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Short title: PSKRs maintain growth under mannitol stress

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Title:

PSK signaling controls ABA homeostasis and promotes shoot growth

under mannitol stress

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One-sentence summary
PSK receptor signaling is required to delay cotyledon greening in response to
mannitol and ABA nad it promotes shoot growth under mannitol stress by controlling
ABA levels and ABA responsiveness.

Footnotes

Author contributions: MS conceived the project. MS, MDS and KR designed the
experiments. BH performed ABA measurements and data analysis. MDS and KR
performed experiments. MDS and KR analyzed data. MS wrote the manuscript with
contributions from MDS and BH.

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Funding: This work was funded by the Deutsche Forschungsgemeinschaft through
grants SA495/13-1 and SA495/13-2.

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ABSTRACT

We hypothesized that the growth-promoting activity of the peptide hormone
phytosulfokine (PSK), may be important to maintain growth under abiotic stress. To test
this hypothesis, we employed mannitol as a stressor and analyzed the involvement of
abscisic acid (ABA) that mediates a subset of mannitol responses. Inhibition of seed
germination by ABA or mannitol was independent of PSK receptor signaling whereas
repression of cotyledon greening was partially dependent on PSKR signaling with
receptor null *pskr1-3 pskr2-1* seedlings showing enhanced greening. Mannitol led to
dose-dependent shoot growth inhibition that was alleviated by PSKR signaling. With
mannitol, *pskr1-3 pskr2-1* seedlings had strongly reduced shoot fresh and dry weights
incompared to wild type. Analysis of *pskr1-3* and *pskr2-1* single receptor loss-of-function
lines revealed that signaling via *PSKR1* is crucial for shoot growth promotion under
mannitol stress. Mannitol and ABA induced expression of *PSK3* and *PSKR1* and ABA
promoted expression of *PSK2* and *PSK4*. In turn, PSKR signaling was required for
mannitol-induced accumulation of ABA in the shoot revealing a regulatory feedback
loop. PSKRs repressed expression of *UGT71B6* encoding an ABA UDP-
glucosyltransferase and maintained expression of *BG1*, an ABA glucosidase which may
lead to reduced ABA-glucose conjugation and enhanced ABA remobilization. Marker
gene expression analyses supported the conclusion that PSKR and mannitol signaling
pathways crosstalk, a conclusion that was supported by the observation that PSK
receptor signaling enhanced sensitivity to ABA in mannitol-stressed shoots. In
conclusion, PSKR signaling maintains shoot growth under mannitol stress in part by
interfering with the ABA pathway.

INTRODUCTION

The non-ionic osmolyte mannitol is a metabolite produced by plants and microorganisms

that is frequently used in osmotic stress and plant growth research (Nikonorova et al.,

2018; Kalve et al., 2020). Plants respond to mannitol by reduced growth and by stoma

closure that reduces water loss (Munemasa et al., 2015). The plant hormone abscisic

acid (ABA) accumulates in plants exposed to osmotic stress and controls core plant

responses to counteract water deficit (Bartels and Sunkar, 2005; Yamaguchi-Shinozaki

and Shinozaki, 2006; Tuteja, 2007 Finkelstein, 2013). Active ABA levels are determined

by synthesis, degradation, inactivation and remobilization. ABA is synthesized from

xanthophylls with 9-*cis*-epoxycarotenoid dioxygenase (NCED) catalyzing a key regulated

step. Indeed, elevation of ABA levels during drought conditions goes along with elevated

NCED activity (Finkelstein, 2013; Dejonghe et al., 2018). Degradation of ABA is initiated

by ABA 8'-hydroxylase, an enzyme that is encoded by four members of the cytochrome

P450 CYP707A family in Arabidopsis (Kushiro et al., 2004; Saito et al., 2004). ABA

hydroxylation has been identified as the key step in ABA catabolism (Dejonghe et al.,

2018). However, inactivation of ABA also occurs through conjugation to glucose by ABA

UDP-glucosyltransferase (UGT) encoded by *UGT71B6-B8*, in Arabidopsis (Dong and

Hwang 2004; Dong et al., 2014). ABA-glucose ester is a storage form of ABA that can

be remobilized by ABA glucosidases BG1 and BG2 (Lee et al., 2006). Thus, ABA

homeostasis depends on synthesis and inactivation pathways whereby many of the

genes involved are regulated in response to dehydration and other stresses (Xu et al.,

2013).

Shoot growth is inhibited by mannitol in a dose-dependent manner with inhibition

observed at low concentrations (25-50 mM), and high levels of ABA (Saab et al., 1990;

Skirycz et al., 2010; Skirycz and Inzé, 2010; Verelst et al., 2013). Growth reduction as a

response to abiotic stresses is thought to save resources that can be used to provide

stress resistance and ensure plant survival and reproduction in an adverse environment.

The mechanisms that balance growth and stress responses are however not much
explored.

PSK is a secreted signaling peptide that is perceived by a receptor at the plasma
membrane that belongs to the leucine-rich repeat receptor-like kinase family. The
Arabidopsis genome encodes two genes, *PSKR1* and *PSKR2* (Matsubayashi et al.,
2006; Sauter, 2015). Knockout of both receptor genes results in reduced root elongation
and shoot growth whereas exposure of wild type seedlings to PSK promotes growth by
enhancing cell expansion (Kutschmar et al., 2009; Stührwohldt *et al.*, 2011). At the
molecular level, PSKR1 interacts with the co-receptor BRASSINOSTEROID-
INSENSITIVE 1 (BAK1) and the H^+-ATPases AHA1 and AHA2, and indirectly through
BAK1 and AHAs with the CYCLIC NUCLEOTIDE-GATED CHANNEL 17 (CNGC17).
These proteins assemble in a nanocluster at the plasma membrane and were proposed
to form a functional unit that drives cell expansion (Ladwig et al., 2015). PSKR signaling
was shown to cause protoplast expansion in a CNGC17-dependent manner and was
proposed to lead to cell wall acidification, water uptake, accompanied by osmotic
adjustment, and consequently to expansion of cells. Based on the growth-promoting
activity of PSKRs, we hypothesized that PSK signaling may also contribute to maintain
growth under mannitol stress thereby providing a molecular mechanism that integrates
growth and mannitol stress responses. To test this hypothesis, we employed the *pskr1-3*
pskr2-1 double knockout mutant that is deficient in PSKR signaling (Hartmann *et al.*,
2013) and compared shoot growth under mannitol, that is well suited to study growth
regulation under mild stress conditions (Skirycz *et al.*, 2011*c*; Van den Broeck *et al.*,
2017), to that of wild type.Our results show that PSK signaling maintains shoot growth
under moderate mannitol stress. In the shoot, PSKR, mannitol and ABA interact at the
level of gene expression resulting in PSKR-dependent induction of ABA under mild
mannitol stress. We further show that PSKR signaling is required for the delay of
cotyledon greening induced by mannitol and ABA. Together, these findings reveal that
PSKR signaling interacts with ABA and mannitol pathways to control early seedling
development and shoot growth. under abiotic stress.

RESULTS

PSK receptors mediate inhibition of cotyledon greening in response to ABA and

mannitol

To answer the question if PSK receptor signaling controlled early seedling development
under stress conditions we used the uncharged osmolyte mannitol and the stress
hormone abscisic acid (ABA) which have unique but also overlapping signaling
pathways (Yoshida et al., 2014). We first studied seed germination under mannitol
stress. Seeds of wild type, the PSK receptor null line *pskr1-3 pskr2-1*, and PSKR1
overexpressors were exposed to 1 µM PSK, to 350 mM mannitol or a combination of
both and seed germination was scored for up to 21 days (Supplemental Fig. S1). No
significant differences in germination rate were detected between genotypes and
treatments. ABA inhibited seed germination, but treatment with 1 µM PSK in the
presence or absence of 1 µM ABA did not alter seed germination (Supplemental Fig.
S2). Likewise, knockout or overexpression of PSK receptors had no influence on seed
germination at any given treatment indicating that seed germination was not controlled
by PSK signaling.

We next studied the role of PSKR signaling in cotyledon greening. In the absence
of an effector, cotyledon greening did not differ between wild type, *pskr1-3 pskr2-1*, and
PSKR1 overexpressors (Fig. 1A; Supplemental Fig. S3). Seedling development was
delayed by 1 µM ABA while 1 µM PSK did not have an effect (Fig. 1B; Supplemental
Fig. S3). However, wild type seedlings that were treated with PSK in addition to ABA
showed enhanced inhibition of cotyledon greening indicative of a synergistic effect
between ABA and PSK signaling. This conclusion was supported by the finding that the
degree of inhibition by ABA was genotype-dependent (Fig. 1B; Supplemental Fig. S3). In
wild type, ABA inhibited cotyledon greening by 65% compared to control conditions
whereas greening was reduced by only 18% in the PSK receptor null line *pskr1-3 pskr2-*
1 and by 81-96% in lines overexpressing PSKR1 indicating that the ABA-induced delay
in seedling development was enhanced by PSKR signaling. The response to 350 mM
mannitol was similar to that of ABA. A delay in seedling development was observed that
was enhanced by PSK (Fig. 1C). Furthermore, *pskr1-3 pskr2-1* seedlings were less
responsive to mannitol whereas PSKR1 overexpressors showed a hypersensitive
response. Taken together, these findings revealed crosstalk between PSKR and
mannitol and between PSKR and ABA signaling pathways in cotyledon greening.

PSKR1 promotes shoot growth under mannitol stress

To study seedling growth regulation by PSKR signaling in response to mannitol, seedlings were pre-grown for 4 days without mannitol and subsequently transferred to plates containing 0, 25 mM, 50 mM, 100 mM or 200 mM mannitol (Fig. 2). By chosing this experimental setup, we circumvented the effects of mannitol on cotyledon greening described above. During pre-growth under control conditions, early seedling development was completed after 4 days in all genotypes (Supplemental Figs. S1, S2 and S3). Wild type seedlings that were transferred to mannitol displayed a dose-dependent inhibition of shoot size, shoot fresh weight and shoot dry weight that was exacerbated in *pskr1-3 pskr2-1* seedlings (Fig. 2A, B, and C). The strongest growth inhibition compared to wild type was observed at low concentrations of 25 mM and 50 mM mannitol suggesting that PSKR signaling maintains shoot growth during mild mannitol stress. Growth reduction was brought about mainly by reduced leaf size, and reduced leaf number (Fig. 2D; Supplemental Fig. S4). Exacerbated growth inhibition in *pskr1-3 pskr2-1* seedlings was also seen with sorbitol (Supplemental Fig. S5). Unlike shoot growth, root elongation was unaffected by mannitol up to 100 mM in wild type and *pskr1-3 pskr2-1*. Root growth was inhibited by At 200 mM mannitol in both genotypes with a significantly stronger inhibition in *pskr1-3 pskr2-1* (Fig. 2E).

To pinpoint which of the two PSK receptors mediated resistance to mannitol-induced growth inhibition of the shoot, we used single PSK receptor gene knock out lines (Kutschmar *et al*., 2009) (Fig. 3). After 2 and 3 weeks, growth inhibition by 50 mM mannitol was comparable in *pskr1-3* and *pskr1-3 pskr2-1* whereas *pskr2-1* plants showed wild-type growth indicating that PSKR1 promotes growth of plant shoots exposed to mannitol (Fig. 3A, B).

To test whether the PSKR-dependent maintenance of shoot growth was a response to low water potential, we exposed wild type and *pskr1-3 pskr2-1* seedlings to PEG6000 at concentrations between 0 and 10% (Supplemental Fig. S6). While shoot fresh and dry weights were reduced in a PEG6000 dose-dependent manner, the growth reduction was not significantly different between wild type and *pskr1-3 pskr2-1* indicating that the response to mannitol was due to a specific chemical property of mannitol rather than a water-stress condition.

Mannitol and ABA promote expression of *PSKR* and *PSK* genes

To investigate whether expression of *PSK* and *PSKR* genes was regulated by mannitol

and ABA in leaves, we employed *promoter:GUS* lines that were described previously

(Kutschmar *et al*., 2009; Stührwohldt *et al*., 2011) to obtain spatial resolution. Of the five

PSK precursor genes, *PSK2*, *PSK3*, *PSK4* and *PSK5* were expressed in the shoot in

accord with the previous observation that *PSK1* is root-specific (Kutschmar *et al*., 2009)

(Fig. 4A). *PSK3* promoter activity was particularly high in young, expanding leaves.

Regulation of PSK precursor gene expression by 200 mM mannitol or 5 µM ABA was

studied by qPCR (Fig. 4B-F). In wild type, *PSK3* was significantly induced by mannitol

while *PSK2*, *PSK3* and *PSK4* were induced by ABA revealing, in part, differential

responses to the two signals. Knockout of PSK signaling in *pskr1-3 pskr2-1* resulted in

elevated *PSK2* and *PSK4* expression at control conditions suggestive of a feedback

inhibitory loop between PSK signaling and precursor gene expression. Interestingly,

PSK1, *PSK3* and *PSK5* were hyperinduced in the receptor-deficient background

compared to wild type revealing that *PSK1*, *PSK3* and *PSK5* are negatively controlled by

PSKR signaling during mannitol stress. Induction of *PSK3* mRNA levels by ABA was

abolished in *pskr1-3 pskr2-1* indicating that *PSK3* is upregulated by ABA in a PSKR-

dependent manner pointing to cross-talk between these signaling pathways.

PSKR1:GUS activity was detected in cotyledons, true leaves and in the root (Fig.

5A-F) while *PSKR2:GUS* activity was overall low in the shoot (Fig. 5G). *PSKR1:GUS*

seedlings exposed to 50 mM mannitol displayed increased GUS activity specifically in

young true leaves (Fig. 5D), a finding that was confirmed by qPCR analysis (Fig. 5H).

PSKR1 transcripts increased in response to mannitol or ABA at low and high

concentrations (Fig. 5H). By contrast, *PSKR2* mRNA levels increased to a minor degree

at high mannitol or ABA levels (Fig. 5I) in accord with the observation that PSKR1 is

crucial for maintenance of growth (Fig. 3).

The data revealed highly differential PSK gene regulation in young leaves by a

network of ABA-dependent and ABA-independent mannitol stress signaling that

crosstalk with the PSK signaling pathway. As a consequence, mannitol and ABA induce,

both, *PSKR1* and *PSK* precursor genes which promote shoot growth during mannitol
stress.

PSKR signaling controls ABA levels and ABA responsiveness

Hyperinduction of *PSK1*, *PSK3* and *PSK5* by mannitol in the PSK receptor null
background (Fig. 4B-D) revealed crosstalk between PSK and mannitol signaling.
Induction of *PSK3* by mannitol and ABA suggested that ABA may participate in PSK-
dependent growth promotion under mannitol stress. To learn more about this regulatory
network, we next asked whether ABA levels were regulated by PSKR signaling. Analysis
of ABA levels by mass spectrometry revealed a dose-dependent increase in ABA in
shoots and roots in response to mannitol in wild type (Fig. 6A, B). By contrast, ABA
levels did not increase in *pskr1-3 pskr2-1* shoots in response to mannitol suggesting that
PSKR signaling is required for ABA accumulation under mannitol stress. In roots, ABA
levels increased in *pskr1-3 pskr2-1* seedlings at 200 mM mannitol albeit overall levels
were lower than in wild type. Genotypic differences in ABA accumulation in response to
mannitol were confirmed using the ABA sensor ABAleon2.1 (Waadt et al. 2014) that was
introduced in wild type and *pskr1-3 pskr2-1*. Photobleaching-based FRET analysis
(Supplemental Fig. S7) revealed a decreased FRET efficiency, reporting elevated ABA,
in wild type but not in *pskr1-3 pskr2-1* in response to mannitol (Fig. 6C).The difference in
absolute FRET efficiency between genotypes may be owed to the fact that the lines
were transformed rather than introgressed.

We next explored whether PSKR signaling affected the sensitivity to ABA in
mannnitol-exposed seedlings. A dose-response analysis showed that ABA at 0.1 µM
and higher inhibited shoot growth in wild type under control conditions in a concentration
dependent manner whereas *pskr1-3 pskr2-1* seedling growth was inhibited at 0.3 µM
ABA and higher (Fig. 6D, E). In the presence of mannitol, shoot growth of wild type was
promoted at 0.01 µM ABA and inhibited at 0.3 µM ABA and higher while growth of
pskr1-3 pskr2-1 seedlings increased between 0.1 and 1 µM ABA and decreased at
higher ABA concentrations indicating that PSKR signaling altered the sensitivity to ABA
under mild mannitol stress. The reduced leaf number in mannitol exposed *pskr1-3*

pskr2-1 seedlings was restored to wild type level at 0.3-1 µM ABA (Supplemental Fig.
S4). In summary, the responsiveness of seedlings that lack PSKR receptors is shifted to
higher ABA concentrations compared to wild type. The need for higher ABA required to
promote shoot growth may be explained by a lower endogenous ABA content fostering
the idea that PSKR promotes growth in part by increasing ABA in response to mannitol.
It should be noted, however, that growth inhibition by mannitol was only partially
alleviated by ABA in *pskr1-3 pskr2-1* suggesting that other levels of regulation exist. To
gain more insight into the network that connects ABA with mannitol and PSKR
pathways, we analyzed expression of genes involved in ABA homeostasis (Fig. 6F).

To identify the molecular targets of PSKR signaling in ABA metabolism, we
analyzed key ABA biosynthetic *NCED* genes, *CYP707A1-4* genes coding for ABA 8'-
hydroxylases that degrade ABA to phaseic acid (Kushiro et al., 2004; Saito *et al*., 2004;
Okamoto et al., 2006), *UGT71B6-8* genes coding for ABA uridine diphosphate
glucosyltransferases that catalyze ABA inactivation through glycosylation (Dong et al.,
2014), and *BG1* and *BG2* genes encoding glucosidases that mobilize ABA from ABA-
glucose ester (Lee et al., 2006; Xu et al., 2012) (Fig. 6F). *NCED3* and *5* transcripts were
more abundant in young leaves than *NCED9* transcripts (Fig. 7A). *NCED3* was
upregulated by mannitol whereas *NCED5* was induced by ABA (Fig. 7B-D). However,
PSKR signaling did not significantly alter *NCED* expression.

CYP707A2 and *A3* were expressed at higher levels than *CYP707A1* and
CYP707A4 confirming a previous report (Fig. 8A) (Kushiro *et al*., 2004). A more detailed
analysis revealed induction of *CYP707A1*, *A2* and *A4* by 1 µM and 5 µM ABA in wild
type indicating increased ABA degradation when plants encounter high ABA (Fig. 8B-E;
Supplemental Fig. S8). Mannitol did not alter mRNA abundance of *CYP707A* genes. In
pskr1-3 pskr2-1, *CYP707A1* transcripts were elevated over wild type revealing
repression of this gene by PSKR signaling (Fig. 8B). By contrast, *CYP707A2* and *A4*
transcripts decreased in PSKR-deficient plants indicative of gene activation by PSKR
signaling (Fig. 8C) while transcript levels of *CYP707A3* were not significantly different
between mutant and wild type (Fig. 8D; Supplemental Fig. S8). Taken together,
CYP707A1, *A2* and *A4* are targets of PSK receptor signaling. Since *CYP707A1* was
upregulated and *CYP707A2* and *CYP707A4* were downregulated in mannitol stressed

pskr1-3 pskr2-1 plants, it is difficult to assess the contribution of ABA degradation to
overall ABA levels.

Among the three ABA UDP-glucose transferase genes *UGT71B6-B8* (Fig. 9),
UGT71B6 transcripts were elevated in wild type and hyperinduced in *pskr1-3 pskr2-1*
plants exposed to mannitol (Fig. 9B). *UGT71B7* was upregulated by mannitol and ABA
in both genetic backgrounds (Fig. 9C), while *UGT71B8* was not regulated. These data
suggested that ABA conjugation is enhanced under mannitol stress in PSKR-deficient
plants compared to wild type.

Genes coding for the ABA glucosidases BG1 and BG2 were upregulated by ABA
in wild type and *pskr1-3 pskr2-1* while mannitol reduced *BG1* expression in *pskr1-3*
pskr2-1 compared to wild type (Fig. 9E-G; Supplemental Fig. S9) suggesting that PSKR
signaling increases ABA levels by releasing it from the ABA-glucose pool. In summary,
repression of *UGT71B6* and enhanced expression of *BG1* by PSKR signaling may be
responsible for ABA accumulation in response to mannitol.

PSKR-dependent marker gene expression in response to ABA and mannitol

Since ABA responsiveness was controlled by PSKR signaling (Fig. 1A, B, Fig. 6D, E,
Supplemental Fig. S3), we studied expression of ABA- and mannitol-responsive genes
in wild type and PSKR-deficient seedlings (Fig. 10A-C). The dehydration-responsive
element/C-repeat (DRE/CRT)-binding protein 2 (DREB2) transcription factor plays a key
role in ABA-independent gene expression in response to osmotic stress such as induced
by mannitol while also interacting with ABA-dependent gene expression (Yoshida et al.,
2014). *DREB2A* transcripts were elevated in *pskr1-3 pskr2-1* but not in wild-type
seedlings in response to mannitol but not ABA (Fig. 10A). Similarly, the ABA receptor
gene *PYL6* was induced by mannitol in the receptor null mutant compared to wild type
(Fig. 10B) as was the basic helix-loop-helix transcriptional repressor gene *bHLH129*
(Tian et al., 2015) (Fig. 10C) providing evidence that these genes are repressed by
PSKRs during mannitol stress signaling possibly to dampen the stress response and to
allow for seedling growth. Analysis of knockout lines for these and other genes related to
ABA synthesis (*ABA2, NCED3, NCED9*) and signaling (*PYL6, OST1, SnRK2.9, ABI1,*

ABI3, *bHLH129*, *DREB2A*) revealed that their response to mannitol with regard to shoot

growth was indistinguishable from wild type and did hence not phenocopy *pskr1-3*

pskr2-1 seedlings (Fig. 10D) leading us to conclude that these genes are not required

for or act redundantly in PSKR-mediated growth control during mannitol stress.

DISCUSSION

Inhibition of cotyledon greening by ABA or mannitol is dependent on PSK receptor signaling

Seed germination and seedling establishment are stringently controlled by environmental conditions to ensure seedling survival. In particular, water availability is a requirement for seedling establishment. Under water-limited conditions, ABA acts as a hormonal signal that prevents delays germination and early seedling development. Here we showed that ABA and mannitol delayed seed germination independent of PSKR signaling whereas inhibition of cotyledon greening by ABA or mannitol was PSKR-dependent. *pskr1-3 pskr2-1* seedlings displayed accelerated cotyledon greening and *PSKR1* overexpressors were hypersensitive to ABA and mannitol with delayed cotyledon greening suggesting that PSKR signaling altered the responsiveness to ABA and mannitol pointing to crosstalk between these pathways.

PSK ligand and receptor are induced by mannitol and ABA to promote shoot growth

Growth of plant shoots was supported by PSKR signaling particularly during mannitol stress. Plants exposed to mannitol displayed elevated transcript levels of *PSKR1* and *PSK3,* that were also induced by ABA suggesting that the PSK signal pathway is promoted by mannitol signaling through ABA to actively maintain shoot growth. A crucial role of *PSKR1* in promoting mannitol resistance was revealed in single receptor gene knockout lines. *pskr1-3* seedlings displayed the same growth retardation as seedlings of the double receptor knock out line *pskr1-3 pskr2-1* whereas *pskr2-1* seedlings had a wild type phenotype. Mannitol and ABA exerted common but also differential control of PSK signaling genes pointing to a fine-tuned regulatory network rather than a linear pathway of growth control. *PSK2* and *PSK4* were induced by ABA but not by mannitol revealing ABA regulation of PSK signaling in a pathway that is unrelated to mannitol. Intricate regulatory loops were revealed by hyperinduction of *PSK1*, *PSK3* and *PSK5* by mannitol

in the PSK receptor null background compared to wild type which suggested that PSK
signaling feedback-inhibits expression of ligand precursor genes under mannitol stress
possibly to balance growth (Fig. 11). The regulated signaling genes *PSK3* and *PSKR1*
were expressed in young expanding leaves in accord with their role in cell expansion
(Hartmann et al., 2013; Ladwig et al., 2015). It was suggested that plant cells
communicate via extracellular signals and plasma membrane-bound receptors despite
of a continuous network of plasmodesmata that enable cell-cell communication because
apoplastic signals allow for signal integration and output coordination (Chivasa and
Goodman, 2020). Induction of PSK signaling may allow for coordinated leaf growth in
particular when leaves encounter local mannitol accumulation e.g. from mannitol-
producing pathogens (Jennings et al., 2002; Mosher et al., 2013; Meena et al., 2015).
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373 **ABA homeostasis under mannitol stress is controlled through the PSKR pathway**
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Exposure to mannitol increased ABA levels in a PSKR-dependent manner raising the
question how PSK signaling controls ABA homeostasis at the molecular level. The
steady-state level of active ABA is determined by ABA synthesis, catabolism,
inactivation and remobilization (Cutler and Krochko, 1999; Nambara and Marion-Poll,
2005). Nine-*cis*-epoxycarotenoid dioxygenases (NCEDs) are key enzymes of ABA
synthesis that cleave 9-*cis*-xanthophylls to xanthoxin, a precursor of ABA. Arabidopsis
NCED3 was previously described as the major stress-induced *NCED* gene in leaves
with *NCED5* and *NCED9* being induced to a minor degree in response to water-deficit
(Tan et al., 2003). In this study, *NCED3* was induced by mannitol in wild type and
hyperinduced in the PSKR null mutant pointing to elevated ABA synthesis in PSKR-
deficient shoots. On the other hand, *CYP707A1* encoding an ABA degrading ABA 8'-
hydroxylase (Kushiro et al., 2004) was likewise hyperinduced in the PSK receptor null
mutant compared to wild type in the presence of mannitol while *CYP707A2* transcript
levels went down. Elevated synthesis and elevated degradation rates in *pskr1-3 pskr2-1*
seedlings compared to wild type could result in increased flux in the ABA
synthesis/degradation pathway but do not explain why ABA levels did not increase
under mannitol stress. The *CYP707A3* gene was previously shown to be repressed in

the shoot by the bHLH transcription factor bHLH122 under drought stress conditions resulting in up-regulated ABA levels (Liu et al., 2014). In this study, *CYP707A3* was not significantly regulated by mannitol or ABA in young leaves.

Aside from synthesis and degradation, ABA is subject to inactivation through conjugation to glucose by UDP-glucose transferases UGT71B6, UGT71B7 and UGT71B8 (Dong et al., 2014) and by remobilization of ABA from ABA-glucose stores by ABA-glucose ß-glucosidases BG1 and BG2 (Lee et al., 2006; Xu et al., 2012). Regulation of   reversible inactivation is one level to control ABA homeostasis (Ma et al., 2018). BGs were previously described as key regulators of osmotic stress resistance (Xu et al., 2012). *BG1* is regulated by miR165/166. Downregulation of miR165/166 resulted in elevated *BG1* expression and in elevated ABA levels (Yan et al., 2016). A comparison between wild type and *pskr1-3 pskr2-1* seedlings exposed to mannitol revealed that PSKR signaling repressed induction of *UGT71B6* and promoted expression of *BG1* possibly shifting the equilibrium between conjugation and remobilization toward more free ABA. Vice versa, increased conjugation and reduced ABA release from ABA-glucose ester in *pskr1-3 pskr2-1* could prevent accumulation of free ABA in response to mannitol in this genotype.

A molecular link between ABA and PSKR pathways was established by marker gene expression. The ABA receptor gene *PYL6* (Ma et al., 2009; Aleman et al., 2016) was upregulated in PSKR null plants and hyperinduced by mannitol suggesting that PSKR signaling dampens PYL6-induced ABA responses at the level of receptor abundance. Plants respond to osmotic stress through ABA-dependent and ABA-independent pathways (Yoshida et al., 2014). The dehydration-responsive element/C-repeat (DRE/CRT), and DRE-/CRT-binding protein 2A (DREB2A) integrates ABA-dependent and ABA-independent drought stress signaling. DREB2A promotes stress-response genes and at the same time inhibits growth (Qin et al., 2008; Kim et al., 2011). However, the PSKR-dependent pathway that confers resistance to growth inhibition by mannitol was not observed when plants were dehydrated by PEG suggesting that PSKRs do not mediate a drought response mimicked by PEG6000. Mannitol has chemical properties beyond being an osmolyte that may be recognized in the growth-related pathway that links it to PSKR signaling. *DREB2A* was induced in the PSKR knockout line suggesting that repression of *DREB2A* may contribute to growth

maintenance by PSKRs under mannitol stress. However, even though *DREB2A* was
reported to have adverse effects on plant growth (Yoshida et al., 2014), the loss-of-
function mutant *dreb2* showed wild-type shoot growth in the presence of mannitol. A
wild-type growth phenotype was also observed for other ABA signaling and synthesis
mutants exposed to mannitol possibly indicating redundant activities from other
members of the gene families that encode the ABA synthesis and signaling components
(Nambara and Marion-Poll, 2005; Joshi-Saha, 2011).
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CONCLUSION

PSKR signaling mediates the delay in cotyledon greening in response to ABA and
mannitol and supports shoot growth in plants exposed to mannitol. ABA, mannitol and
PSKR signaling pathways are intricately linked as evident from the regulation of *PSK*
and *PSKR* genes by mannitol and ABA and by the regulation of ABA levels by PSKR
signaling under mannitol stress. Regulation of ABA levels could result from PSKR-
dependent repression of *UGT71B6* responsible for ABA conjugation and upregulation of
BG1 responsible for release of ABA from ABA-glucose. Our study reveals a role of
PSKR signaling in balancing growth during mannitol stress through interaction with ABA
homeostasis.
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METHODS

Plant material and growth conditions

All experiments were performed with *Arabidopsis thaliana* (L.) Heynh. ecotype Columbia (Col-0) and mutants in the Col-0 background. The following lines were described previously: *pskr1-3* (Kutschmar *et al*., 2009; Stührwohldt *et al*., 2011), *pskr2-1* (Amano *et al*., 2007; Stührwohldt *et al*., 2011), *pskr1-2 pskr2-1* (Stührwohldt *et al*., 2011; Hartmann *et al*., 2013), *PSKR1ox2* and *PSKR1ox12* (Hartmann *et al*., 2013), *35S:PSKR1-GFP* (Hartmann *et al*., 2015). For GUS analyses of PSK receptors the lines *PSKR1:GUS-4* (Kutschmar *et al*., 2009; Stührwohldt *et al*., 2011) and *PSKR2:GUS-3* were used. For growth on plates, seeds were surface-sterilized for 25 min with 2% (w/v) sodium hypochlorite (NaOCl) followed by four washing steps with autoclaved water and placed on square plates containing half-strength MS medium (Murashige & Skoog, 1962; basal salt mixture, Duchefa Biochemie) and 1% (w/v) sucrose except for PEG6000 experiments with 0.5% (w/v) sucrose (Supplemental Fig. S6), solidified with 0.4% (w/v) Gelrite (Duchefa Biochemie). After two days of stratification at 4°C in the dark, plates were transferred to long day with a 16 h light (70 µM photons·m^{-2}·s^{-1}) and 8 h dark at 22°C and 60% humidity.

For germination and greening assays, wild type and mutant parental plants were grown and harvested at the same time to ensure equal seed quality. Seeds were placed on medium supplemented with or without 1 µM (+)-*cis*, *trans*-abscisic acid (ABA) (Duchefa Biochemie), 350 µM mannitol and/or 1 µM PSK (Pepscan). PSK and ABA were always added freshly. ABA was diluted right before use. The penetration of the endosperm or testa by the embryo radicle was counted as successful germination event. Three independent experiments were performed with 100 seeds each per genotype per treatment.

For shoot growth analyses under stress conditions, seedlings were pregrown vertically under sterile conditions for 4 days to complete germination and cotyledon greening (Supplemental Fig. S3) and subsequently transferred to new plates supplemented with mannitol, sorbitol, polyethylene glycol 6000 (PEG6000), and/or ABA

as indicated and grown for the times indicated. Growth was quantified with a fine scale
as shoot fresh weight or shoot dry weight. Plant pictures are shown on a black
background for better visualization. Primary root lengths were determined 7 days after
transfer of 4-day-old seedlings to mannitol because the roots reached the bottom of the
plate after longer times making it impossible to measure root lengths lateron.

Histochemical GUS analysis

To analyze spatial distribution of *PSKR* and *PSK* expression *β*-glucuronidase (GUS)
assays were performed as described (Weigel & Glazebrook, 2002) with minor changes.
Seedlings were collected in 90% (v/v) isopropanol, incubated for 10 minutes and
washed with 50 mM sodium phosphate buffer (pH 7.2). Staining was performed for 15 h
and stopped by transferring the seedlings to 70% (v/v) ethanol. Tissues were cleared
with a chloral hydrate:deionized water:glycerol 6:2:1 (g/ml/ml) mixture that was added on
microscopy slides instead of water. Seedlings were visualized under bright-field
illumination with a Nikon SMZ18 binocular (Nikon) and photographed with a DIGITAL
SIGHT-Ri1 camera (Olympus).

RNA isolation, RT-PCR and quantitative real time PCR

Total RNA was isolated from true leaves using TRI Reagent (Merck) following
manufacturer's protocol. cDNA was synthesized from 1 µg DNase I-treated (Thermo
Fisher Scientific) total RNA by oligo(dT)-primed reverse transcription using RevertAid
Reverse Transcriptase (Thermo Fisher Scientific). To avoid gDNA contamination and to
ensure an equal amount of RNA input, cDNA was tested by PCR for *ACTIN2*
(At3g18780) transcripts prior to qPCR analysis with the primers ACT2for
5'-CAAAGACCAGCTCTTCCATCG-3' and ACT2rev 5'-
CTGTGAACGATTCCTGGACCT-3'. qPCR was used to examine the expression of
PSKR1, PSKR2, PSK1, PSK2, PSK3, PSK4, PSK5, NCED3, NCED5, NCED9,
CYP707A1, CYP707A2, CYP77A3, CYP707A4, UGT71B6, UGT71B7, UGT71B8, BG1,

BG2, *DREB2A*, *PYL6* and *bHLH129* with primers listed in Supplemental Table 1 using

the Rotor Gene SYBR Green PCR Kit (Qiagen) according to manufacturers' protocol in

a Rotor gene Q cycler (Qiagen). Ten ng cDNA per sample were applied in a total volume

of 15 µl. Estimation of raw data was done with the Rotor-Gene Q 2.3.1.49 (Qiagen)

program.

The relative transcript abundance was calculated based on the $\Delta\Delta$CP method

including primer efficiency to normalize the data with two reference genes (Pfaffl, 2001;

Van Desompele *et al.*, 2007). In relation to each reference gene (*ACT2* and

GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE 1 (*GAPC1*)) (Supplemental

Table 1) values were averaged from three independent biological replicates with two

technical replicates each. The expression of wild type under control conditions was set

to 1 and all other values were calculated as fold change of that.

ABA measurements

Four-day-old seedlings were transferred to medium containing mannitol as indicated and

grown for additional 7 days. Roots and shoots were harvested separated and

immediately frozen in liquid nitrogen. About 50 mg of homogenized, frozen material was

extracted with 500 µl of methanol containing isotope-labelled internal standard $^2H_6$-ABA

(0.1 ng µl^{-1}) followed by centrifugation. The supernatant was diluted with 4.5 ml water

and subjected to solid-phase extraction on HR-XC (Chromabond, Macherey-Nagel,

Düren, Germany) column. Fractions containing ABA were eluted with acetonitrile and

separated using the ACQUITY UPLC System (Waters, Eschborn, Germany) (Balcke et

al. 2012). Detection of ABA and $^2H_6$-ABA was done by ESI-tandem mass spectrometry

(MS/MS) using a 3200 Q TRAP® LC/MS/MS mass spectrometer (Waters) (Balcke et al.,

2012). ABA content per sample was calculated using the ratio of ABA and $^2H_6$-ABA peak

heights. Data were obtained from 5 biological replicates each.

To an alternative method to measure changes in ABA levels in response to

mannitol, we obtained the *ABAleon2.1* line and the plasmid *barII-UT-ABAleon2.1* from

Rainer Waadt (Waadt et al. 2014) that we used to generate a homozygous *pskr1-3*

pskr2-1 ABAleon2.1 line. Plants were transformed with *Agrobacterium tumefaciens*

EHA105, containing the *barII-UT-ABAleon2.1* construct with the floral dip method
(Clough and Bent, 1998). The progeny were selected with BASTA[®]. In the T2 generation
the seedlings were additionally screened with the FastGene[®] Blue/Green LED Flashlight
(Nippon Genetics Europe GmbH) with an orange/blue filter to exclude silencing of the
transgene. Acceptor photobleaching Förster resonance energy transfer (FRET) was
used to measure relative differences in ABA levels in each genotype using a Leica SP5
CLSM. Cells were excited sequentially at 458 and 514 nm and emission recorded with
adequate filter sets. Post-bleach images were captured at 458 nm excitation
(Supplemental Fig. S7). FRET is visualized as an increase in mTurquoise fluorescence
following cpVenus173 photobleaching (Supplemental Figure S7). FRET efficiency was
calculated according to the formula $FRET_{eff} = (D_{post} - D_{pre})/D_{post}$ with D_{post}=fluorescence
intensity of the donor after acceptor photobleaching and D_{pre}=fluorescence intensity of
the donor before acceptor photobleaching.

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561　**Statistical analysis**

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563　Statistical analyses were done using Minitab® 16.1. Data that were not ditributed
564　normally were evaluated using a Kruskal-Wallis or Mann-Whitney test for pairwise
565　comparison. Normally distributed data were tested for equal variance. In the case of
566　equal variance, ANOVA, otherwise a *t*-test for pairwise comparison was chosen.

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569　**Accession numbers**

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ACT2 - At3g18780, *GAPC1* - At3g04120, *PSKR1* - At2g02220, *PSKR2* - At5g53890,
PSK1 - At1g13590, *PSK2* - At2g22860, *PSK3* - At3g44735, *PSK4* - At3g49780, *PSK5* -
At5g65870, *NCED3* - At3g14440, *NCED5* - At1g30100, *NCED9* - At1g78390,
CYP707A1 - At4g19230, *CYP707A2* - At2g29090, *CYP707A3* - At5g45340, *CYP707A4*

- At3g19270, *UGT71B6* - At3g21780, *UGT71B7* - At3g21790, *UGT71B8* - At3g21800,

BG1 - At1g52400, *BG2* - At2g32860, *DREB2A* - At5g05410, *PYL6* - At2g40330,

bHLH129 - At2g43140.

ACKNOWLEDGEMENTS

Hagen Stellmach (IPB Halle) is acknowledged for helping in ABA measurements. We

are grateful to Rainer Waadt for providing the *ABAleon2.1* construct and line and to

Lena Carstens for generating the *pskr1-3 pskr2-1 ABAleon2.1* reporter line.

FIGURE LEGENDS

Figure 1. Repression of early seedling development by ABA or mannitol is mediated by PSK receptor signaling.

A Cotyledon greening of wild type, *pskr1-3 pskr2-1*, and *PSKR1* overexpressing seedlings exposed to 1 µM ABA or 350 mM mannitol or no treatment for the times indicated. The scheme on the lower left side indicates the genotypes grown on each plate

B Cotyledon greening of 8-day-old wild type seedlings, *PSKR* knockout and of three independent *PSKR1* overexpressing lines treated with 1 µM PSK, 1 µM ABA, or both. Data are means ±SE of 3 independent experiments each evaluating 100 seeds per genotype. Different letters indicate significantly different values (one-way ANOVA, Tukey's test, $p<0.05$).

C Cotyledon greening of 8-day-old wild type seedlings, *PSKR* knockout and of three independent *PSKR1* overexpressing lines treated with 1 µM PSK, 350 mM mannitol, or both. Data are means ±SE of 3 independent experiments each evaluating 100 seeds per genotype. Different letters indicate significantly different values (one-way ANOVA, Tukey's test, $p<0.05$).

Figure 2. PSK receptor signaling promotes shoot growth under mannitol stress.

Four-day-old wild type and *pskr1-3 pskr2-1* seedlings were transferred to media containing mannitol as indicated.

A Shoot phenotypes of wild type (wt) and *pskr1-3 pskr2-1* plants grown for 2 weeks. Scale bars = 10 mm.

B Shoot fresh weights of wt and *pskr1-3 pskr2-1* plants grown as in A.

C Shoot dry weights of wt and *pskr1-3 pskr2-1* plants analyzed in B.

D Leaf numbers, sizes and morphology of wild type and *pskr1-3 pskr2-1* plants grown on mannitol-free medium or on 25 mM mannitol for 3 weeks. Scale bar = 10 mm.

619 **E** Primary root lengths of seedlings grown for 7 days after transfer. (B, C, E) Significantly
620 different values within a genotype are denoted by different letters (Kruskal-Wallis,
621 Tukey's ,test, $p<0.05$, $n≥36$, 3 independent experiments). Asterisk indicates significant
622 differences between genotypes (Mann-Whitney test, $P<0.05$).
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Figure 3. *PSKR1* promotes growth under mild mannitol stress.
Four-day-old wild type, *pskr1-3*, *pskr2-1,* and *pskr1-3 pskr2-1* seedlings were transferred
to media with or without 50 mM mannitol.
A Shoot phenotypes after 2 weeks; scale bar = 10 mm.
B Mean (±SE) shoot fresh weights of seedlings after 3 weeks. Different letters indicate
significant differences (Kruskal-Wallis, Tukey's test, $p<0.05$, $n≥36$, 3 independent
experiments).
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Figure 4. *PSK* genes are differentially regulated by mannitol, ABA and *PSKR*
signaling.
A GUS staining of *PSK1:GUS-3*, *PSK2:GUS-2*, *PSK3:GUS-3*, *PSK4:GUS-4* and
PSK5:GUS-1 seedlings; scale bar = 2 mm.
(B-F) Seven-day-old seedlings were exposed to 200 mM mannitol or 5 µM ABA for 1 day
for qPCR analyses in first true leaves. Results (±SE) are averages from 3 biological
replicates with two technical repeats each. Different letters indicate significant
differences.
B Transcript levels of PSK genes relative to *PSK3* that was set to 1.
C-F Relative transcript levels of *PSK1-5* in wild type and in *pskr1-3 pskr2-1* seedlings
treated with mannitol or ABA as indicated (B, F: Kruskal-Wallis, Tukey's test, $p<0.05$; C-
E: one-way ANOVA, Tukey's test, $p<0.05$).
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Figure 5. *PSKR1* expression is induced by mannitol and ABA.
A-F *PSKR1:GUS-4* activity in 7-day-old seedlings treated with 50 mM mannitol for 1 day
or left untreated as a control. (A-C) Expression in shoot, and root under control

conditions. (D-F) Expression in shoot, and root under mannitol. Arrowheads point at true

leaves; scale bar = 0.5 mm (A, D), = 0.1 mm (B, E), = 2 mm (C, F).

G *PSKR2:GUS-3* activity in the shoot; scale bar = 0.5 mm.

H, I Seven-day-old seedlings exposed to 50 mM, 200 mM mannitol, 1 µM or 5 µM ABA

for 1 day or left untreated as a control. Relative transcript levels of (H) *PSKR1* and (I)

PSKR2 were analyzed by RT-qPCR in true leaves. Values are means (±SE); different

letters indicate significant differences (one-way ANOVA, Tukey's test, $p<0.05$, 3

biological replicates).

Figure 6. PSKR and ABA pathways interact.

A Four-day-old wild type and *pskr1-3 pskr2-1* seedlings were transferred to 0 mM, 50 mM or 200

mM mannitol and ABA levels in the shoot were determined after 7 days. Different letters indicate

statistically significant differences (Kruskal-Wallis, Tukey's test, $p<0.05$, 5 biological replicates).

B ABA levels in roots of seedlings treated as in A (one-way ANOVA, Tukey's test, $p<0.05$, 5

biological replicates).

C ABA levels in the first true leaf were compared by photobleaching-based FRET analysis in

wild type and *pskr1-3 pskr2-1* seedlings treated as in A. Decreased FRET efficiency indicates

elevated ABA levels. Different capital and minor letters indicate significantly different values

between treatments (Mann-Whitney test, $p<0.05$, n≥142, 3 independent experiments).

D Shoot fresh weights of wild type seedlings that were transferred after 4 days to plates

containing ABA and mannitol at the concentrations indicated were determined after 2 weeks.

E Shoot fresh weight of *pskr1-3 pskr2-1* seedlings grown as described in (D). (D, E) Different

capital and minor letters indicate significantly different values within a given treatment (Kruskal-

Wallis, Tukey's test, $p<0.05$; n=36).

F Overview of genes encoding for enzymes of ABA synthesis (*NCED*s), degradation

(*CYP707A*s), inactivation (*UGT71B*s) and mobilization (*BG*s). PA=phaseic acid.

Figure 7. *NCED* genes are differentially regulated by mannitol and ABA.

Seven-day-old wild type and *pskr1-3 pskr2-1* seedlings were exposed to 200 mM

mannitol or 5 µM ABA for 1 day to analyze relative *NCED3, 5* and *9* transcript levels in

true leaves.

A Relative *NCED* mRNA levels in wild type under control conditions (Kruskal-Wallis,
Tukey's test, $p<0.05$; 3 biological replicates with two technical replicates each).
B-D Changes in *NCED3*, *NCED5* and *NCED9* transcript levels in response to mannitol,
ABA and genotype. Values are means (±SE) with different letters indicating significant
differences (Kruskal-Wallis, Tukey's test, $p<0.05$; n=6, 3 biological replicates).
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Figure 8. Regulation of *CYP707A* ABA-8'-hydroxylase transcripts by mannitol,
ABA and PSKR signaling.
Seven-day-old wild type and *pskr1-3 pskr2-1* seedlings were exposed to 200 mM
mannitol or 5 µM ABA for 1 day to analyze gene expression in true leaves.
A Relative *CYP707A* transcript levels in wild type under control conditions. Values are
means (±SE) with different letters indicating significant differences (Kruskal-Wallis,
Tukey's test, $p<0.05$, n=6; 3 biological replicates).
B-E Relative *CYP707A1-4* transcript levels in response to genotype and treatment
(Kruskal-Wallis, Tukey's test, $p<0.05$, n=6, 3 biological replicates).
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Figure 9. Regulation of *UGT71B* and *BG* transcripts by mannitol, ABA and PSKR
signaling.
Seven-day-old wild type and *pskr1-3 pskr2-1* seedlings were exposed to 200 mM
mannitol or 5 µM ABA for 24 h for qPCR analysis in true leaves. Values are means (±
SE) of 3 biological replicates with different letters indicating significant differences
A Relative *UGT71B6-8* transcript abundance in wild type under control conditions.
B-D Relative mRNA levels of *UGT71B6-8* in response to genotype and treatment
(Kruskal-Wallis, Tukey's test, $p<0.05$).
E Relative *BG* transcript abundance in wild type under control conditions.
F, G Relative mRNA levels of *BG1 and 2* in response to genotype and treatment (one-
way ANOVA, Tukey's test, $p<0.05$).
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Figure 10. Regulation of ABA and mannitol-responsive genes and their impact on growth under low mannitol stress.

Seven-day-old wild type and *pskr1-3 pskr2-1* seedlings were exposed to 200 mM mannitol or 5 µM ABA for 24 h to analyze gene expression in true leaves. Values are means (±SE) of 3 biological replicates with different letters indicating significant differences.

A Relative transcript levels of the osmotic stress response gene *DREB2A* (Kruskal-Wallis, Tukey's test, $p<0.05$).

B Relative transcript level of the ABA receptor gene *PYL6* (one-way ANOVA, Tukey test, $p<0.05$).

C Relative transcript level of the transcriptional repressor *bHLH129* (Kruskal-Wallis, Tukey's test, $p<0.05$).

D Four-day-old wild type and knockout seedlings were exposed to 50 mM mannitol for 21 days. Capital letters indicate significant differences between lines under control conditions. Percentages show values of treated compared to untreated seedlings within each genotype. Minorcase letters indicate significant differences between lines exposed to mannitol (one-way ANOVA, Tukey's test*, $p<0.05$*; n≥18, 2 biological experiments).

Figure 11. Model of shoot growth control during mannitol stress by PSKR1 and ABA.

Mannitol leads to elevated ABA that promotes PSK and PSKR gene expression. PSKR signaling, in a feedback regulatory loop, targets ABA metabolic genes that may control ABA accumulation. PSKR signaling maintains shoot growth in the presence of low levels of mannitol likely by interacting with ABA synthesis and signaling.

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A Cotyledon greening of wild type, *pskr1-3 pskr2-1*, and *PSKR1* overexpressing seedlings exposed to 1 µM ABA or 350 mM mannitol or no treatment for the times indicated. The scheme on the lower left side indicates the genotypes grown on each plate

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B Shoot fresh weights of wt and *pskr1-3 pskr2-1* plants grown as in A.
C Shoot dry weights of wt and *pskr1-3 pskr2-1* plants analyzed in B.
D Leaf numbers, sizes and morphology of wild type and *pskr1-3 pskr2-1* plants grown on mannitol-free medium or on 25 mM mannitol for 3 weeks. Scale bar = 10 mm.
E Primary root lengths of seedlings grown for 7 days after transfer. (B, C, E) Significantly different values within a genotype are denoted by different letters (Kruskal-Wallis, Tukey's ,test, *p*<0.05, n≥36, 3 independent experiments). Asterisk indicates significant differences between genotypes (Mann-Whitney test, *p*<0.05).

A

control

50 mM
mannitol

wt   *pskr1-3* *pskr2-1* *pskr1-3*
                            pskr2-1

B

Figure 3. *PSKR1* promotes growth under mild mannitol stress.
Four-day-old wild type, *pskr1-3, pskr2-1,* and *pskr1-3 pskr2-1* seedlings were transferred to media with or without 50 mM mannitol.
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G *PSKR2:GUS-3* activity in the shoot; scale bar = 0.5 mm.
H, I Seven-day-old seedlings exposed to 50 mM, 200 mM mannitol, 1 μM or 5 μM ABA for 1 day or left untreated as a control. Relative transcript levels of (H) *PSKR1* and (I) *PSKR2* were analyzed by RT-qPCR in true leaves. Values are means (±SE); different letters indicate significant differences (one-way ANOVA, Tukey's test, $p<0.05$, 3 biological replicates).

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C ABA levels in the first true leaf were compared by photobleaching-based FRET analysis in wild type and *pskr1-3 pskr2-1* seedlings treated as in A. Decreased FRET efficiency indicates elevated ABA levels. Different capital and minor letters indicate significantly different values between treatments (Mann-Whitney test, $p<0.05$, n≥142, 3 independent experiments).
D Shoot fresh weights of wild type seedlings that were transferred after 4 days to plates containing ABA and mannitol at the concentrations indicated were determined after 2 weeks.
E Shoot fresh weight of *pskr1-3 pskr2-1* seedlings grown as described in (D). (D, E) Different capital and minor letters indicate significantly different values within a given treatment (Kruskal-Wallis, Tukey's test, $p<0.05$; n=36).
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B-E Relative *CYP707A1-4* transcript levels in response to genotype and treatment (Kruskal-Wallis, Tukey's test, *p*<0.05, n=6, 3 biological replicates).

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Seven-day-old wild type and *pskr1-3 pskr2-1* seedlings were exposed to 200 mM mannitol or 5 µM ABA for 24 h for qPCR analysis in true leaves. Values are means (± SE) of 3 biological replicates with different letters indicating significant differences

A Relative *UGT71B6-8* transcript abundance in wild type under control conditions.

B-D Relative mRNA levels of *UGT71B6-8* in response to genotype and treatment (Kruskal-Wallis, Tukey's test, *p*<0.05).

E Relative *BG* transcript abundance in wild type under control conditions.

F, G Relative mRNA levels of *BG1 and 2* in response to genotype and treatment (one-way ANOVA, Tukey's test, *p*<0.05).

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