



# PYL8 mediates ABA perception in the root through non-cell-autonomous and ligand-stabilization-based mechanisms

Borja Belda-Palazon<sup>a</sup>, Mary-Paz Gonzalez-Garcia<sup>b</sup>, Jorge Lozano-Juste<sup>a</sup>, Alberto Coego<sup>a</sup>, Regina Antoni<sup>a</sup>, Jose Julian<sup>a</sup>, Marta Peirats-Llobet<sup>a</sup>, Lesia Rodriguez<sup>a</sup>, Ana Berbel<sup>a</sup>, Daniela Dietrich<sup>c</sup>, Maria A. Fernandez<sup>a</sup>, Francisco Madueño<sup>a</sup>, Malcolm J. Bennett<sup>c</sup>, and Pedro L. Rodriguez<sup>a,1</sup>

<sup>a</sup>Instituto de Biología Molecular y Celular de Plantas, Consejo Superior de Investigaciones Científicas–Universidad Politécnica de Valencia, ES-46022 Valencia, Spain; <sup>b</sup>Centro Nacional de Biotecnología–Consejo Superior de Investigaciones Científicas, Cantoblanco, E-28049 Madrid, Spain; and <sup>c</sup>Centre for Plant Integrative Biology, School of Biosciences, University of Nottingham, Nottingham LE12 5RD, United Kingdom

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The phytohormone abscisic acid (ABA) plays a key role regulating root growth, root system architecture, and root adaptive responses, such as hydrotropism. The molecular and cellular mechanisms that regulate the action of core ABA signaling components in roots are not fully understood. ABA is perceived through receptors from the PYR/PYL/RCAR family and PP2C coreceptors. PYL8/RCAR3 plays a nonredundant role in regulating primary and lateral root growth. Here we demonstrate that ABA specifically stabilizes PYL8 compared with other ABA receptors and induces accumulation of PYL8 in root nuclei. This requires ABA perception by PYL8 and leads to diminished ubiquitination of PYL8 in roots. The ABA agonist quinabactin, which promotes root ABA signaling through dimeric receptors, fails to stabilize the monomeric receptor PYL8. Moreover, a PYL8 mutant unable to bind ABA and inhibit PP2C is not stabilized by the ligand, whereas a PYL8<sup>SKR</sup> mutant is more stable than PYL8 at endogenous ABA concentrations. The PYL8 transcript was detected in the epidermis and stele of the root meristem; however, the PYL8 protein was also detected in adjacent tissues. Expression of PYL8 driven by tissue-specific promoters revealed movement to adjacent tissues. Hence both inter- and intracellular trafficking of PYL8 appears to occur in the root apical meristem. Our findings reveal a non-cell-autonomous mechanism for hormone receptors and help explain the nonredundant role of PYL8-mediated root ABA signaling.

ABA | PYL8 | non-cell-autonomous | ABA biosensor | root

Responses to environmental conditions in plant roots are coordinated by different hormones. Thus, hormone signaling regulates root growth, root system architecture, and tropic root responses (1–3). Abscisic acid (ABA) mediates root responses to different environmental factors, such as the presence of nitrate in the soil, water deficit, moisture gradients, and salt or nutrient deficiency (4). ABA signaling through the PYRABACTIN RESISTANCE1 (PYR1)/PYR1-LIKE (PYL)/REGULATORY COMPONENTS OF ABA RECEPTORS (RCAR)-Protein phosphatases type 2C (PP2Cs) and ABA-activated SNF1-related protein kinases (SnRK2s) core components is linked to different plant adaptive responses to water deficit and osmotic and salt stress, such as the maintenance of primary root elongation and the repression of lateral root formation (4–10). For example, in maize seedlings under water-deficit stress the primary root growth is maintained through ABA action, which acts partially through ethylene antagonism (5). In *Arabidopsis* roots exposed to salt stress, ABA also has a growth-promoting role during the recovery phase (11). Additionally, ABA signaling is required for root hydrotropism, an adaptive response that facilitates soil exploration under heterogeneous water availability (3). Regulation of root growth by ABA is closely connected with hydrotropism, as the hydrotropic response involves asymmetric ABA signaling in the root cortex through the PYR/PYL/RCAR-PP2C-SnRK2 core signaling pathway (3, 12, 13). Other environmental cues, such as salinity, induce root adaptations

that are mediated by ABA (10, 14, 15). Nutrient-induced root plasticity is also regulated by ABA, for example, the suberization of the endodermis in response to either sodium chloride treatment or sulfur or potassium deficiencies (14). Thus, harmful minerals can be excluded by the endodermis.

Although the role of ABA in root physiology has been well studied, the molecular and cellular mechanisms that operate to coordinate the action of core components are not well known. For example, the expression of the ABA-activated kinase SnRK2.2 is observed in all root tissues, but expression of the ABA receptor promoters is restricted to some of them (3, 13). Therefore, it is not well known how ABA perception is connected with the activation of SnRK2.2 in different root tissues. Additionally, different PYR/PYL/RCAR ABA receptors are expressed at high levels and contribute to the quantitative regulation of ABA sensitivity in the root, but uniquely the *pyl8/rcar3* single knockout shows reduced sensitivity to ABA-mediated inhibition of root growth (8, 13). Therefore, PYL8/RCAR3 plays a nonredundant role for ABA signaling in the root, which relies on PYL8-mediated inhibition of at least five clade A PP2Cs, i.e., HAB1, HAB2, ABI1, ABI2, and PP2CA (13). Compared with other ABA receptors, PYL8 shows a unique expression pattern in the root epidermis and lateral root cap (LRC) (13). Recent studies investigating the degradation of ABA receptors in seedlings have revealed

## Significance

The phytohormone abscisic acid (ABA) controls root responses to environmental signals such as abiotic stress. ABA signaling in roots depends on the nonredundant role of the PYL8 receptor. This study reveals special features of this ABA receptor. ABA binding triggers hormone-dependent stabilization of PYL8 through reduced ubiquitination and induces nuclear localization of the receptor. ABA-induced stabilization also allows movement of the PYL8 receptor from the root epidermis and stele to adjacent tissues. Hence, like mobile transcription factors that regulate plant development, the PYL8 protein can move between cells. In summary, our study reports a novel non-cell-autonomous mechanism to regulate hormone perception and root growth.

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<sup>1</sup>To whom correspondence should be addressed. Email: prodriquez@ibmcp.upv.es.

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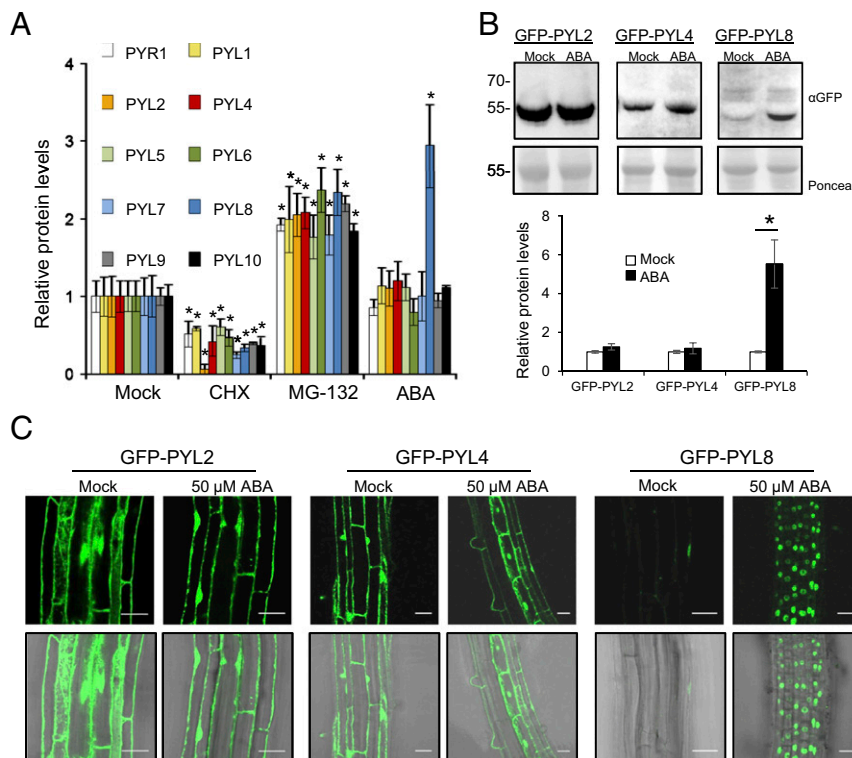
that PYL8 is ubiquitinated and degraded by the 26S proteasome in *Arabidopsis thaliana* (16, 17). In those studies, we found that ABA treatment increased PYL8 protein levels, but had no significant effect on other receptors such as PYR1 and PYL4 (17). Moreover, ABA treatment limited PYL8 degradation in seedlings and reduced PYL8 polyubiquitination (16). It is currently unknown whether such a mechanism operates in root tissues or whether ligand perception by either PYL8 or other receptors is required to stabilize PYL8. Further investigation of ligand-induced effects on PYL8 stability might help explain its nonredundant role for ABA signaling in roots.

Studies to investigate how different hormones control root growth, tropic root responses, or stress adaptation have revealed single tissue layers or discrete spatial domains that are differentially targeted by hormones (1). For example, auxin targets elongating epidermal cells during the gravitropic response whereas ABA targets elongating cortical cells during the hydrotropic response (3, 18). On the other hand, endodermal ABA signaling promotes lateral root quiescence under saline conditions (9). ABA also promotes quiescence of the quiescent center (QC), which may be considered as positive regulation of root growth as it promotes QC maintenance (19). However, ABA also inhibits cell division in the proximal part of the *Arabidopsis* root meristem, which can explain the inhibitory effect of high ABA concentrations on root growth (19). In contrast, low levels of ABA promote root elongation through an increased rate of cell production and elongation (3). ABA signaling is also important in the mature root, where most of the absorption of minerals and water takes place (8). In agreement with the above-mentioned physiological studies, the

expression pattern of SnRK2.2 indicates that ABA signaling is required in all root tissues (3). Altogether, these studies suggest that ABA perception in different root domains is important to regulate root physiology and root growth; however, a detailed molecular and cellular understanding of root ABA perception is still lacking in the different root tissues where ABA acts.

## Results

**ABA Specifically Stabilizes the PYL8 Receptor.** ABA receptor stability and degradation is an emerging topic in ABA signaling (16, 17, 20, 21). To obtain a comprehensive picture of the turnover of ABA receptors, we analyzed protein dynamics of 10 epitope (HA)-tagged receptors (PYR1, PYL1, PYL2, PYL4, PYL5, PYL6, PYL7, PYL8, PYL9, and PYL10, the most highly expressed gene products of the gene family) in 2-wk-old plants. Treatment with the translation inhibitor cycloheximide (CHX) led to diminished protein synthesis of all ABA receptors, whereas treatment with the proteasome inhibitor MG132 led to their accumulation (Fig. 1A). Interestingly, addition of ABA specifically led to the accumulation of PYL8 protein (Fig. 1A). ABA treatment of transgenic lines that express GFP-tagged versions of PYL2, PYL4, and PYL8 also revealed a selective ABA-induced accumulation of PYL8 (Fig. 1B and C). qRT-PCR analyses corroborated that this effect was not caused by changes in the expression of 35S promoter-driven 3HA- or GFP-tagged transgenes (*SI Appendix, Fig. S1*). ABA therefore appears to enhance PYL8 accumulation in these lines through a posttranscriptional mechanism. Confocal laser scanning microscopy (CLSM) also revealed that GFP-PYL8 exhibited a predominantly nuclear localization in root cells following ABA treatment, whereas



**Fig. 1.** ABA treatment specifically increases PYL8 protein levels in seedlings. (A) Effect of CHX, MG132, or ABA treatment on protein levels of HA-tagged receptors. The 10-d-old seedlings expressing HA-tagged receptors were either mock or chemically treated with 50  $\mu$ M CHX, MG132, or ABA for 6 h. Immunoblot analysis using anti-HA was performed to quantify protein levels. A single asterisk (\*) indicates  $P < 0.05$  (Student's  $t$  test) compared with the corresponding mock-treated sample. (B) Effect of ABA treatment on GFP-PYL2, GFP-PYL4, and GFP-PYL8 protein levels. Seedlings expressing GFP-tagged PYL proteins were either mock- or 50  $\mu$ M ABA-treated for 6 h. Immunoblot analysis using anti-GFP was performed to quantify protein levels. (C) ABA treatment leads to selective accumulation of GFP-PYL8 in the nucleus. CLSM analysis of the *Arabidopsis* root differentiation zone in lines expressing GFP-tagged PYL proteins that were either mock- or ABA-treated for 1 h. (Scale bars, 30  $\mu$ m.)

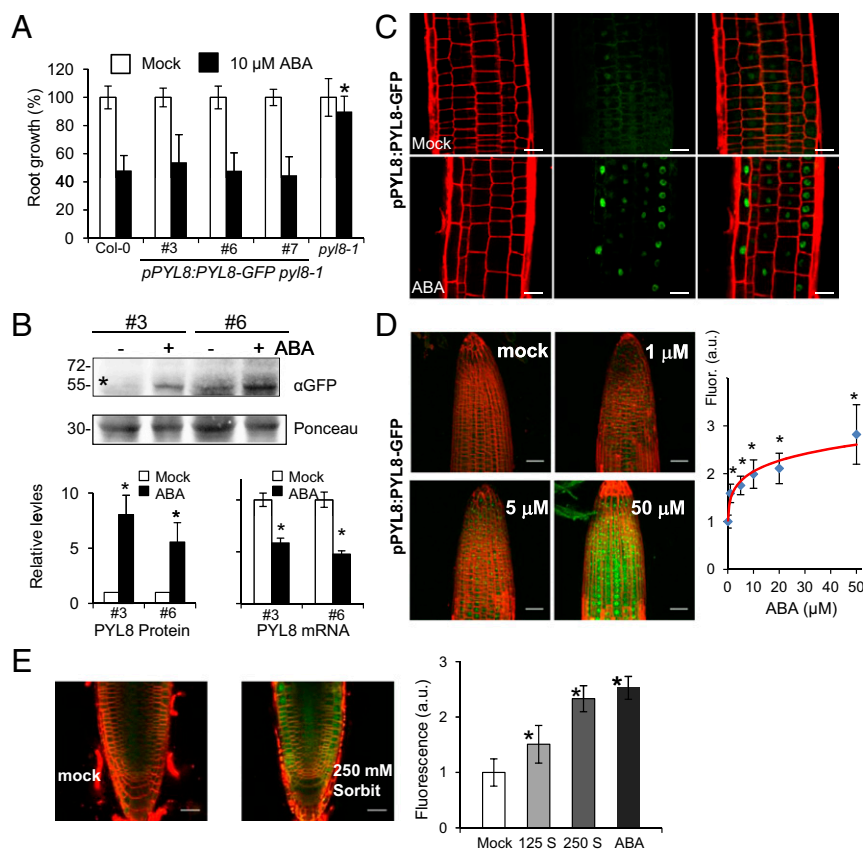
GFP-PYL2 and GFP-PYL4 localized to both the nucleus and cytosol of mock or ABA-treated roots (Fig. 1C).

To gain insight on the root localization of PYL8, we expressed PYL8-GFP driven by its own promoter in a *pyl8-1* mutant background (*ProPYL8:PYL8-GFP pyl8-1*). PYL8-GFP complemented the ABA-insensitive *pyl8-1* phenotype in a root growth assay, indicating that PYL8-GFP is functional (Fig. 2A). Next, we analyzed PYL8-GFP protein levels in roots by immunoblotting and found that these protein levels increased five- to sevenfold after ABA treatment (Fig. 2B). qRT-PCR analysis showed that ABA treatment does not induce up-regulation of the *PYL8* transcript; in fact, ABA down-regulates *PYL8* gene expression (Fig. 2B), in agreement with previous reports in seedlings (22, 23). Instead, ABA treatment led to an accumulation of PYL8-GFP in the nucleus, as observed for GFP-PYL8 expressed from a 35S promoter (Figs. 1C and 2C). Next, we investigated whether PYL8-GFP fluorescence may report changes in ABA concentration in the root. A dose-response analysis indicated that PYL8-GFP fluorescence was sensitive to changes in ABA concentration induced by exogenous ABA addition or osmotic stress (Fig. 2D and E and *SI Appendix, Fig. S2 A and B*). Finally, a kinetic analysis of PYL8-GFP fluorescence was performed in response to 10  $\mu$ M ABA treatment,

and a gradual increase of the fluorescent signal, which could be detected from 30 min after ABA treatment, was observed (*SI Appendix, Fig. S2C*). We conclude that ABA specifically stabilizes the PYL8 receptor and leads to its accumulation in root-cell nuclei.

### PYL8 Stabilization in Roots Is Triggered by Ligand Binding and Requires PP2C Interaction.

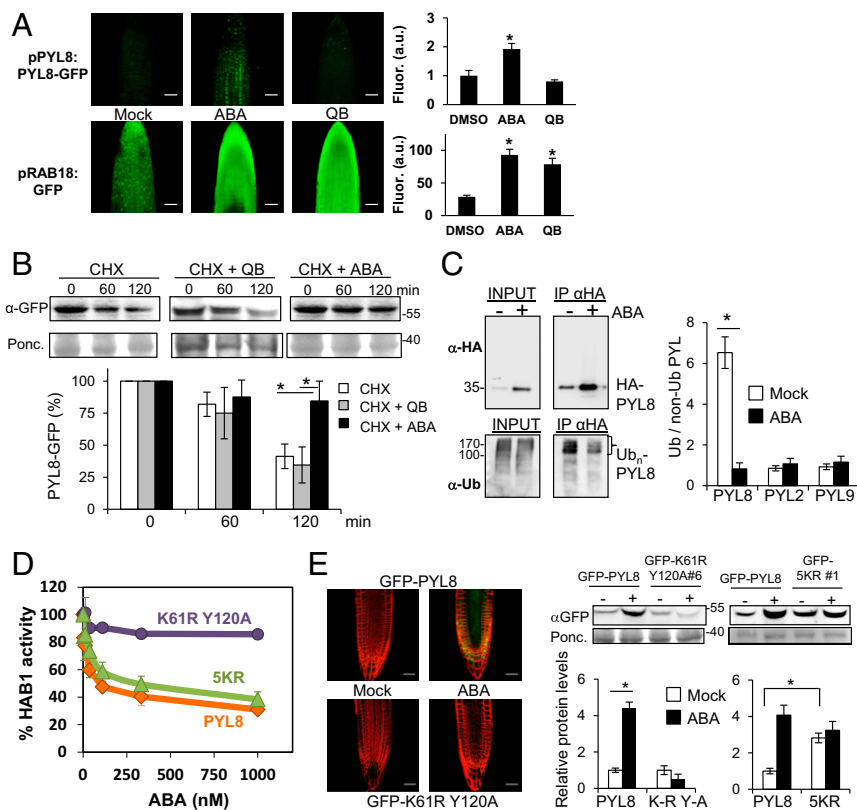
To investigate whether the enhanced PYL8-GFP fluorescence observed after ABA treatment requires ligand perception by PYL8 or simply reflects hormone signaling through other ABA receptors that also operate in the root (13), we switched on ABA signaling through quinabactin (QB) treatment. QB is an ABA agonist that does not activate the PYL8 receptor (*SI Appendix, Fig. S3A*) but instead activates ABA signaling primarily through dimeric ABA receptors such as PYR1, PYL1, and PYL2, which are expressed at a high level in the root and contribute to the quantitative regulation of ABA signaling (13, 24, 25). QB treatment was able to up-regulate the expression of the ABA-responsive ProRAB18:GFP reporter, but, in contrast to ABA, QB did not enhance PYL8-GFP fluorescence (Fig. 3A). Therefore, the PYL8-GFP accumulation appears to require ABA perception by PYL8.



**Fig. 2.** ABA increases PYL8 protein levels in roots through a posttranscriptional mechanism. (A) PYL8-GFP complements the ABA-insensitive *pyl8-1* phenotype. The 5-d-old seedlings germinated on Murashige and Skoog plates were transferred to new plates lacking or supplemented with 10  $\mu$ M ABA, and quantification of root growth was performed after 10 d. Data are averages  $\pm$ SD from three independent experiments ( $n = 20$ ). A single asterisk (\*) indicates  $P < 0.05$  (Student's  $t$  test) compared with Col-0 in the same assay conditions. (B) ABA treatment leads to accumulation of PYL8-GFP protein and down-regulation of *PYL8-GFP* mRNA in roots. The 10-d-old seedlings expressing PYL8-GFP were either mock- or 50  $\mu$ M ABA-treated for 3 h and protein or RNA extracted from root tissue. Immunoblot analysis using anti-GFP was performed to quantify protein levels of PYL8-GFP (asterisk) in roots. A major 30-kDa root protein was used to normalize protein loading. qRT-PCR analyses were performed to quantify mRNA expression of PYL8-GFP. A single asterisk (\*) indicates  $P < 0.05$  (Student's  $t$  test) compared with mock-treated samples. (C) ABA treatment leads to accumulation of PYL8-GFP in the nucleus. CLSM analysis of *Arabidopsis* root expressing ProPYL8:PYL8-GFP in the *pyl8-1* background after mock or ABA treatment for 6 h. (Scale bars, 25  $\mu$ m.) (D) Dose-response analysis of PYL8-GFP accumulation in response to treatment with the indicated ABA concentrations for 6 h. Fluorescence was quantified in arbitrary units (a.u.) using images acquired by CLSM. (E) Accumulation of PYL8-GFP after 250 mM sorbitol treatment. Fluorescence was measured after treatment with 125 or 250 mM sorbitol (S) or 50  $\mu$ M ABA for 3 h. (Scale bars, 30  $\mu$ m.) A single asterisk indicates  $P < 0.05$  (Student's  $t$  test) compared with mock-treated samples.

To ascertain whether ABA treatment leads to decreased degradation of PYL8 in roots, we performed a CHX  $\pm$  ABA experiment using the *ProPYL8:PYL8-GFP pyl8-1* line and analyzed PYL8 protein levels in roots (Fig. 3B). While CHX treatment in the absence of ABA led to a 60% reduction of PYL8 after 120 min, the simultaneous presence of ABA slowed PYL8 degradation to a reduction of only 20%. QB was not effective in slowing PYL8 degradation (Fig. 3B). ABA may prevent degradation of PYL8 in roots through reduced polyubiquitination of the receptor (16). To investigate this possibility, we performed immunoprecipitation of HA-PYL8 in mock and ABA-treated root samples. Immunoprecipitated HA-PYL8 was analyzed using anti-HA and anti-Ub (P4D1) antibodies and the ratio of Ub(n)-PYL8 to PYL8 was found to be approximately sixfold higher in mock compared with ABA-treated roots (Fig. 3C). Thus, even though the total PYL8 protein level was increased about fourfold after ABA treatment, the amount of polyubiquitinated PYL8 was diminished in ABA-treated roots compared with mock conditions (Fig. 3C). In contrast, ABA treatment did not affect the ubiquitination ratio of PYL2 and PYL9 compared with mock conditions (Fig. 3C).

The results described above using QB treatment suggest that PYL8 stabilization and/or accumulation requires ABA perception by the receptor. To obtain further evidence, we analyzed the  $\text{PYL8}^{\text{K61R Y120A}}$  mutant, which is predicted to be unable to bind ABA because it is impaired in the salt bridge formed between the highly conserved K61 residue and the ABA carboxylate, and the hydrogen bond formed by Y120 with the ABA carboxylate group through an internal water molecule (13). Accordingly, the recombinant  $\text{PYL8}^{\text{K61R Y120A}}$  protein was unable to inhibit PP2C HAB1 (Fig. 3D). We generated GFP- $\text{PYL8}^{\text{K61R Y120A}}$  transgenic lines and analyzed them following ABA treatment (Fig. 3E). Both CLSM and immunoblot analysis of root protein extracts revealed that GFP- $\text{PYL8}^{\text{K61R Y120A}}$  fails to accumulate after ABA treatment, in contrast to wild-type PYL8 (Fig. 3E). We conclude that either ABA perception and/or PP2C interaction are required to trigger PYL8 stabilization. Recent proteomic studies led to the identification of ubiquitinated residues in PYL8 (26). In contrast to the K61 residue that affects ABA binding, other N-terminal Lys residues of PYL8 are not predicted to be involved in ABA binding (26). We therefore decided to mutate those Lys residues that are



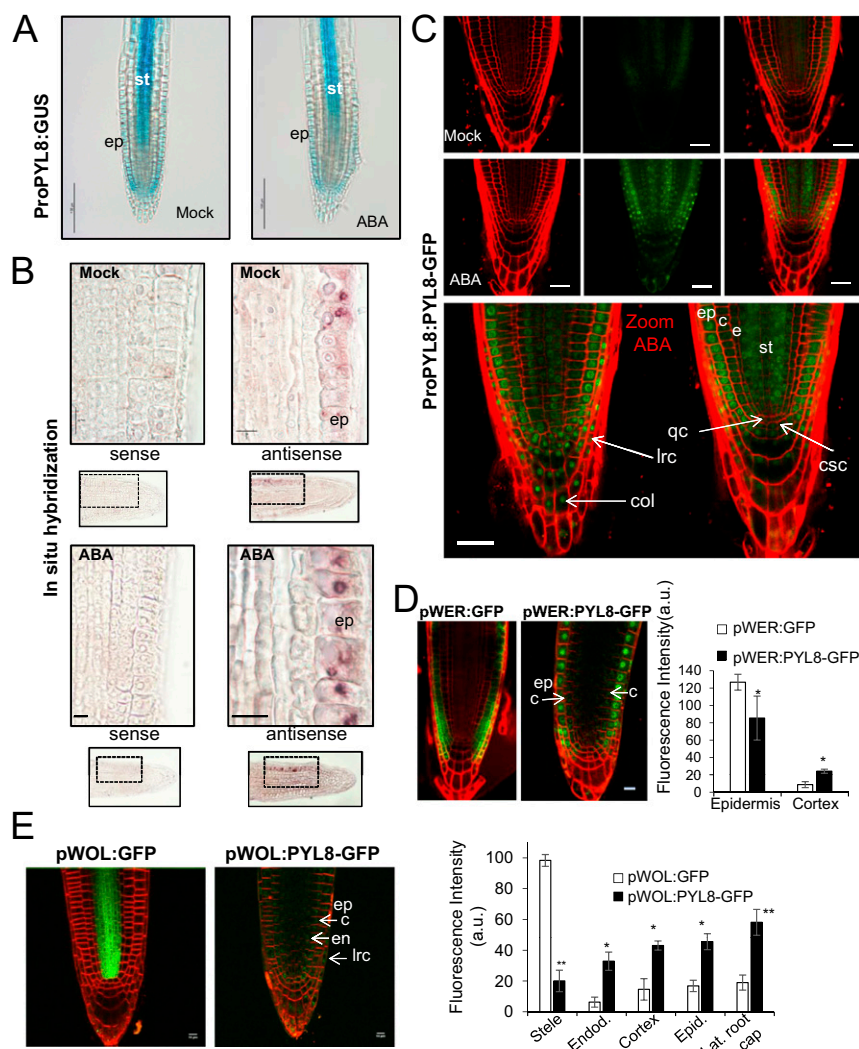
**Fig. 3.** ABA perception by PYL8 is required to trigger its stabilization via reduced receptor ubiquitination. (A) QB treatment does not lead to accumulation of PYL8-GFP. QB induces ABA signaling in the root as revealed by the pRAB18:GFP reporter. CLSM analysis of *Arabidopsis* root apex expressing either ProPYL8:PYL8-GFP in the *pyl8-1* background or ProRAB18:GFP in wild type after mock, 20  $\mu\text{M}$  ABA, or 50  $\mu\text{M}$  QB treatment for 1 h. A single asterisk indicates  $P < 0.05$  (Student's *t* test) compared with mock (DMSO)-treated sample. (B) ABA prevents degradation of PYL8-GFP in roots whereas QB does not. The 10-d-old seedlings expressing PYL8-GFP were treated with 50  $\mu\text{M}$  ABA for 6 h to induce accumulation of PYL8. After washing out ABA, a CHX treatment in the absence or presence of 50  $\mu\text{M}$  ABA or QB was performed for 60 or 120 min. Protein extracts of roots were analyzed using an anti-GFP antibody ( $\alpha$ -GFP). The histogram shows the quantification of the PYL8-GFP protein during the CHX treatment. A single asterisk indicates  $P < 0.05$  (Student's *t* test) when CHX + ABA treatment was compared with CHX or CHX + QB treatments, respectively. (C) ABA treatment increases total HA-PYL8 protein levels in root but reduces polyubiquitinated PYL8 forms. Protein extracts were prepared from mock or ABA-treated root samples and submitted to immunoprecipitation using anti-HA antibodies. Immunoprecipitated PYL8 (IP  $\alpha$ HA) was analyzed by immunoblotting using anti-HA and anti-Ub (P4D1) antibodies. The ratio of polyubiquitinated to non-Ub PYL8, PYL2, and PYL9 protein was quantified in mock- and ABA-treated samples. A single asterisk indicates  $P < 0.05$  (Student's *t* test) compared with the ABA-treated sample. (D) The  $\text{PYL8}^{\text{K61R Y120A}}$  mutant is unable to inhibit PP2C HAB1, whereas activity of  $\text{PYL8}^{\text{5KR}}$  is similar to PYL8 wild type. Phosphatase activity of HAB1 was measured in the presence of PYL8 wild type,  $\text{PYL8}^{\text{K61R Y120A}}$ , or  $\text{PYL8}^{\text{5KR}}$  mutants and different ABA concentrations. (E) CLSM of *Arabidopsis* root apex (Left) and immunoblot analysis of root protein extracts reveal that the  $\text{PYL8}^{\text{K61R Y120A}}$  mutant is not stabilized by ABA. Transgenic seedlings expressing GFP-PYL8, GFP- $\text{PYL8}^{\text{K61R Y120A}}$ , or GFP- $\text{PYL8}^{\text{5KR}}$  were either mock- or 50  $\mu\text{M}$  ABA-treated for 3 h, root protein extracts were prepared, and immunoblot analysis was performed using anti-GFP to quantify protein levels (Right). A single asterisk (\*) indicates  $P < 0.05$  (Student's *t* test) when the indicated samples were compared. (Scale bars, 30  $\mu\text{m}$ .)

potential ubiquitination sites (26) but presumably do not impair PYL8 function—i.e., Lys24, Lys38, Lys59, Lys70, and Lys84—and generated the quintuple Lys-Arg PYL8 mutant (abbreviated as 5KR). We found that in vitro activity of the 5KR mutant was comparable to wild-type PYL8 (Fig. 3D). Interestingly, GFP- and HA-tagged lines of PYL8<sup>5KR</sup> showed a two- to threefold increase of protein levels compared with wild type in the absence of exogenous ABA treatment (Fig. 3E and *SI Appendix, Fig. S3B*). We analyzed seedling establishment in the presence of 0.5  $\mu$ M ABA and ABA-mediated inhibition of root growth in response to 10  $\mu$ M ABA (*SI Appendix, Fig. S3 C and D*). In both cases, HA-tagged lines of PYL8<sup>5KR</sup> showed enhanced sensitivity to ABA compared with lines expressing wild-type PYL8. These results suggest that ubiquitination and regulation of PYL8 protein stability is crucial for proper response to ABA.

To investigate whether intracellular movement of PYL8 affects plant sensitivity to ABA, we compared subcellular localization and ABA sensitivity of GFP-PYL8, GFP-PYL8<sup>5KR</sup>, and

GFP-PYL8<sup>K61R Y120A</sup> lines (*SI Appendix, Fig. S4*). The line expressing GFP-PYL8, which accumulates GFP-PYL8 in the nucleus after ABA treatment, shows enhanced sensitivity in ABA-mediated inhibition of root growth and repression of lateral root formation compared with wild-type Col-0 (*SI Appendix, Fig. S4*). Some nuclear accumulation of GFP-PYL8<sup>5KR</sup> was observed at endogenous ABA levels (*SI Appendix, Fig. S4A*), which correlated with enhanced sensitivity to ABA compared with GFP-PYL8 line (*SI Appendix, Fig. S4 B and C*; see also *SI Appendix, Fig. S3 C and D*). In contrast, lines expressing GFP-PYL8<sup>K61R Y120A</sup>, which does not accumulate in the nucleus after ABA treatment, behave as wild-type Col-0 in root growth assays (*SI Appendix, Fig. S4*). Therefore, nuclear accumulation of GFP-PYL8 induced by ABA is required for ABA response.

**PYL8 Behaves Non-Cell-Autonomously in Root Tissues.** To study the effect of ABA treatment on PYL8 expression in the root apex, we performed  $\beta$ -glucuronidase (GUS) staining after mock or 50  $\mu$ M



**Fig. 4.** Expression of PYL8 transcript and protein in roots. (A) GUS expression driven by the ProPYL8:GUS gene in the root apex. GUS staining after mock or 50  $\mu$ M ABA treatment. (Scale bars, 100  $\mu$ m.) (B) Localization of PYL8 mRNA in the root apex. In situ hybridization was performed on longitudinal sections of the root apex of mock- or 50  $\mu$ M ABA-treated seedlings using PYL8 antisense or sense probes. The PYL8 transcript was visualized using anti-digoxigenin-AP antibody and nitro-blue tetrazolium/5-bromo-4-chloro-3-indolyl-phosphate staining. (Scale bars, 10  $\mu$ m.) (C) CLSM visualization of PYL8-GFP driven by the PYL8 promoter after mock or ABA treatment. Localization of PYL8-GFP after ABA treatment was detected in the root apical meristem, columella, and LRC. (Scale bars, 25  $\mu$ m.) c, cortex; col, columella; csc, columella stem cells; e, endodermis; ep, epidermis; lrc, LRC; qc, quiescent center; st, stele. (D and E) CLSM visualization of GFP or PYL8-GFP proteins expressed under the control of the pWER and pWOL promoters in *pyl8-2* background. To stabilize PYL8, seedlings were treated with 50  $\mu$ M MG132 and ABA for 6 h. (Scale bars, 10  $\mu$ m.) Histograms indicate tissue-scale measurements of CLSM images using CellSeT software. \* $P < 0.05$  and \*\* $P < 0.01$  (Student's *t* test) compared with GFP control.

ABA treatment for 3 h (Fig. 4A). In control root apices, GUS expression driven by the *PYL8* promoter was detected in LRC, root epidermis, and stele cells (*SI Appendix*, Fig. S5A and B), as previously reported (13). This *PYL8* expression pattern was similar in ABA-treated plants, although some attenuation of *PYL8* expression was apparent (Fig. 4A). To gain further insight about the expression of *PYL8* in the root apex, we performed *in situ* hybridization using a digoxigenin-labeled antisense RNA probe to detect the *PYL8* mRNA in Col-0 (Fig. 4B). Under both mock and ABA-treatment conditions, the *PYL8* transcript was detected mainly in the epidermis. Weak staining of stele cells using the antisense RNA probe was also detected, but was attenuated after ABA treatment (Fig. 4B).

Since ABA signaling has been reported to regulate distinct processes in different root tissues (3, 9, 19) and *PYL8* plays a key role in root ABA perception, we investigated the localization of the *PYL8* protein in the root apex. Using CLSM, we analyzed the Pro*PYL8*:*PYL8*-GFP lines after either mock or ABA treatments. Interestingly, expression of *PYL8*-GFP in mock-treated roots was weakly detected in the epidermis and stele, whereas following ABA treatment it was clearly visible in LRC, epidermis, cortex, endodermis, stele, QC, and columella cells (Fig. 4C). *PYL8*-GFP expression in the epidermis was markedly enhanced by ABA treatment (*Movie S1*). Since the *PYL8* transcript was not detected in the cortex or endodermis, we conclude that the *PYL8* protein is translocated to adjacent tissues from cells where it is initially synthesized. This movement is reminiscent of mobile transcription factors (TFs) such as *SHORT ROOT* (*SHR*) that regulate root development (27). To further investigate the movement of *PYL8* between different root layers, we expressed *PYL8*-GFP driven by *WER* and *WOL* tissue-specific promoters (3) (*SI Appendix*) and examined the localization of the fluorescent protein by CLSM (Fig. 4D and E). Quantification of CLSM images was performed with an updated version of CellSeT software (Fig. 4D and E), which performs tissue-scale measurements from confocal microscope images (*SI Appendix*). When *PYL8*-GFP was expressed under control of the *WER* promoter, which drives expression in the epidermis and LRC (as confirmed by a *pWER*:*GFP* control), we could also detect *PYL8*-GFP at least in cortex cells (Fig. 4D). In the case of *WOL*-driven expression, whereas the GFP control was detected in the root vascular cylinder and pericycle as expected, we could detect *PYL8*-GFP additionally in the LRC, epidermis, cortex, and endodermis (Fig. 4E). Taken together, these results suggest that the *PYL8* protein can move from the cells where its transcript is produced.

The ABA-insensitive phenotype of *pyl8-2* in root growth assays was not complemented when *PYL8* was expressed driven by either *WER* or *WOL* promoters (*SI Appendix*, Fig. S6). *PYL8* mRNA expression driven by its endogenous promoter is mostly localized in the LRC, epidermis, and the vascular bundle and is able to complement the ABA insensitivity of *pyl8* in root growth assays (Fig. 2A). Driven by the *WER* promoter, *PYL8* protein was markedly detected in LRC and epidermis and weakly in cortex, suggesting that complementation requires intercellular movement of the protein to other root layers. Driven by the *WOL* promoter, *PYL8* protein was detected in most of root tissues; however, expression levels were markedly lower than those obtained using the endogenous *PYL8* promoter (Fig. 4C and E). Therefore, although intercellular movement of the protein seems to be necessary, it is not sufficient unless suitable levels of the protein are achieved. Taken together, these results suggest that combined expression in the epidermis and vascular bundle is required for complementation of the *pyl8* phenotype (Fig. 2A).

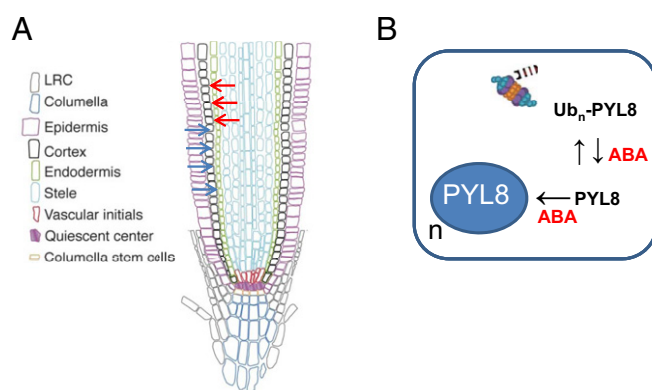
Finally, given the importance of ABA signaling in the mature root, expression of *PYL8*-GFP was examined in the root differentiation zone after ABA treatment and was localized in the epidermis, cortex, endodermis, pericycle, and vascular tissue (*SI Appendix*, Fig. S5C and D). In particular, a 3D reconstruction

after CSLM imaging revealed the presence of *PYL8* in procambial cells of the vascular tissue (*Movie S2*), which suggests a possible role of *PYL8* in vascular development.

## Discussion

We report that, unlike other ABA receptors, *PYL8* exhibits distinct regulatory properties. For example, *PYL8* is transcribed in the epidermis and stele of the root apex, but the *PYL8* protein is also present in the cortex and endodermis. Hence, comparison of the *PYL8* transcript expression with the localization of the *PYL8* protein reveals translocation of the ABA receptor from epidermis or stele to adjacent tissues, including the cortex and endodermis (Fig. 5A). Moreover, when *PYL8*-GFP was expressed driven by the *WOL* promoter, which is specifically expressed in the root vascular cylinder, the protein moved as far as the LRC (Fig. 4E). Hence, *PYL8* appears to regulate ABA signaling in the root apex through a non-cell-autonomous mechanism. However, it seems that both intercellular movement and appropriated protein levels are required for complementation of the ABA-insensitive phenotype of *pyl8* in root growth assays (Figs. 2A and 4C). The regulatory behavior exhibited by *PYL8* is reminiscent of mobile TFs involved in plant development that perform non-cell-autonomous actions by trafficking from cell to cell through plasmodesmata (28, 29). For example, *SHORT ROOT* (*SHR*), which is synthesized in all stele cells except the phloem, moves to adjacent cells including the endodermis and phloem (28, 29). The movement of *SHR* relies on the endomembrane system, interaction with the *SHR* interacting embryonic lethal (*SIEL*) protein, and association with endosomes in a *SIEL*-dependent manner (27). Interestingly, ABA receptors traffic through endosomes (20, 21). In addition to degradation in the vacuole, endosome trafficking can promote signaling functions in both plants and animals by facilitating the movement of proteins between cells (30).

We also report that ABA specifically stabilizes *PYL8* compared with other ABA receptors and induces its accumulation in root nuclei. We demonstrate that this requires ABA perception by *PYL8* and leads to diminished ubiquitination of *PYL8* in roots. Thus, the inactive *PYL8*<sup>K61R Y120A</sup> protein is not stabilized by ABA in roots, and activation of root ABA signaling in the absence of ligand binding by *PYL8* (as occurs after QB treatment) fails to



**Fig. 5.** Proposed model for ABA-dependent stabilization and movement of the non-cell-autonomous ABA receptor *PYL8*. (A) *PYL8* translocation from epidermis (blue arrows) and stele (red arrows) to adjacent tissues. Translocation could be promoted by increased ABA levels or follow a default mechanism that is reinforced by ABA-induced accumulation of *PYL8*. The intercellular movement of *PYL8* is accompanied by intracellular trafficking and increased nuclear accumulation in response to ABA. (B) ABA reduces polyubiquitination of *PYL8* through an unknown mechanism, which stabilizes and increases *PYL8* protein levels. ABA also enhances *PYL8* localization in the nucleus (n), which prevents vacuolar degradation and might represent an additional mechanism to increase *PYL8* levels.

stabilize PYL8. Different reporters for direct visualization of ABA concentration changes have been described (31–34). However, reporters based on the overexpression of PP2Cs or ABA receptors affect ABA sensitivity per se; for example, ABALeon lines show reduced sensitivity to ABA (33) whereas ABACUS lines show enhanced ABA-mediated inhibition of root growth compared with wild type (34). The ProPYL8:PYL8-GFP *pyl8-1* line here described showed wild-type sensitivity to ABA-mediated inhibition of root growth (Fig. 2A), which is a requisite for a root ABA biosensor. Additionally, both kinetic and dose–response analyses indicate that PYL8-GFP might be used as an ABA biosensor in roots to detect exogenous ABA (SI Appendix, Fig. S2). Moreover, the PYL8-GFP biosensor harbors the potential to specifically identify PYL8 agonists through in vivo screening, which is required to confirm the bioactivity of molecules identified by in vitro or in silico screening. However, the current version of the PYL8-GFP biosensor needs to be improved to a ratiometric version to achieve a wider dynamic range of sensitivity to ABA changes (33, 34).

Although the main function of PYL8 is the ABA-dependent inhibition of clade A PP2Cs such as ABI1 and PP2CA (13), an additional role independent of the core ABA-signaling pathway has also been reported (35). Thus, PYL8 promotes lateral root growth by interacting with the TFs MYB77, MYB44, and MYB73 to augment auxin signaling, which points to an additional nuclear role of PYL8 (35). ABA perception by PYL8 in the nucleus is required to inhibit PP2C activity and hence relieve repression of ABA signaling by the SWI/SNF chromatin remodeling ATPase BRAHMA (36). Failure to inhibit nuclear PP2C activity, as exemplified by the phosphatase *abi1<sup>Gly180Asp</sup>* that is refractory to inhibition by ABA receptors, blocks ABA signaling and inhibits ABA response element-

binding bZIPs that mediate transcriptional response to ABA (37, 38). Interestingly, we observed enhanced nuclear localization of PYL8 in root cells after ABA treatment, which suggests that both intra- and intercellular movement of PYL8 occurs (Fig. 5B). Further insight into the cellular mechanisms involved in movement of ABA receptors is a key issue for future research. We note that the enhanced localization of PYL8 in the nucleus, together with diminished polyubiquitination induced by ABA, can reduce degradation of the receptor through the vacuolar pathway (20, 21) and contributes to stabilization of the receptor (Fig. 5B). The mechanism whereby ABA specifically reduces polyubiquitination of PYL8 is another challenging issue to be investigated.

## Materials and Methods

Detailed description is provided in SI Appendix for plant material and growth conditions; generation of HA-tagged and GFP-tagged lines and ProPYL8:PYL8-GFP *pyl8-1* lines; expression of PYL8-GFP in root driven by tissue-specific promoters; generation of PYL8 mutations; in vivo protein analysis and degradation assays; root growth assays; RT-qPCR analysis; GUS staining; PP2C inhibition assays; RNA in situ hybridization; CLSM; and measurements and statistical analysis.

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