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The low-oxygen response is triggered by an ATP-dependent shift in oleoyl-CoA in *Arabidopsis*

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Plant response to environmental stimuli involves integration of multiple signals. Upon low-oxygen stress, plants initiate a set of adaptive responses to circumvent an energy crisis. Here, we reveal how these stress responses are induced by combining (a) energy dependent changes in the composition of the acyl-CoA pool and (b) the cellular oxygen concentration. A hypoxia-induced decline of cellular ATP levels reduces LONG-CHAIN ACYL-COA SYNTHETASE (LACS) activity, which leads to a shift in the composition of the acyl-CoA pool. Subsequently, we show that different acyl-CoAs induce unique molecular responses. Altogether, our data disclose a role for acyl-CoAs acting in a cellular signaling pathway in plants. Upon hypoxia, high oleoyl-CoA levels provide the initial trigger to release the transcription factor RAP2.12 from its interaction partner ACYL-COA BINDING PROTEIN (ACBP) at the plasma membrane. Subsequently, according to the N-end rule for proteasomal degradation, oxygen-concentration dependent stabilization of the subgroup VII ETHYLENE-RESPONSE FACTOR (ERFVII) transcription factor RAP2.12 determines the level of hypoxia-specific gene expression. This research unveils a specific mechanism activating low-oxygen stress responses only when a decrease in the oxygen concentration coincides with a drop in energy.

low oxygen stress | integrative signalling | acyl-CoA | ERFVII | ACBP

Flooding contributes almost 60% to the worldwide cost and damage to crops provoked by natural disasters¹. Due to heavy precipitation and concomitant waterlogging or flooding events in large areas of the world, climate change will cause plants to be even more frequently exposed to oxygen limiting conditions (hypoxia) in the near future².

In plants, subgroup VII ETHYLENE-RESPONSE FACTOR (ERFVII) transcription factors act as key regulators of hypoxic gene expression^{3,4,5,6}. During non-stress conditions, the ERFVII protein RELATED TO APETALA 2.12 (RAP2.12) is sequestered to the plasma membrane via direct interaction with ACYL-CoA BINDING PROTEIN (ACBP)^{3,7,8,9}. Upon hypoxia, RAP2.12 is released from the plasma membrane and subsequently accumulates in the nucleus^{3,7,9}. Further, the stability of ERFVII proteins is tightly controlled in an oxygen-dependent manner employing the Cys-branch of the N-end rule^{3,4}. That is, ERFVII protein degradation is prevented under hypoxic conditions when N-end rule-assisted degradation is impaired due to oxygen limitation¹⁰. Although the homeostatic regulation of adaptive responses to low oxygen stress in plants is well-investigated^{3,4,11}, the identity of the initial trigger to release the ERFVII transcription factors from its membrane docking protein ACBP remains unknown and the existence of multiple signal queues that are integrated into low-oxygen specific responses is likely¹².

ACBPs represent an evolutionary conserved protein family found in *Escherichia coli*, yeast, animals and plants^{13,14} and participate in the regulation of unbound acyl-CoA levels by sequestration and transportation of acyl-CoAs^{15,16}. The interaction between members of a protein family capable of reversibly bind-

ing acyl-CoAs with the ERFVII proteins RAP2.12^{3,7} and RAP2.3^{8,9} provided a first indication that acyl-CoAs can be involved in the release of ERFVII transcription factor protein during hypoxia. We could elaborate this mode of action with experiments on RAP2.12 as a representative member of ERFVII transcription factors.

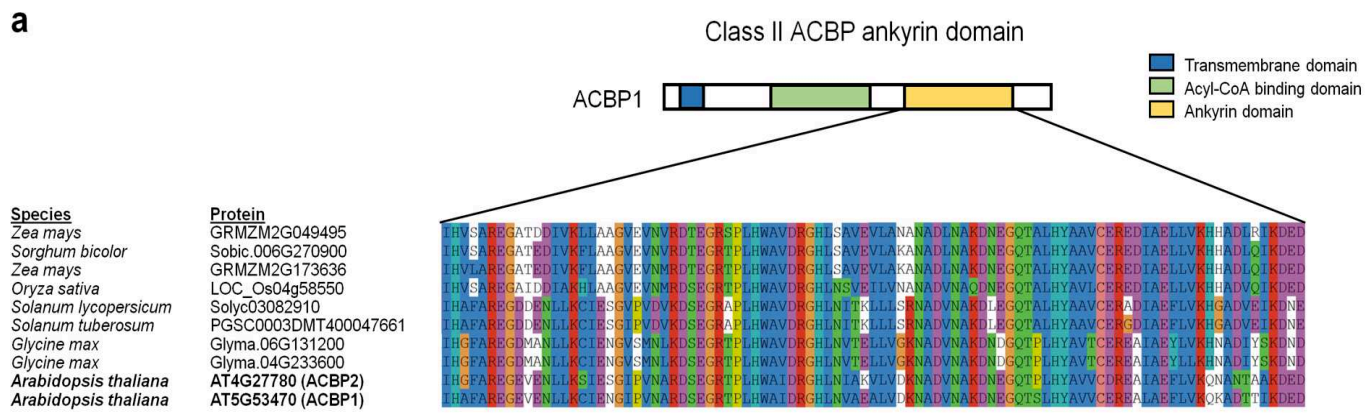
Acyl-CoAs are intermediates in both lipid catabolism and anabolism. In the catabolic pathway, fatty acids are activated in the cytosol by ACYL-CoA SYNTHETASES prior to their transport into the mitochondria or peroxisomes where β -oxidation occurs. In plants, lipid anabolism occurs through two pathways: *de novo* fatty acid synthesis takes place in plastids and the generated fatty acids can be incorporated into complex lipids within the plastid by the so-called prokaryotic pathway. Alternatively, the fatty acid may be exported from the plastid to the cytosol to become substrate for the eukaryotic lipid biosynthesis pathway in the endoplasmic reticulum (ER). Transport of fatty acids from the plastid, through the cytosol into the ER is mainly mediated via palmitoyl-CoA (C16:0-CoA) and oleoyl-CoA (C18:1-CoA) that are produced from palmitic and oleic acid by the enzyme LONG-CHAIN ACYL-CoA SYNTHETASES (LACS) at the outer plastid membrane in root and shoot tissues^{17,18,19,20}. In addition to their involvement in lipid metabolism, acyl-CoAs are also known to modulate the activity of numerous enzymes, ion-channels and transcription factors in animals and microorganisms¹⁵. Examples of acyl-CoAs directly affecting transcription factor activity by functioning as ligands have been reported for humans (HNF-4 α ²¹) and *E. coli* (FadR²²). For plants, direct involvement of acyl-CoAs controlling transcription factor activity was not

Significance

To control adaptive responses to the ever-changing environment that plants are continuously exposed to, plant cells must integrate multiple information to make optimal decisions. Here, we reveal how plants can link information about the cellular energy status with the actual oxygen concentration of the cell in order to trigger a response reaction to low-oxygen stress. We reveal that oleoyl-CoA has a moonlighting function in an energy (ATP) dependent signal transduction pathway in plants, and we provide a model that explains how diminishing oxygen availability can initiate adaptive responses when it coincides with a decreased energy status of the cell.

Reserved for Publication Footnotes

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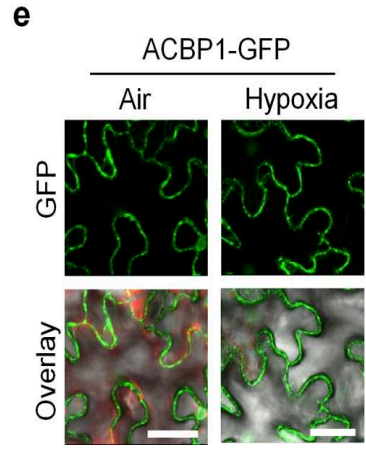
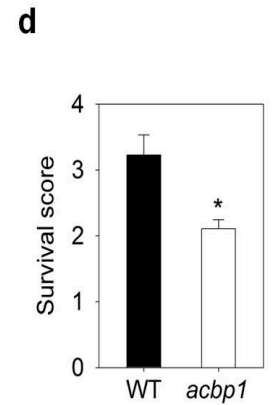
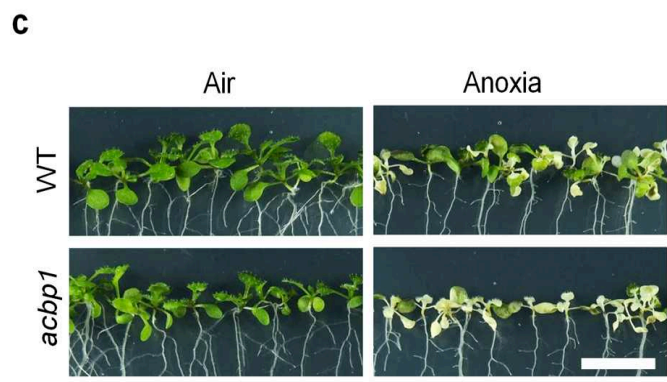
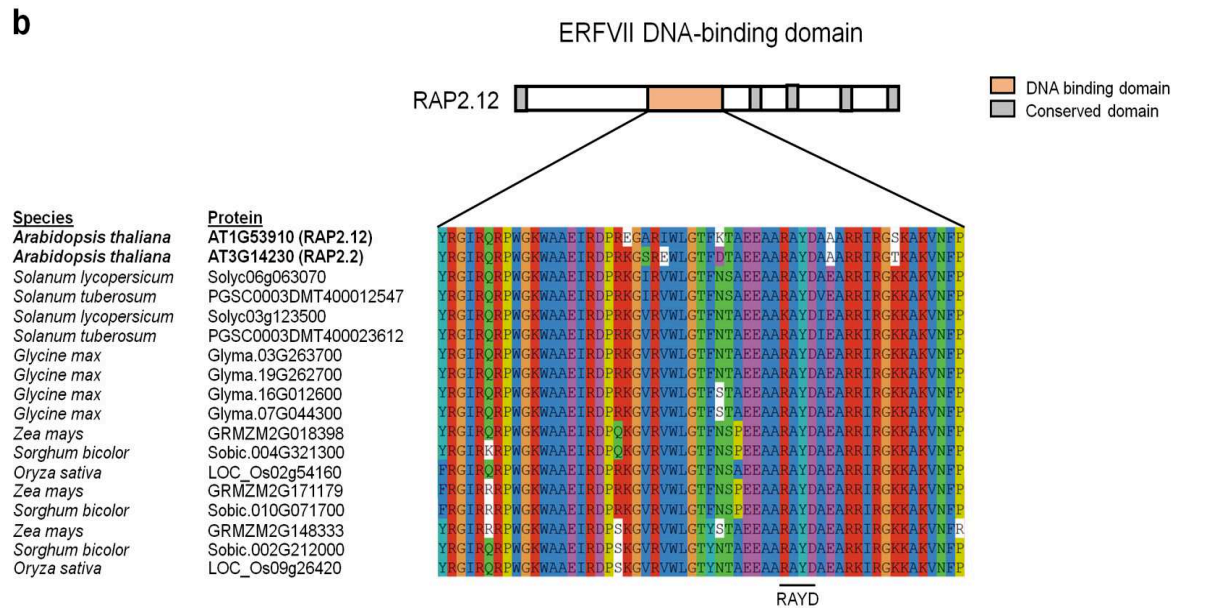


Fig. 1. ACBP is an important element of the low-oxygen stress response pathway in plants **a**, Multiple sequence alignment of Class II ACBP ankyrin domain as compared to ACBP1 and ACBP2 ankyrin domains in *Arabidopsis thaliana*²⁷. **b**, Multiple sequence alignment of ERFVII DNA-binding domain as compared to RAP2.12 and RAP2.2 in *Arabidopsis thaliana*²⁸. Sequences of homologous proteins were obtained from Phytozome v12.0 and aligned with Clustal X. **c**, Eleven-day-old seedlings of wildtype and *acbp1* after 9 h of anoxia and 3 d recovery. Scale bar, 1.0 cm. **d**, Survival scores for wildtype and *acbp1* after 9 h anoxia and 3 d recovery. Data are mean values ± s.d.; * $p < 0.05$, $n = 4$ (15 seedlings per replicate). **e**, Effect of 2 hours of hypoxia treatment (1% O₂) on the localization of GFP-tagged ACBP1 in epidermal cells. Representative pictures are shown. Bar = 10 μm.

demonstrated yet, although an indirect regulatory role has been suggested²³.

Hypoxia has detrimental effects on the plant's cellular homeostasis, in the first place because oxidative phosphorylation in mi-

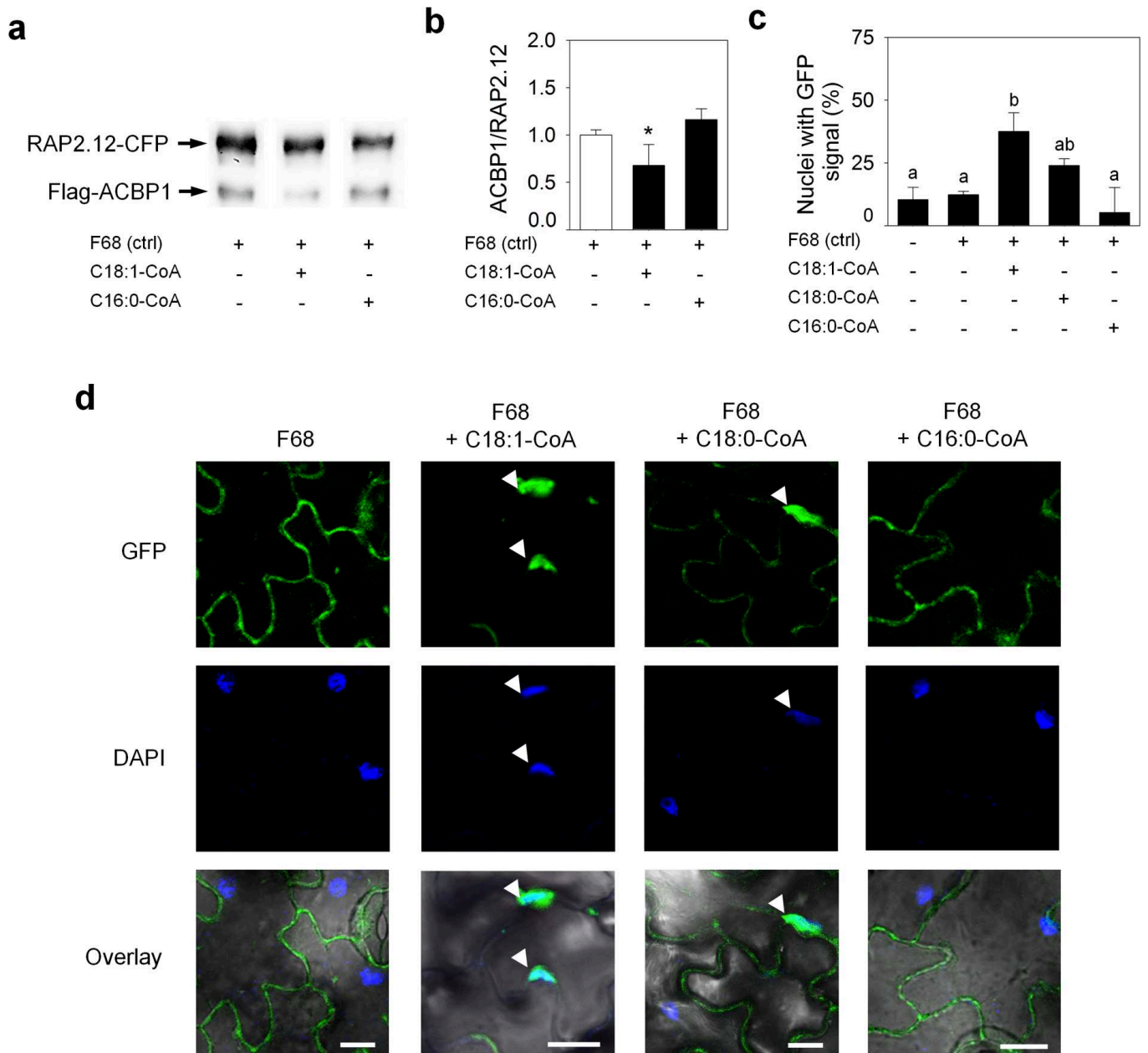


Fig. 2. Application of C18:1-CoA induces RAP2.12 relocation into the nucleus. **a**, Representative Western-blot showing *in vitro* ACBP1-RAP2.12 complex stability after treatment with C18:1-CoA or C16:0-CoA. Pluronic F68 treatment served as control. **b**, Quantification of ACBP1-to-RAP2.12-ratio as shown in panel a. Data are mean values \pm s.d. * $p < 0.05$, $n = 8$. **c**, Percentage of epidermal cells with nuclear localization of RAP2.12-GFP after treatment with different acyl-CoAs. Data are mean values \pm s.d.; * $p < 0.05$. **d**, Localisation of RAP2.12-GFP in detached leaves incubated with 0.1 % C18:1-CoA, C18:0-CoA or C16:0-CoA dissolved in 0.01 % Pluronic F68 under normoxic conditions for 3 hours. Treatment with Pluronic F68 only served as negative control. DAPI staining was used to identify nuclei. Arrows indicate nuclei with GFP signal. Bar = 10 μ m.

tochondria is reduced which ultimately leads to a decrease of the cellular energy charge. This results in ATP-consuming metabolic processes being attenuated, including fatty acid synthesis and processing²⁴. Consequently, the export of newly synthesized fatty acids from the plastid into the cytosol is affected, since the activation to acyl-CoAs is ATP dependent^{18,25}. Therefore, an energy-related impact of hypoxia on acyl-CoA levels in the cytosol is expected and investigated here.

In this study, we reveal a combinatory signaling network by which the reduced energy level under low-oxygen stress is integrated into the ERFVII-dependent hypoxic signaling cascade. We show that dynamic responses of C18:1-CoA and C16:0-CoA levels to hypoxia constitute an early molecular trigger leading to

dissociation of the ACBP:RAP2.12 complex thereby activating the molecular low-oxygen response cascade. We describe an integrative signaling mechanism in which adaptive gene expression upon low-oxygen stress results from the specific combination of (1) low-energy triggered release of the transcription factor RAP2.12 from ACBP as mediated by an acyl-CoA signal; and (2) low-oxygen dependent stabilization of the RAP2.12 protein according to the N-end rule of protein degradation.

Results

C18:1-CoA promotes dissociation of the ACBP:RAP2.12 complex *in vitro* and *in vivo*

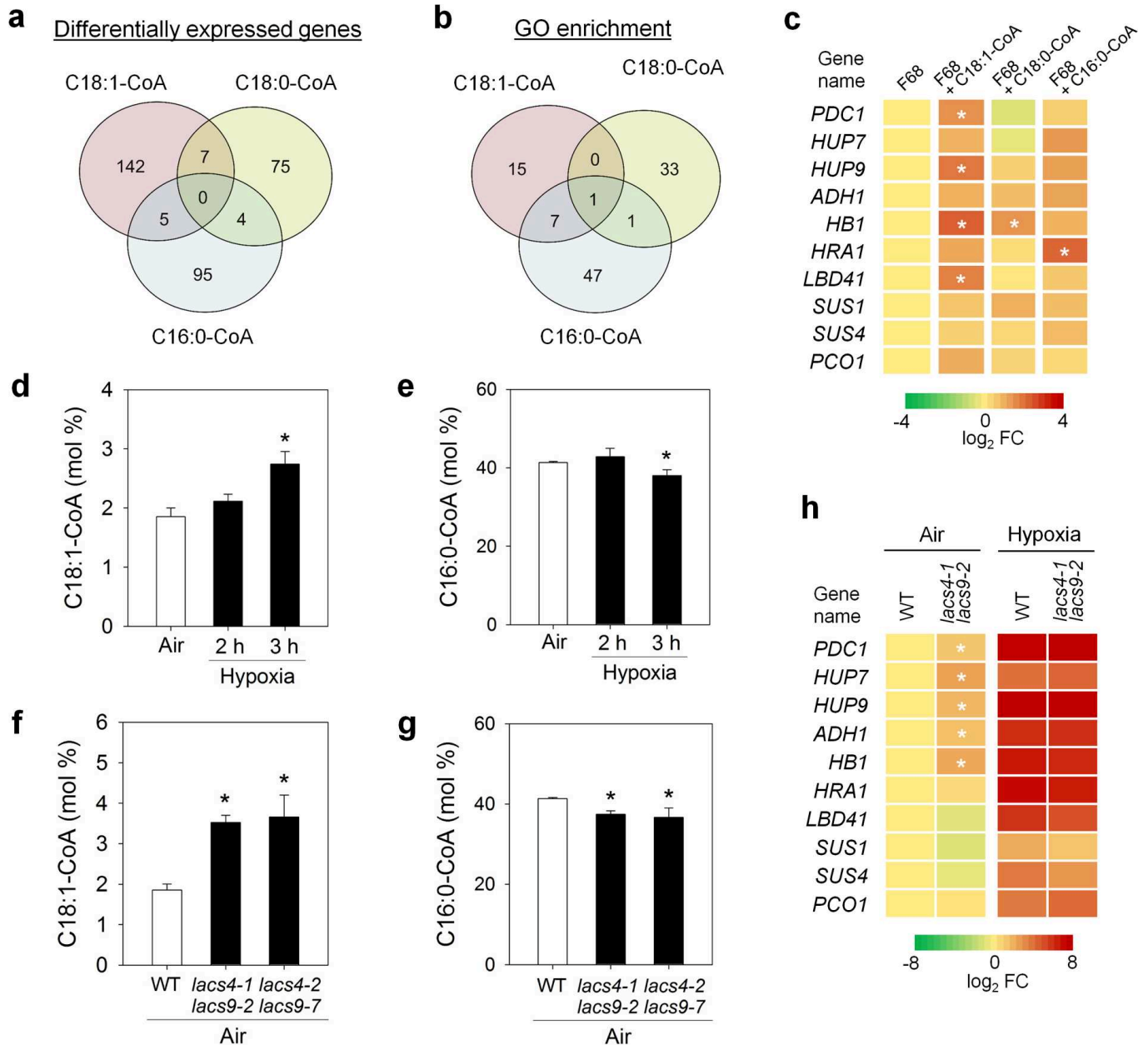


Fig. 3. Changing oleoyl-CoA levels induces low-oxygen responsive gene expression. a, Number of significantly differentially expressed genes in leaves after 1.5 hours treatment with different acyl-CoAs as determined by RNA-Seq (FDR-adjusted p -value < 0.05). b, Number of GO classes in which differentially expressed genes are significantly over-represented under acyl-CoA treatments as shown in a. c, qPCR analysis of differential expression of hypoxia-responsive genes after acyl-CoA treatment in air (reference: F68 only). Data are presented as mean values * $p < 0.05$, $n = 5$. d, C18:1-CoA levels increase upon hypoxia in wildtype. Data are mean values \pm s.d.; * $p < 0.05$, $n = 3$. e, C16:0-CoA levels decrease upon hypoxia in wildtype. Data are mean values \pm s.d.; * $p < 0.05$, $n = 3$. f, C18:1-CoA levels are increased in *lacs4lacs9* double mutants grown in air. Data are mean values \pm s.d.; * $p < 0.05$, $n = 3$. g, C16:0-CoA levels are lowered in *lacs4lacs9* double mutants. Data are mean values \pm s.d.; * $p < 0.05$, $n = 3$. h, Expression data for hypoxia-responsive genes comparing wildtype and *lacs4-1 lacs9-2* in air or hypoxia (2 h 1% O_2 ; mean values, * $p < 0.05$, $n = 4$).

In Arabidopsis, the ERFVII transcription factor RAP2.12 is constitutively expressed but sequestered at the plasma membrane by binding to ACBP1 during normoxic conditions, while it accumulates in the nucleus under oxygen concentrations below 10% (v/v)^{3,7}. The interaction domains of ACBP1 and RAP2.12 were previously identified in Arabidopsis^{3,26,27} and appear to be well conserved among plant species (Fig. 1a-b), indicating that complex formation of both proteins is a general feature in plants. Importantly, changing the expression of ACBPs affects tolerance to low oxygen²⁸ (Fig. 1c-d) similar to what was shown previously for RAP2.12³. During hypoxia GFP-tagged ACBP1

remains at the plasma membrane (Fig. 1e), while GFP-tagged RAP2.12 was shown to accumulate in the nucleus upon hypoxia^{3,7}. This indicates that RAP2.12 dissociates from ACBP1 prior to its relocation to the nucleus. Consequently, the release of RAP2.12 from ACBP1 is considered as a trigger that activates adaptive gene expression in response to hypoxia.

To investigate if acyl-CoAs interfere with the interaction between ACBP1 and RAP2.12, we performed an *in vitro* affinity assay (SI Appendix, Fig. S1) in the presence of either oleoyl-CoA (C18:1-CoA), which is a preferred substrate for ACBP1, or palmitoyl-CoA (C16:0-CoA) that is not a strongly interacting

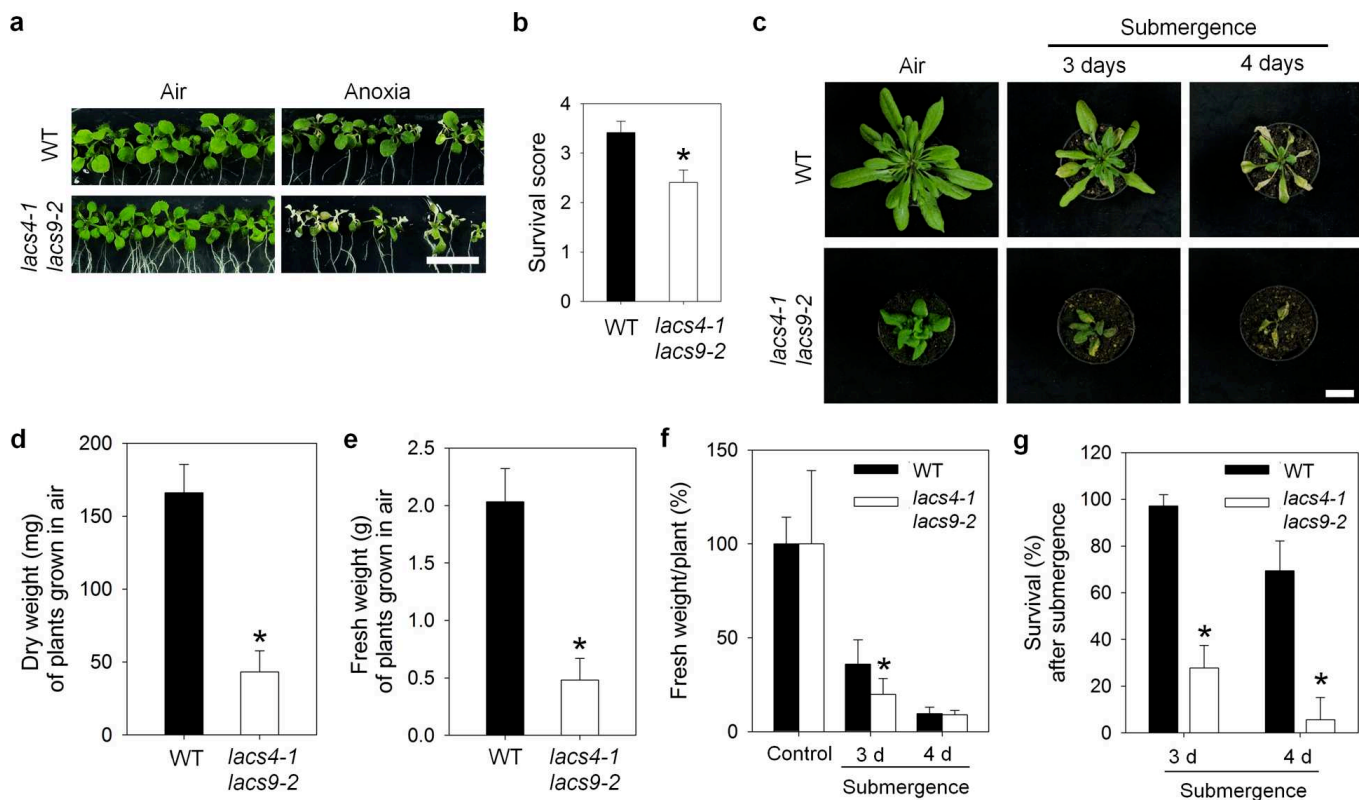


Fig. 4. Decreased tolerance of *lacs4 lacs9* knock-out lines to anoxia and submergence. a, Eleven-day old seedlings of wildtype and *lacs4-1 lacs9-2* after 9 h of anoxia and 3 d recovery. Scale bar, 1.0 cm. b, Survival scores for wildtype and *lacs4-1 lacs9-2* after 9 h anoxia and 3 d recovery. Data are mean values \pm s.d.; * $p < 0.05$, $n = 4$ (15 seedlings per replicate). c, Phenotype of wildtype and *lacs4 lacs9* mutant grown in air (control), or after 3 or 4 days submergence-induced hypoxic treatment. Scale bar = 2 cm. Photographs were taken 4 days after the submergence treatment. d, Absolute dry weight of wild-type and *lacs4-1 lacs9-2* plants grown in air. Data represent mean \pm s.d. (3 replicate experiments with each 12 plants per genotype). Asterisk indicates significant differences after one-way ANOVA ($P < 0.05$). e, Absolute fresh weight of wildtype and *lacs4-1 lacs9-2* plants grown in air. Data represent mean \pm s.d. (3 replicate experiments with each 12 plants per genotype). Asterisk indicates significant differences after one-way ANOVA ($P < 0.05$). f, Relative fresh weight of wildtype and *lacs4-1 lacs9-2* plants grown in air, or after 3 or 4 days of submergence followed by 4 days of recovery. Data represent mean \pm s.d. (3 replicate experiments with each 12 plants per genotype). Asterisk indicates significant differences after one-way ANOVA ($P < 0.05$). g, Percentage of plants that survived the 3 or 4 days of flooding-induced hypoxia, respectively (mean values \pm s.d., 3 replicate experiments with each 12 plants per genotype). * $P < 0.05$ according to one-way ANOVA.

agent^{29,30}. *In vitro* exposure of an ACBP1-RAP2.12 protein complex to C18:1-CoA, but not C16:0-CoA, significantly decreased the binding affinity between the two proteins as indicated by the reduced ratio of Flag-tagged ACBP1 and CFP-tagged RAP2.12 protein (Fig. 2a-b). Apparently, interaction between ACBP1 and C18:1-CoA reduces the binding capacity of ACBP1 for the transcription factor RAP2.12. To confirm that C18:1-CoA-induced dissociation of RAP2.12 from ACBP1 also occurs *in vivo*, we exposed detached leaves of plants expressing *35S:RAP2.12-GFP* to various acyl-CoAs under aerobic conditions. Application of C18:1-CoA, but not C18:0-CoA or C16:0-CoA, significantly induced nuclear accumulation of RAP2.12-GFP, indicating that RAP2.12 was released from ACBP1 *in vivo* after the application of C18:1-CoA, but not by C16:0-CoA (Fig. 2c-d). Translocation of RAP2.12 to the nucleus was previously described to occur during hypoxic conditions^{3,7}. Therefore, we tested if application of acyl-CoA to leaves might have induced hypoxia due to increased beta-oxidation or mitochondrial respiration. However, no increase of the oxygen consumption rate by leaf tissue after treatment with acyl-CoAs was observed, indicating that our experimental treatment did not affect the oxygen concentration of the tissue in this experiment (SI Appendix Fig. S2). We concluded, remobilization of the transcription factor RAP2.12 from the plasma membrane into the nucleus can be triggered *in vivo* by increasing the level of C18:1-CoA.

Acyl-CoAs provoke distinct transcript responses

To determine if specific transcriptional responses are provoked by the application of different acyl-CoAs, RNA-Seq transcriptome analysis was performed on wild-type seedlings exposed to either 1 mM C18:1-CoA, C18:0-CoA or C16:0-CoA. Uptake of these externally applied acyl-CoAs is mediated by ABCD-transporters that first cleave the CoA-group from the acyl-chain, allowing the resulting fatty acid to cross lipid membranes. Once inside the cell, CoA is immediately reattached, which traps the acyl-CoA in the cellular compartment in which it has been imported³¹. This analysis revealed that each of these acyl-CoAs modulates distinct sets of genes (Fig. 3a, SI Appendix, Table S1). The high specificity of induced changes in gene expression underlines the eligibility of acyl-CoAs as signaling molecules in plants. To investigate the biological function of the differentially regulated genes, a Gene Ontology enrichment analysis³² was carried out. While application of C18:0-CoA or C16:0-CoA mainly affected the expression of genes related to reproductive development and hormone signaling, C18:1-CoA mainly modulated the expression of genes associated with hypoxia and low oxygen responses (Fig. 3b, SI Appendix, Table S2). This result was confirmed by qPCR-assisted expression profiling executed on wild-type plants incubated with C18:1-CoA. Indeed, RAP2.12-regulated hypoxia-response genes were induced by C18:1-CoA treatment, while C18:0-CoA and C16:0-CoA had only minor effects on the expression of these genes (Fig. 3c, SI Appendix Table S1). This observation is readily explained by our earlier

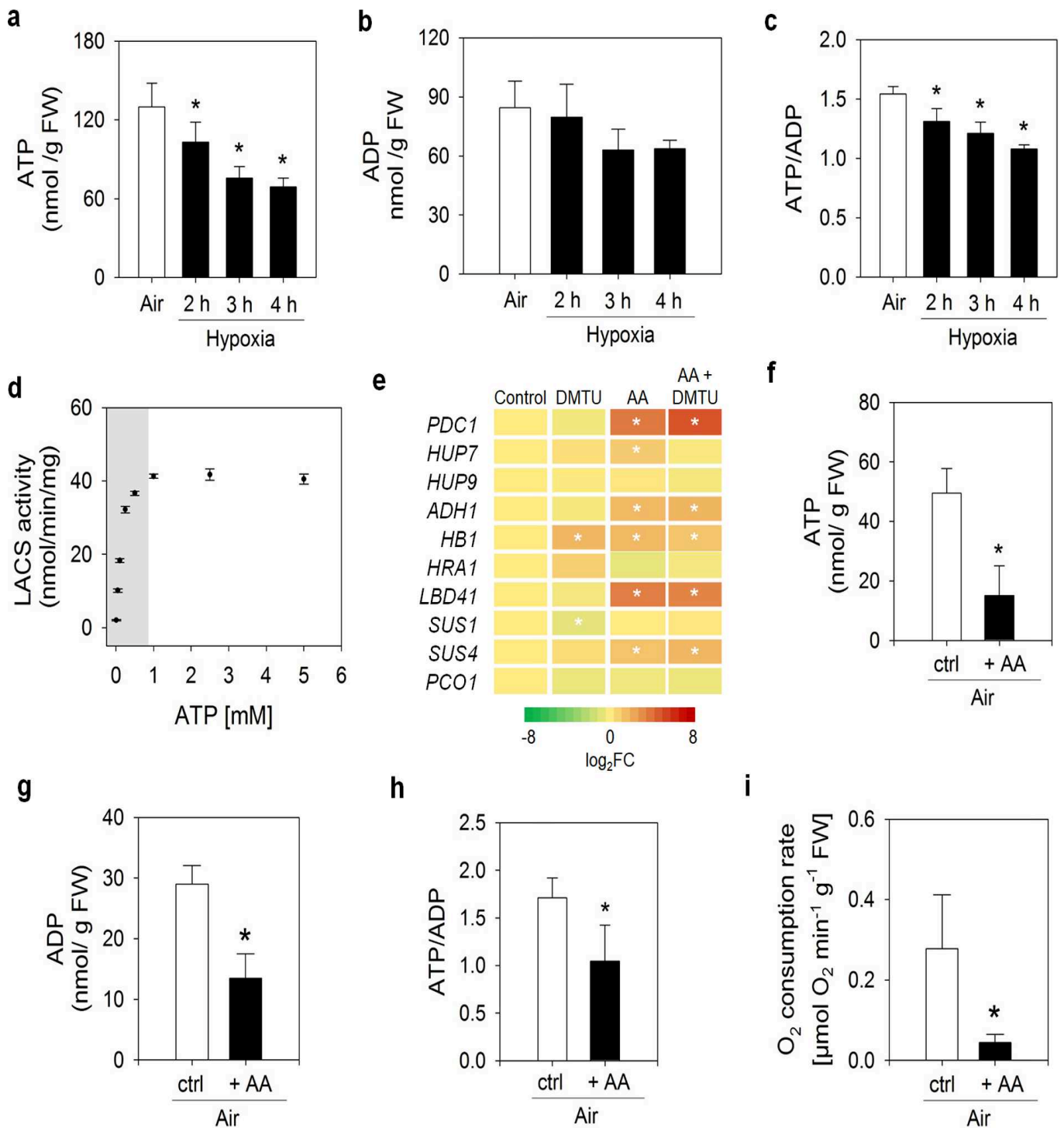


Fig. 5. Decreasing the cellular ATP level constitutes limiting conditions for LACS activity and induces the expression of low-oxygen responsive genes. **a**, ATP levels under hypoxia (mean \pm s.d., * $p < 0.05$, $n = 5$). **b**, Concentration of ADP in wild-type seedlings grown under long-day conditions and exposed to hypoxia. Data shown are given in nmol per gram fresh weight and represent the mean \pm s.d. of independent replicates ($n = 5$). **c**, ATP-to-ADP-ratio under hypoxia (mean \pm s.d., * $p < 0.05$, $n = 5$). **d**, *In vitro* LACS activity depends on ATP concentration (mean \pm s.d., * $p < 0.05$, $n = 5$). The grey area marks the ATP-concentration range usually determined in plant cells. **e**, Differential expression of hypoxia-responsive genes after 3 hours of 1 mM dimethylthiourea (DMTU) and/or 50 μ M antimycin-A (AA) treatment under aerobic conditions (reference: mock-treated control). Data are presented as mean \pm s.d.* $p < 0.05$, $n = 5$. **f**, ATP levels after 3 hours of 50 μ M antimycin-A treatment (AA) (mean \pm s.d., * $p < 0.05$, $n = 5$). **g**, Concentration of ADP in wild-type seedlings exposed to 3 hours of 50 μ M antimycin-A (AA) treatment. Data represent mean \pm s.d. ($n = 5$). Asterisk indicates significant differences after one-way ANOVA ($p < 0.05$). **h**, ATP-to-ADP-ratio after 3 hours of 50 μ M antimycin-A (AA) treatment (mean \pm s.d., * $p < 0.05$, $n = 5$). **i**, Oxygen consumption rate in wild-type leaves upon 3 hours of 50 μ M antimycin-A treatment. Data represent mean \pm s.d. ($n = 7$). Asterisk indicates significant difference after Student's t-test ($p < 0.05$).

observation that RAP2.12 relocalizes to the nucleus upon C18:1-CoA application (Fig. 2c-d). Therefore, it is concluded that

C18:1-CoA provides a specific cellular signal that is substantially

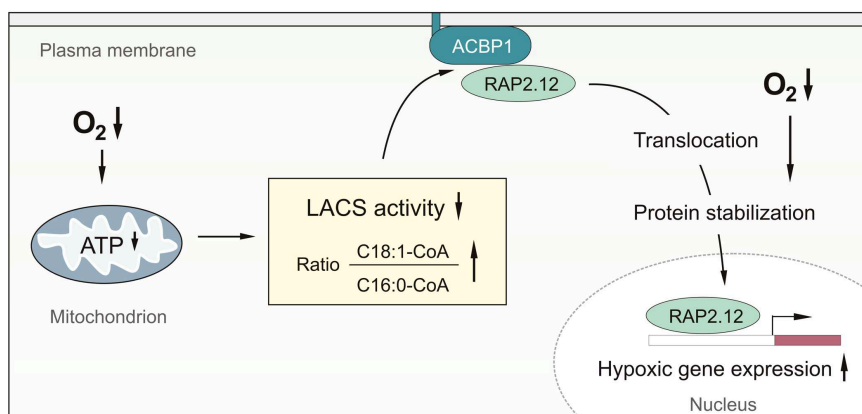


Fig. 6. Triggering low-oxygen responses in plants integrates the cellular energy and oxygen status via modulation of oleoyl-CoA levels. Oxygen limitation reduces cellular ATP levels, which results in increased C18:1-CoA levels. Dissociation of ERFVII protein (as shown here for RAP2.12) bound to ACBP1 at the plasma membrane is promoted by C18:1-CoA. Free ERFVII protein is stable under low-oxygen conditions and relocalizes into the nucleus to activate hypoxic responses.

involved in the control of gene expression by releasing RAP2.12 from ACBP1.

Increase of C18:1-CoA to C16:0-CoA ratio induces hypoxic gene expression *in vivo*

In a physiological context, C18:1-CoA-mediated dissociation of RAP2.12 from ACBP1 only makes sense when the endogenous acyl-CoA pool responds to hypoxia. Indeed, HPLC-assisted quantification of acyl-CoAs revealed a shift to elevated C18:1-CoA (Fig. 3d) and C20:0-CoA (SI Appendix, Fig. S3) levels with less C16:0-CoA (Fig. 3e) after 3 hours of hypoxia, while no significant changes of the total pool of acyl-CoAs included in our analyses were observed (SI Appendix, Fig. S3). These dynamic responses of specific acyl-CoAs to changing environmental conditions as exemplified here for hypoxia are in line with the suggestion that acyl-CoAs in plants can play a role in stress signaling.

A similar shift of the acyl-CoA pool as observed during low-oxygen conditions was observed in transgenic plants in which two LACS genes, *LACS4* and *-9*, were knocked out³³ (Fig. 3f-g, SI Appendix, Fig. S4). Under aerobic conditions, *lacs4lacs9* double knock-out plants have elevated C18:1-CoA and reduced C16:0-CoA levels. To provide further proof that endogenous changes of the C18:1-CoA or C16:0-CoA level can have an effect on low-oxygen responses of plants, we tested the induction of hypoxic gene expression in *lacs4lacs9* plants in air. Indeed, many RAP2.12-dependent hypoxia-response genes were activated under aerobic conditions in *lacs4lacs9* (Fig. 3h, SI Appendix, Table S2). In addition, also tolerance to hypoxia was altered. Performance of *lacs4lacs9* was impaired under both anoxia and submergence conditions as compared to wild-type plants (Fig. 4). Similar observations were described for plants with constitutive activation of the hypoxia stress response pathway³⁴, although it should be mentioned that the impact of constitutive activation of the ERFVII signaling pathway on plant performance under stress conditions also appears to depend on the experimental growth conditions and the recovery treatment^{4,35}. Altogether, our data give rise to a model describing that the control of endogenous acyl-CoA levels through LACS activity is a prerequisite to properly induce hypoxia tolerance responses in plants.

LACS activity is reduced by depletion of ATP

To explain the mechanism by which LACS activity in plants is affected by hypoxic conditions, we analyzed LACS activity in dependence of its substrate adenosine-tri-phosphate (ATP). First, we monitored the cellular energy status in wild-type plants grown under hypoxia. Already after 2 hours, the ATP level as well as the ATP-to-ADP ratio were significantly reduced as compared to the air-treated control (Fig. 5a-c). To examine at which ATP concentration LACS activity becomes substrate limited, an *in vitro* LACS activity assay was performed. This experiment showed that the activity of *LACS4* was ATP dependent at ATP concentrations

below 0.8 mM (Fig. 5d), which is close to the estimated cytosolic ATP concentration under aerobic conditions *in planta*^{36,37,38}. Since ATP concentrations in plant cells decrease during hypoxia²⁴, LACS activity is expected to diminish concomitantly. However, it should be mentioned that variations of the ATP concentration between tissues or even within a cell (between organelles) might lead to different local ATP-limiting conditions for LACS during hypoxic stress. Moreover, hypoxia-induced low-energy status will also influence other processes that are not covered by the analyses that we describe here.

To verify that a drop in ATP can trigger hypoxia responses of plants in air, we chemically inhibited mitochondrial respiration using antimycin-A. Indeed, after three hours of 50 μM antimycin-A treatment of rosettes in air, several hypoxia responsive genes were significantly induced (Fig. 5e, SI Appendix Table S3), while ATP levels and the ATP-to-ADP ratio were reduced (Fig. 5f-h). Since application of antimycin-A strongly reduced the oxygen consumption rate of the tissue (Fig. 5i), it is unlikely that the induction of hypoxia responsive genes is the consequence of low-oxygen concentrations here. Also an antimycin-A induced ROS burst appeared unlikely to be responsible for the gene induction, since the induced genes responded similarly when in addition to antimycin-A also 1 mM of the hydrogen peroxide scavenger dimethylthiourea (DMTU)^{39,39} was supplied (Fig. 5e). Although it cannot be concluded that reduced ATP levels are exclusively responsible for triggering hypoxia responses in plants without performing dose response analyses of individual and combined compounds, the data provide evidence that the cellular energy status is involved in the regulation of hypoxic gene expression.

Discussion

In this study, we demonstrate that acyl-CoAs provoke distinct transcriptional responses in plants, suggesting that they are involved in different signaling pathways. Specifically, binding of C18:1-CoA to ACBP triggers dissociation of the ACBP:RAP2.12 complex upon an hypoxia-induced energy crisis, resulting in mobilization of the transcription factor RAP2.12 into the nucleus. Consequently, RAP2.12-mediated gene expression is induced. Therewith we reveal the trigger of the ERFVII-mediated signaling cascade to activate cellular hypoxia-tolerance responses in plants (Fig. 6).

When the oxygen availability to cells diminishes, mitochondria produce less ATP due to a reduced activity of oxidative phosphorylation⁴¹. Indeed, our plants showed a rapid decrease of their energy status upon hypoxia. Already within two hours, the ATP-to-ADP ratio dropped significantly and remained decreasing throughout the rest of the experiment (Fig. 5c). Consequently, the activity of ATP-mediated reactions within the cell is expected to

953 reduce too²⁴. Here, we show that ATP concentration-dependent
954 LACS activity reaches its maximum at an ATP concentration of 1
955 mM (Fig. 5d) which resembles the concentration in a non-stressed
956 plant cell^{36,37,38}. This means that any decrease of the cellular
957 energy status is translated into a reduction of LACS activity. The
958 enzyme LACS is among others located in the plastidial outer
959 envelope where it is provided with C16:0 and C18:1 fatty acids
960 from the stroma by thioesterases that are located in the inner
961 envelope^{42,43}. Using CoA and ATP as co-substrates, LACS acti-
962 vates the fatty acids and releases them as C16:0-CoA and C18:1-
963 CoA in the cytosol¹⁸. When the level of ATP drops and LACS
964 activity decreases, the export rate of fatty acids will be reduced. As
965 the elongation and rapid desaturation reactions in the plastidial
966 stroma from C16:0 to C18:1 commence, the ratio C18:1 compared
967 to C16:0 that is provided to LACS from the stroma is likely to
968 increase through time under these conditions. As a consequence,
969 the ratio of C18:1-CoA to C16:0-CoA that is released by LACS
970 into the cytosol will increase and would readily explain why we
971 observe an increased level of C18:1-CoA as compared to C16:0-
972 CoA in plants that were exposed to low oxygen (Fig. 3d,e) as well
973 as in *lacs4lacs9* double knockout lines in air (Fig. 3f,g).

974 Acyl-CoA fatty acid esters bind to ACBP proteins. Here, we
975 show that specifically the interaction between C18:1-CoA with
976 ACBP1 results in release of RAP2.12 from the ACBP1:RAP2.12
977 complex while C16:0-CoA does not affect the interaction between
978 RAP2.12 and ACBP1 (Fig. 2). A shift of the ratio between C18:1-
979 CoA and C16:0-CoA as described above, will therefore lead to
980 the release of RAP2.12 from ACBP. Indeed, application of C18:1-
981 CoA, but not C16:0-CoA, increased the number of nuclei in which
982 GFP-tagged RAP2.12 accumulated (Fig. 2c, d). Consequently,
983 also upregulation of hypoxia responsive marker genes was ob-
984 served (Fig. 3a-c).

985 Similar to this external application of acyl-CoAs, also an
986 endogenous shift of the C18:1-CoA to C16:0-CoA ratio as ob-
987 served in *lacs4lacs9* mutant lines resulted in the upregulation
988 of hypoxia responsive genes already in aerobic conditions (Fig.
989 3h). Altogether, these data describe how the ultimate trigger for
990 release of RAP2.12 from ACBP is constituted by an energy-crisis
991 provoked response of the acyl-CoA pool under hypoxia (Fig. 6).

992 Changes of the cellular energy status happen all the time as
993 most biotic and abiotic stress conditions affect energy metabolism
994 in one way or another⁴⁴. It would be most detrimental for
995 plant fitness, when each fluctuation of the ATP-level immediately
996 led to the activation of hypoxic gene expression³⁴. Therefore,
997 the lifetime of ERFVII proteins depends on the actual cellu-
998 lar oxygen concentration via the Cys-branch of the N-end rule
999 for proteasomal protein degradation^{3,4,11}. Only when an energy
1000 crisis is provoked by low-oxygen conditions, the stabilization of
1001 RAP2.12 enables the protein to accumulate in the nucleus in a
1002 sufficient amount to activate hypoxic gene expression. However,
1003 when RAP2.12 is released from ACBP due to an energy deficit
1004 that is not related to low-oxygen stress, the protein will be rapidly
1005 degraded due to proteasomal activity. Therefore, we propose that
1006 the ACBP:RAP2.12 complex forms the initial hub capable of
1007 integrating signal inputs related to the cellular energy charge with
1008 oxygen-concentration dependent determination of the life-time
1009 of RAP2.12 protein (Fig. 6). Subsequently, RAP2.12 protein that
1010 is newly synthesized after the onset of hypoxia does still undergo
1011 N-end-rule-assisted stabilization but may not be linked directly to
1012 the energy status of the cell.

1013 Constitutive activation of the molecular stress response to
1014 low-oxygen in the *lacs4lacs9* mutant background lead to reduced
1015 tolerance to low-oxygen as well as to flooding stress (Fig. 4).
1016 This observation is congruent with earlier observations that con-
1017 stitutive activation of the hypoxia stress response in plants *via*
1018 overexpression of a stable version of RAP2.12 protein reduced

1019 the tolerance of the plants to hypoxia³⁴ although other studies
1020 indicate that the latter phenotype is likely conditional to growth
1021 conditions and recovery treatment too^{4,34}. This underlines the im-
1022 portance of a timely control of stress responses that are optimally
1023 adjusted to the actual environmental conditions. The integration
1024 of (a) energy-dependent changes in C18:1-CoA levels as cellular
1025 trigger signal with (b) the homeostatic control of the lifetime of
1026 RAP2.12 in an oxygen-concentration dependent manner provides
1027 a highly specific control mechanism to initiate hypoxic responses.
1028 The mechanism guarantees that a full low-oxygen response is
1029 activated only when hypoxia is detrimental for the plant's energy
1030 status.

1031 The ATP dependence of oleoyl-CoA synthesis by LACS in
1032 combination with the impact of oleoyl-CoA on the interaction
1033 between RAP2.12 and ACBP exposes mitochondrial activity as
1034 an early trigger for hypoxia signaling. Consistently, manipulating
1035 mitochondrial ATP synthesis using inhibitors of specific respi-
1036 ratory complexes like antimycin-A induced RAP2.12-controlled
1037 hypoxic gene expression even under aerobic conditions⁴⁵ (Fig.
1038 5e). It is striking that the induction of hypoxic gene expression
1039 in air by acyl-CoAs (Fig. 3c,h) or antimycin-A (Fig. 5e) was
1040 lower as compared to the induction of these genes by hypoxic
1041 conditions (Fig. 3h). This observation stresses the impact of
1042 additional oxygen-dependent regulatory mechanisms, such as the
1043 N-end rule-mediated reduction of RAP2.12 life-time in air. In
1044 this context, it is worth mentioning that the control of low-oxygen
1045 stress responses is not only linked to the oxygen and energy status
1046 of the cell, but it is also known to be influenced by other cellular
1047 factors such as nitric oxide^{46,47}, hydrogen peroxide⁴⁸, calcium
1048^{49,50}, and potassium⁵¹. In the near future, it will be intriguing
1049 to expand the mechanistic explanation on how the energy and
1050 oxygen status of a cell are integrated upon low-oxygen stress with
1051 these additional signaling components¹².

1052 ACBPs are found in all kingdoms of life, while ERFVII are
1053 highly conserved among higher plants. Moreover, the interaction
1054 domains of both protein families are highly conserved in plants
1055 (Fig. 1). Therefore, the ACBP:ERFVII signaling hub as presented
1056 here may represent a universal mechanism in plants to initiate
1057 hypoxia-induced stress responses via the integration of multiple
1058 cellular signals. Moreover, the specific interaction of ACBPs to
1059 various acyl-CoAs on the one hand (Fig. 2) and the distinct cellular
1060 responses provoked by individual acyl-CoAs on the other hand
1061 (Fig. 3a,b) suggest that many additional possibilities may exist
1062 of how acyl-CoAs can modulate cellular signaling pathways in
1063 plants.

1064 Materials and Methods

1065 **Plant materials.** Arabidopsis thaliana ecotype Col-0 was used as wildtype
1066 for all analyses. 35S:RAP2.12-GFP line and *lacs4-1 lacs9-2* and *lacs4-2 lacs9-7*
1067 double knock-out lines were described previously^{3,33}. The *acbp1* knock-out
1068 line (SAIL_683_C03) was obtained from NASC (SI Appendix, Fig. S5).

1069 **Growth conditions and analysis of oxygen deprivation response.** For
1070 testing anoxia tolerance of seedlings, seeds were sown on half-strength MS
1071 medium containing 0.5% (w/v) sucrose, stratified for 48 hours at 4°C and
1072 germinated at 21°C day / 18°C night with a photoperiod of 16 h light (150
1073 $\mu\text{mol m}^{-2} \text{s}^{-1}$) and 8 h dark. At day 11, seedlings were exposed to full anoxia,
1074 by placing the culture plates in an environment containing 100% nitrogen,
1075 for 9 h in the dark to avoid photosynthetic oxygen production. After 3 days
1076 of recovery, the survival score was determined as previously described⁴. For
1077 submergence assays, seeds were sown in moist soil, stratified at 4°C in the
1078 dark for 48 h and germinated at 21°C day / 18°C night with a photoperiod of
1079 16 h light and 8 h darkness. 4-week-old plants were submerged with water in
1080 40 cm high plastic containers and kept in the dark to avoid photosynthetic
1081 oxygen production. Leaves stayed 10 cm under the water surface. After 3 or 4
1082 days, water was removed from the boxes and plants were placed back under
1083 photoperiodic conditions (16 h/8 h, light/dark). Submergence tolerance was
1084 assayed after 4 days of recovery.

1085 For acyl-CoA pool measurements, plants were grown on horizontal agar
1086 plates containing 0.8 % agar in ½ MS medium (pH 5.7) with 15 mM sucrose
1087 for two weeks under long-day conditions (16 h in 150 $\mu\text{mol photons m}^{-2}$
1088 s^{-1} at 21°C and 8 h in 0 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ at 19°C). After 2.5 h in light,

1089 they were subjected to hypoxia in the dark by exposition to a stream of
1090 air containing 1% (v/v) oxygen, supplemented with nitrogen and 350 ppm
1091 carbon dioxide. Plants were harvested by freezing in liquid nitrogen after
1092 2 h, 3 h, and 4 h of hypoxia. For normoxic control, untreated plants were
1093 harvested simultaneously with the start of hypoxic treatment.

1094 For expression analysis after acyl-CoA treatment, wild-type seeds were
1095 sown in 24-well plates containing half-strength liquid MS-medium, stratified
1096 for 48 hours at 4°C and germinated at 21°C day / 18°C night with a photo-
1097 period of 16 h light (150 μmol m⁻² s⁻¹) and 8 h dark. At day 14, seedlings
1098 were treated with different acyl-CoAs at a final concentration of 0.1% in
1099 0.01% Pluronic F68. Pluronic is a non-fatty acid based detergent which means
that the detergent properties of pluronic in solubilising fatty acyls are not
confounded by fatty acyls derived from the detergent itself⁵²

1100 **Cloning of constructs.** Coding sequences (CDSs) were amplified from
1101 a cDNA template using Phusion High Fidelity DNA polymerase (Thermo
1102 Scientific). The ACBP1 CDS was cloned into pENTR-D and recombined into
1103 pK7FWG2⁵¹ to fuse it with GFP. For *in vitro* expression, the CDS of ACBP1
1104 was fused N-terminally with a Flag-tag by PCR and cloned into pF3A WG
1105 BYDV (Promega), while the CDS of RAP2.12 was fused C-terminally to CFP by
1106 PCR and cloned into pF3A WG BYDV (Promega). A complete list of all primers
used is provided in **SI Appendix, Table S4**.

1107 **Plant transformation.** Transgenic ACBP1-GFP plants were generated by
1108 transforming wild-type plants with the vector pK7FWG2⁵³ containing the
1109 ACBP1 CDS fused in frame to GFP at its C-terminus. T0 seeds were screened for
kanamycin resistance and the presence of GFP signals by confocal microscopy.

1110 **qRT-PCR.** RNA extraction, digestion of genomic DNA, cDNA synthesis
1111 and qRT-PCR analysis were performed as described previously⁵⁴. For all
1112 experiments, 4-5 independent biological replicates were used, as indicated in
1113 the figure and table legends. For normalization, UBIQUITIN10 expression was
1114 used according to³ Primers for hypoxia core genes, LACS genes and UBI10
are given in **SI Appendix, Table S4**.

1115 **RNA-SEQ analysis.** Illumina HiSeq sequencing was performed according
1116 to standardized protocols as described in detail in the SI Appendix. Trans-
1117 scriptome analysis was performed by means of CLC Genomics Workbench
1118 v.6 using the Arabidopsis thaliana reference sequence (Tair10). Expression
1119 values were normalized using quantile normalisation and pair-wise statistical
analyses comparing the treatments performed using FDR-corrected p-values
based on Baggerly's test⁵⁵.

1120 **Confocal imaging.** For protein localization studies, GFP signals were im-
1121 aged and analysed with a Leica DM6000 TCS SP8 confocal microscope (Leica
1122 Microsystems). Nuclear staining was performed by using DAPI (molecular
1123 probes) according to the manufactures instructions. For quantification of
1124 nuclear translocation of RAP2.12 after acyl-CoA treatment, twenty DAPI-
1125 stained nuclei per plant (5 plants in total) were analyzed per treatment.
1126 Leaves of 5-week-old soil-grown 35S:RAP2.12-GFP plants were incubated
1127 for 3 h with different acyl-CoAs at a final concentration of 0.1% in 0.01%
Pluronic F68 in a 24-well plate under continuous shaking in the light. The
experiments were repeated three times.

1128 **In vitro binding assay.** The method to determine whether acyl-coAs
1129 affect the interaction between ACBP1 and RAP2.12 is explained in detail
1130

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1157 in the SI Appendix, Supplementary Information text and Fig. S1. In brief,
1158 both proteins were synthesized using wheat germ extract⁵⁴. The full CDS of
1159 RAP2.12 was fused C-terminally with the CDS of CFP, and the CDS of ACBP1
1160 was N-terminally fused with a FLAG-tag. RAP2.12-CFP protein was bound to
1161 GFP-Trap-A beads (Chromotek) and incubated with ACBP1 protein overnight.
1162 Subsequently, beads were resuspended in wash buffer containing different
1163 acyl-CoAs at a final concentration of 0.1% in 0.01% Pluronic F68, or as a
1164 mock control only 0.01% F68. After one night of incubation, the buffer was
replaced and the composition of the protein complex retained to the beads
was analysed on a Western blot.

1165 **Analysis of acyl-CoA esters.** Acyl-CoAs were extracted, derivatized, and
1166 analysed using HPLC as described earlier⁵⁶. Detailed information about the
1167 method is provided in the SI Appendix.

1168 **LACS4 in vitro enzyme assay.** The *in vitro* LACS enzyme assay was
1169 carried out as described previously¹⁷ using protein that was heterologously
expressed in *E. coli*⁵⁷. Details of the method are explained in the SI Appendix.

1170 **ATP and ADP quantification** ATP and ADP were extracted with 16 %
1171 trichloroacetic acid³³ and analysed after derivatisation by HPLC as described
1172 previously⁵⁸. Details of the procedure are described in the SI Appendix.

1173 **Analysis of oxygen consumption rates.** For the determination of oxygen
1174 consumption rates four-week-old plants grown on soil under short-day
1175 conditions (8 h in 160 μmol photons m⁻² s⁻¹ at 20 °C and 16 h in 0 μmol photons
1176 m⁻² s⁻¹ at 16 °C) were used. Starting three hours prior to measurement, the
1177 plants were sprayed every hour either with 50 mM MES buffer (pH 6.5)
1178 containing 50 μM antimycin-A⁵⁹ or with 50 mM MES buffer for control.
1179 This treatment was done in the last hour of dark phase and two hours
1180 into the light phase, and then measurement of oxygen consumption rates
1181 at normoxic conditions was performed as described before³⁴ using the
1182 respective spraying solution. In a similar setup the effect of different acyl-
CoAs on the oxygen consumption rate was tested by incubating leaf disks in
acyl-CoAs at a final concentration of 0.1% in 0.01% Pluronic F68.

1183 **Statistical analysis.** Statistical evaluation of significant variation be-
1184 tween treatments or genotypes was done by performing Student's t-test or
1185 one-way ANOVA where appropriate.

1186 **Data availability.** The RNAseq gene expression data are available in
1187 NCBI's Gene Expression Omnibus (GEO) through GEO Series accession number
1188 GSE97186.

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1194 experiments. R.S., M.F., M.V.P, M.A., F.P., D.A.W., M.K., T.L., G.B., and J.H.S
1195 performed experiments. F.L., I.A.G. and P.G. provided expertise and feedback.
1196 R.S., J.H.S. and J.T.vD. wrote the manuscript. All authors commented on the
1197 manuscript. R.S., J.H.S. and J.T.vD. conceived the project.

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