard cells [74]. Recent biochemical analyses revealed that phosphorylation of RBOHD at distinct sites by CPKs and BOTRYTIS-INDUCED KINASE 1 (BIK1) is required for stomatal immunity to bacteria [75,76], indicating that RBOH and the downstream ROS production are key for the signal interaction between ABA and biotic signaling in guard cells. The detailed mechanisms were recently reviewed by [2].

Chemical genetics identified a novel small molecule 5-(3,4-dichlorophenyl)furan-2-yl]-piperidine-1-yl-methanethione (DFPM) that interferes with ABA signaling, including in guard cells [77]. DFPM inhibits ABA-induced stomatal closure and S-type anion channel activation. DFPM does not inhibit ABA-dependent interaction of PYR1 and ABI1 and ABA activation of SnRK2 protein kinases [77]. DFPM suppresses imposed Ca²⁺ oscillation-induced stomatal closure, suggesting that DFPM targets the Ca²⁺-dependent branch of ABA signaling. DFPM signaling requires *PHYTOALEXIN DEFICIENT4* (*PAD4*), and *ENHANCED DISEASE SUSCEPTIBILITY1* (*EDS1*). PAD4/EDS1 are known as central regulators of basal and effector-triggered immunity [77,78]. Furthermore, natural variation in the DFPM response among *Arabidopsis* accessions identified the immune-receptor-like VICTR (VARIATION IN COMPOUND TRIGGERED ROOT growth response) further establishing a link of DFPM to effector-triggered immune signaling [78]. Thus, DFPM provides a small molecule that enables specific dissection of crosstalk between an R-protein mediated-effector triggered immune responses and ABA signaling. Together these studies imply that multiple biotic signal inputs crosstalk with ABA signaling in guard cells.

Perspectives

Recent studies have proven that chemical control of ABA signaling is a promising potential strategy to improve drought tolerance of crop species. It was shown that synthetic ABA agonists can be utilized to induce stomatal closure and enhance drought tolerance [79,80]. In addition, a recent study elegantly proved the potential of controlling the ABA response by an engineered ABA receptor [81]. These findings also highlight the importance of basic research in this field towards addressing drought tolerance in crops. Because guard cells can synthesize ABA in a cell-autonomous manner and also take up ABA, a key question is which pathway is dominantly activated when guard cells respond to various stresses. Noninvasive single-cell imaging using ABA biosensors can answer this question in the future. Recent studies identified novel regulators that control plasma membrane localization and protein turnover of PYR/PYL/RCAR proteins [82,83], and their roles in guard cell ABA signaling remains to be determined. Single-cell metabolome and proteome analyses have identified an array of possible candidates as modulators of guard cell ABA and biotic signaling [84,85], but their function and regulation need to be investigated in detail. Electrophysiological studies using *Xenopus* oocyte systems have led to significant advances in our mechanistic understanding of guard cell ABA signaling and enable rapid testing of signaling mechanisms and models. However, observations from in planta analyses cannot be fully explained by these studies suggesting a more complex in planta network [39]. For example, in planta analyses demonstrate a strong dependence of Ca²⁺-dependent signaling on the Ca²⁺-independent ABA signaling pathway [39]. Along with oocyte electrophysiological and biochemical analyses, in planta analyses (e.g. higher-order mutants) will be required to understand in vivo guard cell ABA signaling.

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Highlight

- ABA triggers a robust signal network that controls stomatal closing
- Guard cell ABA levels are controlled by biosynthesis, catabolism, and transport
- SnRKs and CPKs are key for ABA activation of anion channels in guard cells
- PP2Cs down-regulate both Ca²⁺-independent and Ca²⁺-dependent ABA signaling branches
- Multiple biotic signal inputs target ABA signaling in guard cells

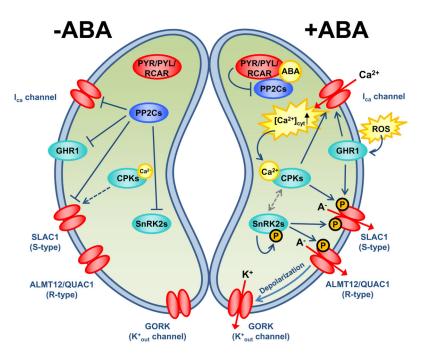


Figure 1. Schematic model of ABA signal transduction mechanisms in guard cells. (Left) In the absence of ABA, PP2Cs dephosphorylate SnRK2 protein kinases and the S-type anion channel SLAC1. Note that non-specific Ca²⁺ elevations are prohibited from activating stomatal closing mechanisms, as direct dephosphorylation of SLAC1 by PP2Cs prevents non-specific [Ca²⁺]_{cvt} activation of S-type anion channels [39]. (**Right**) In the presence of ABA, PYR/PYL/RCAR ABA receptors bind to and inhibit PP2Cs, followed by activation of the Ca²⁺-independent protein kinases SnRK2s, including OST1, possibly by autophosphorylation. Hyperpolarization-dependent Ca^{2+} -permeable cation (I_{Ca}) channels are released from PP2C-dependent down regulation, resulting in ABA-responsive [Ca²⁺]_{cvt} increases that activate CPKs. CPKs also are required for activation of ICa channels. ABAinduced Ca²⁺ release from intracellular Ca²⁺ stores is not shown in this figure for simplicity and due to the need to further characterize the detailed signaling mechanisms. The active SnRK2s and CPKs phosphorylate SLAC1 with preferential affinities at different sites and activate the channel. The SnRK2 protein kinase OST1 also phosphorylates and activates the R-type anion channel ALMT12/QUAC1. In planta roles of CPKs and PP2Cs in ALMT12/ QUAC1 regulation and possible direct cross-regulation of CPKs and SnRK2s need to be further investigated. Activation of the two types of anion channels causes sustained plasma membrane depolarization, which drives K⁺ efflux through the voltage-dependent outward K⁺ (K⁺_{out}) channel GORK. The loss of K⁺ and anion leads to guard cell turgor decrease and stomatal closure. NAD(P)H oxidase-mediated ROS production is involved in guard cell ABA signaling. The ROS possibly activate GHR1 that mediates ABA activation of I_{Ca} and S-type anion channels. Phosphorylation sites in SLAC1 mediated by GHR1 need to be identified.