The Mitochondrial Sulfur Dioxygenase ETHYLMALONIC ENCEPHALOPATHY PROTEIN1 Is Required for Amino Acid Catabolism during Carbohydrate Starvation and Embryo Development in Arabidopsis1[C][W]  

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The sulfur dioxygenase ETHYLMALONIC ENCEPHALOPATHY PROTEIN1 (ETHE1) catalyzes the oxidation of persulfurides in the mitochondrial matrix and is essential for early embryo development in Arabidopsis (Arabidopsis thaliana). We investigated the biochemical and physiological functions of ETHE1 in plant metabolism using recombinant Arabidopsis ETHE1 and three transfer DNA insertion lines with 50% to 99% decreased sulfur dioxygenase activity. Our results identified a new mitochondrial pathway catalyzing the detoxification of reduced sulfur species derived from cysteine catabolism by oxidation to thiosulfate. Knockdown of the sulfur dioxygenase impaired embryo development and produced phenotypes of starvation-induced chlorosis during short-day growth conditions and extended darkness, indicating that ETHE1 has a key function in situations of high protein turnover, such as seed production and the use of amino acids as alternative respiratory substrates during carbohydrate starvation. The amino acid profile of mutant plants was similar to that caused by defects in the electron-transfer flavoprotein/electron-transfer flavoprotein:ubiquinone oxidoreductase complex and associated dehydrogenases. Thus, in addition to sulfur amino acid catabolism, ETHE1 also affects the oxidation of branched-chain amino acids and lysine.

Protein recycling is involved in many cellular processes, including metabolic regulation and programmed cell death. Damaged or dispensable proteins and entire organelles are degraded to provide carbohydrates and nitrogen for energy production and the synthesis of new material. In plants, this turnover is essential for tissue remodeling during senescence and seed production as well as for survival under nutrient-limiting stress conditions (Li and Vierstra, 2012). Catabolism of the sulfur-containing amino acids Cys and Met is still largely unknown. Several enzymes have been shown to release sulfur from Cys. L-Cys desulfurases (nitrogen fixation1 homolog [Saccharomyces cerevisiae; NFS1] and NFS2; EC 2.8.1.7) provide persulfide for the biosynthesis of iron-sulfur clusters, thiamine, biotin, and molybdenum cofactor (van Hoewyk et al., 2008; Balk and Pilon, 2011). β-Cyanoalanine synthase (EC 4.4.1.9) detoxifies cyanide under the consumption of Cys and releases β-cyanoalanine and sulfide (Hatzfeld et al., 2000). Cytosolic L-Cys desulphydrase (DES1; EC 4.4.1.1) and mitochondrial D-Cys desulphydrase (EC 4.4.1.15) catalyze β-elimination reactions of L- or D-Cys to pyruvate, ammonium, and hydrogen sulfide (H₂S; Riemenschneider et al., 2005; Alvarez et al., 2010). Since their expression increases with age, Cys desulphydrases have been suggested to be involved in the catabolism of sulfur-containing amino acids during senescence (Riemenschneider et al., 2005; Jin et al., 2011).

Recently, several regulatory functions of sulfide in plants have emerged. Sulfide increases drought resistance by inducing stomatal closure (Garcia-Mata and Lamattina 2010; Jin et al., 2011, 2013) and is also protective against other abiotic stresses such as heat and heavy metals (Zhang et al., 2008, 2010; Li et al., 2012). It negatively

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[C] Some figures in this article are displayed in color online but in black and white in the print edition.
[W] The online version of this article contains Web-only data. www.plantphysiol.org/cgi/doi/10.1104/pp.114.239764
involved in plant sulfur catabolism. In Arabidopsis and, therefore, constitutes a good candidate to be analyzed (Birke et al., 2012). The presence of an additional, so far unknown mechanism in mitochondria was revealed but not further analyzed (Birke et al., 2012).

ETHYLMALONIC ENCEPHALOPATHY PROTEIN1 (ETHE1) is a sulfur dioxygenase (SDO; EC 1.13.11.18) that oxidizes persulfides in the mitochondrial matrix and, therefore, constitutes a good candidate to be involved in plant sulfur catabolism. In Arabidopsis (Arabidopsis thaliana), ETHE1 (AT1G53580) is critical for seed production. A loss-of-function mutation causes alterations in the mitochondrial ultrastructure and an arrest of embryo development at early heart stage (Holdorf et al., 2012). However, the precise biochemical and physiological roles of ETHE1 in plant mitochondria have not been established. Mutations in the human homolog ETHE1 lead to the fatal metabolic disease ethylmalonic encephalopathy (Tiranti et al., 2004). The primary cause for the disease is a disruption of the mitochondrial sulfide detoxification pathway that oxidizes sulfide to either thiosulfate or sulfate in four steps catalyzed by sulfide:quinone oxidoreductase, ETHE1, a sulfurtransferase, and sulfate oxidase (Hildebrandt and Grieshaber, 2008; Tiranti et al., 2009). Increased sulfide concentrations in the bloodstream severely damage the vascular endothelium and thus cause the main symptoms of ethylmalonic encephalopathy: rapidly progressive necrosis in the brain, chronic diarrhea, and microangiopathy (Giordano et al., 2012). In addition, sulfide interferes with mitochondrial energy metabolism. It reversibly inhibits COX at low micromolar concentrations (Tiranti et al., 2009), and chronic exposure destabilizes specific COX subunits (Di Meo et al., 2011). ETHE1 deficiency also affects the mitochondrial catabolism of fatty acids and branched-chain amino acids (BCAA), leading to an accumulation of ethylmalonic acid as well as C4 and C5 acylcarboxinines and acylglycines (Tiranti et al., 2009; Hildebrandt et al., 2013).

Here, we show that in Arabidopsis, the mitochondrial SDO ETHE1 is part of a sulfur catabolic pathway that catalyzes the oxidation of sulfide or persulfides derived from amino acids to thiosulfate and sulfate. ETHE1 has a key function in situations of high protein turnover, such as seed production or unfavorable environmental conditions leading to carbohydrate starvation and the use of amino acids as alternative respiratory substrates.

RESULTS

We analyzed three transfer DNA (T-DNA) insertion lines of the AT1G53580 gene to investigate the physiological function of ETHE1 in Arabidopsis. In the mutant line ethel-1, the T-DNA is inserted into the 5′ untranslated region 64 bp upstream of the start codon (Fig. 1A), leading to a decrease in ETHE1 transcript level by 75% (Fig. 1B). Immunolabeling showed that only trace amounts of ETHE1 protein were present in purified mitochondria of this line (Fig. 1C). In ethel-2 and ethel-3, the T-DNA insertion is localized in the promoter region of the gene (335 and 327 bp upstream of the start codon; Fig. 1A). The ETHE1 transcript level was 60% to 70% of the wild type, and ETHE1 protein abundance was also decreased in these lines (Fig. 1, B and C).

SDO activity was measured as oxygen consumption upon the addition of 1 mm reduced glutathione (GSH) and elemental sulfur using a Clarke-type oxygen electrode. The elemental sulfur rings react with GSH nonenzymatically to form polysulfane compounds including glutathione persulfide (GSSH), the substrate of the SDO reaction (Rohwerder and Sand, 2003). Mitochondria isolated from wild-type Arabidopsis cell suspension culture had an SDO activity of 36.0 ± 8.4 nmol oxygen min⁻¹ mg⁻¹ protein under standard conditions, which was comparable to the SDO activity in mitochondria isolated from wild-type rosette leaves (44.2 ± 2.7 nmol oxygen min⁻¹ mg⁻¹ protein; n = 3). By contrast, almost no SDO activity was detectable in mitochondria from the ethel-1 line, and the activity was decreased by 24% and 64% in ethel-2 and ethel-3, respectively (Fig. 1D).

The ETHE1 gene excluding the mitochondrial targeting sequence was expressed in Escherichia coli and purified using a C-terminal 6× His tag. Recombinant Arabidopsis ETHE1 protein had a specific activity of 35.3 ± 1.8 μmol oxygen min⁻¹ mg⁻¹ protein in the standard activity test for SDO, which is 1,000 times higher than that in isolated mitochondria. The pH optimum of Arabidopsis ETHE1 was around pH 9.0 and the temperature optimum was 55°C, compared with pH 7.5 and 35°C for human ETHE1 (Supplemental Fig. 1, B and C). These results confirm that ETHE1 in Arabidopsis is an SDO (EC 1.13.11.18).

ETHE1 Oxidizes GSSH to Sulfite

Recombinant Arabidopsis ETHE1 was highly specific for GSSH as a substrate. SDO activity comparable to the standard assay using GSH and elemental sulfur as a substrate was only observed in the presence of oxidized glutathione (GSSG) and sulfide, which also form GSSH in a nonenzymatic reaction (Fig. 2A). Free sulfide and 3-mercaptoppyruvate were not oxidized, and GSSH could not be replaced by other thiols such as Cys, 3-mercaptopetanol, and dithiothreitol (Supplemental Table S1).

Human ETHE1 is known to catalyze the reaction GSSH + oxygen + water → GSH + sulfite + 2H⁺ (Kabil and Banerjee, 2012). To confirm that sulfite is also the product of ETHE1 in Arabidopsis, we measured thiol levels during the course of the SDO activity assay (Fig. 2B). Sulfite was only detected after the addition of elemental sulfur and increased proportionately to the oxygen consumed. The total amount of sulfite produced, which was limited by 250 nmol of oxygen available in the electrode chamber, was 218 ± 42.4 nmol
Thiosulfate was not produced by recombinant ETHE1.

ETHE1 Is Part of a Mitochondrial Sulfur Catabolic Pathway

To test which sulfur compounds can serve as substrates for the ETHE1-dependent pathway, we measured oxygen consumption by isolated mitochondria upon the addition of a range of potential substrates (Fig. 2C; Supplemental Table S1). In order to discriminate between ETHE1-dependent oxygen consumption and other mitochondrial reactions, we compared activities in wild-type samples with those in ethe1-1 and ethe1-3. In agreement with the identified substrates for recombinant ETHE1, specific SDO activity could be observed in isolated mitochondria after the addition of GSH and elemental sulfur or GSSG and sulfide (Fig. 2C). Interestingly, the presence of 3-mercaptopyruvate also resulted in a significant rate of oxygen consumption in wild-type mitochondria, which was absent in ethe1-1 and strongly decreased in ethe1-3 mitochondria, indicating that this reaction is ETHE1 dependent (Fig. 2C). Sulfide or thiosulfate was not oxidized by the mitochondria, whereas L- or D-Cys addition led to a low rate of ETHE1-independent oxygen consumption (Supplemental Table S1).

The main product of mitochondrial GSSH oxidation was thiosulfate (Fig. 2D). During the standard activity test using GSH and elemental sulfur as a substrate (0.25 mg mL⁻¹ mitochondrial protein, 15 min), mitochondria produced 55 ± 18 μM thiosulfate and 9 ± 10 μM sulfite while consuming 103 ± 25 μM oxygen (n = 5). Thus, most of the sulfite produced by the SDO reaction is immediately converted to thiosulfate in Arabidopsis mitochondria, similar to the pathway in animals (Hildebrandt and Grieshaber, 2008).

The Mitochondrial Sulfur Catabolic Pathway Is Involved in Sulfide Detoxification

To test a potential role of ETHE1 in the detoxification of excess H₂S in vivo, wild-type and ethe1-1 plants were exposed to a sublethal concentration of H₂S (1 μL L⁻¹) for 12 d. We measured leaf contents of Cys and GSH, which are produced from sulfide during the sulfur assimilation pathway, as well as of the Cys precursor O-acetylserine (OAS). In addition, the inorganic products of sulfide oxidation, thiosulfate, sulfite, and sulfate, were analyzed (Fig. 3). Under control conditions, ethe1-1 plants had significantly higher contents of Cys, GSH, and sulfate than the wild type but decreased levels of thiosulfate and OAS.

In wild-type plants, H₂S exposure resulted in a 5-fold increase of the endogenous sulfide concentration. Cys and GSH accumulated with a concomitant decrease in the precursor OAS, indicating that part of the excess sulfide was incorporated into amino acids. In addition, we found evidence for sulfide oxidation. Concentrations of thiosulfate, sulfite, and sulfate were significantly higher in H₂S-treated than in control plants. Thiosulfate increased
most drastically (1,588-fold), from 3.8 ± 0.3 to 6,002 ± 117 pmol mg⁻¹ fresh weight, so that after the H₂S exposure it became one of the most abundant sulfur compounds present in the leaves. The accumulation of thiosulfate and sulfite upon sulfide exposure was significantly less pronounced in ethe1-1 plants than in the wild type, and the sulfate concentration even decreased, indicating a role of the ETHE1-dependent mitochondrial sulfur catabolic pathway in sulfide oxidation. Thus, the results of in planta analysis of ethe1 mutants are in full agreement with the biochemical characterization of ETHE1 recombinant protein and isolated mitochondria and demonstrate the relevance of ETHE1 for the detoxification of sulfide derived from Cys degradation.

Low Levels of ETHE1 Are Sufficient for the Survival of Arabidopsis Plants, But Development Is Delayed

While complete knockout of the ETHE1 gene is embryo lethal (Holdorf et al., 2012), seeds of the strong knockdown mutant ethe1-1 were viable. However, we observed a severe delay in embryo development (Fig. 4, A and B). Five days after pollination, most of the ethe1-1 embryos were still at the globular stage and reached the heart stage only 7 d after pollination, whereas wild-type embryos were already at the heart stage and the bent cotyledon or mature stage. The development of ethe1-1 plants grown under long-day conditions was also delayed (Fig. 4, C and D). Growth rates of ethe1-1 rosettes expressed as diameter and number of leaves were about 60% of the wild-type rates (Supplemental Fig. S2). There were no apparent differences regarding embryo development or growth phenotype between wild-type plants and the weaker knockdown lines ethe1-2 and ethe1-3.

ETHE1 Is Involved in Mitochondrial Amino Acid Catabolism

We used the information available from a proteomic approach in combination with coexpression analysis to elucidate in which physiological context ETHE1 activity...
is most relevant for plant metabolism. Mitochondria isolated from wild-type and ethel-1 cell suspension cultures were analyzed by isoelectric focusing (IEF)/SDS-PAGE, and 73 proteins were identified in 45 spots with a significantly changed volume (Table I; Supplemental Fig. S3; Supplemental Table S2).

Our results confirm the predicted role of ETHE1 in plant sulfur metabolism. Several enzymes involved in Cys synthesis (Ser acetyltransferase and Ser hydroxymethyltransferase) or degradation (β-cyanoalanine synthase, Asp aminotransferase, NSF1, nitrogen fixation factor U-like domain containing protein4 [NFU4], and NFU5) were affected in ethel-1 mitochondria. Interestingly, we also found indications for differences in energy metabolism between ethel-1 and the wild type. Tricarboxylic acid cycle dehydrogenases (malate dehydrogenase, succinate dehydrogenase, subunits of pyruvate and 2-oxoglutarate dehydrogenase complexes) as well as enzymes involved in the oxidation of amino acids as alternative substrates of the mitochondrial respiratory chain (e.g. electron-transfer flavoprotein [ETF], electron-transfer flavoprotein:ubiquinone oxidoreductase [ETFQO], branched-chain α-keto acid dehydrogenase, fumarylacetoacetate hydrolase, methylcrotonoyl-CoA carboxylase, and Glu dehydrogenase) were detected in spots with a changed volume (Table I). This data set provides valuable information about which mitochondrial pathways in general are affected by the ETHE1 knockdown. However, care must be taken not to overinterpret the results. Regulation patterns of individual enzymes cannot be concluded, since spot volume is not always equivalent to the total abundance of one specific protein.

The potential role of ETHE1 in amino acid catabolism is further supported by coexpression analysis using Genevestigator (www.genevestigator.com). ETHE1 expression was up-regulated in experiments that stimulate nutrient remobilization, such as prolonged darkness, drought, abscisic acid treatment, and germination. Enzymes involved in protein degradation and amino acid catabolism as well as peroxisomal fatty acid β-oxidation were most clearly coexpressed with ETHE1 under these conditions (Supplemental Table S3). In particular, several enzymes of the BCAA and Lys catabolic pathway (ETF, isovaleryl-CoA dehydrogenase, 3-hydroxyisobutyrate dehydrogenase, branched-chain α-keto acid dehydrogenase subunits, and aminoadipate-semialdehyde dehydrogenase) showed an expression pattern similar to ETHE1. Thus, equivalent to the situation in animals, Arabidopsis ETHE1 is probably involved in sulfur metabolism as well as mitochondrial amino acid oxidation.

ETHE1 Has an Essential Function in the Use of Amino Acids as Respiratory Substrates during Carbohydrate Starvation

The identification of a potential role of ETHE1 in amino acid catabolism prompted us to further investigate the phenotype and amino acid profiles of ethel-1 compared with wild-type plants under conditions with increased protein degradation. These include senescence, decreased light availability (short-day conditions), and severe carbohydrate starvation caused by extended darkness (Fig. 5). The ethel-1 mutant was sensitive to changes in the photosynthetically active period, showing premature senescence under light-limiting conditions. When the plants were grown under long-day conditions (16 h of light/8 h of dark), rosette leaves of ethel-1 plants appeared pale green compared with the wild type, but otherwise senescence proceeded in a similar fashion (Fig. 5A; Supplemental Fig. S4A). Under short-day conditions (8 h of light/16 h of dark), the oldest

Figure 3. Products of sulfide metabolism in wild-type (wt) and ethel-1 plants. Sulfur-containing metabolites were extracted from aerial parts of wild-type and ethel-1 plants grown under short-day conditions for 4 weeks followed by exposure to 0 (–) or 1 (+) ppm H2S for 12 d and quantified using HPLC (n = 3). FW, Fresh weight. Asterisks indicate values significantly different (P < 0.05) from the wild type by Student’s t test.
leaves of ethel-1 plants became chlorotic after 7 weeks of growth starting at the edges (Fig. 5B, arrows). In the further course of development, leaves of the mutant plants turned upward and showed progressive signs of senescence, while wild-type rosettes continued to grow and stayed dark green (Supplemental Fig. S4B). This phenotype became more pronounced when plants were grown in extended darkness (Fig. 5C).

To test whether an increase in reactive oxygen species (ROS) production contributes to premature leaf senescence in ethel-1 plants, we analyzed hydrogen peroxide (H$_2$O$_2$) and superoxide levels in young leaves of plants grown under short-day conditions by 3,3’-diaminobenzidine (DAB) and nitroblue tetrazolium (NBT) staining, respectively (Supplemental Fig. S5). H$_2$O$_2$ production was not significantly different in ethel-1 compared with the wild type and was clearly restricted to necrotic leaf areas (Supplemental Fig. S5A). In contrast, NBT-stained portions of ethel-1 leaves (37% ± 26%) were significantly larger than in the wild type (19% ± 9%) and not correlated to visible signs of senescence. Interestingly, formazan production is not specific for superoxide, but NBT is also rapidly reduced by GSSH (Supplemental Fig. S5D). Thus, our results indicate a general increase in ROS or reactive sulfur species in ethel-1 plants.

In agreement with the postulated function of ETHE1 in protein catabolism, we found an accumulation of all detectable amino acids in seeds from ethel-1 plants compared with the wild type during early embryo development (4–5 d after pollination), resulting in a 1.8-fold increase of total free amino acid content (Supplemental Table S4). The amino acid composition was not changed in senescent rosette leaves of ethel-1 plants grown under long-day conditions (Fig. 5D; Supplemental Table S5). However, under short-day conditions, concentrations of the compounds related to sulfur metabolism (Cys, glutathione, and Ser) as well as the BCAA Val, Leu, and Ile were significantly higher in the mutant than in the wild type (Fig. 5D; Supplemental Table S5). The effect on amino acid content became more pronounced when plants were subjected to complete darkness for 7 d. The largest differences between ethel-1 and the wild type occurred in sulfur-containing amino acids (2- to 5-fold) and BCAA (3- to 6-fold). In addition, extended darkness generally led to a drastic (50- to 60-fold) increase in the nitrogen-rich amino acids Arg and Asn, and concentrations were slightly higher in ethel-1 than in wild-type leaves (Supplemental Table S5). As a consequence, the total concentration of free amino acids increased 4-fold in wild-type leaves and 5-fold in ethel-1.
Table I. Proteins with potentially changed abundance in ethe1-1 mitochondria

Mitochondrial proteins from wild-type and ethe1-1 cell culture were separated by IEF/SDS-PAGE (Supplemental Fig. S3). Gels from three biological replicates were analyzed by Delta2D (Decodon), and the proteins in spots with at least 1.5-fold changes in volume were identified by nano-liquid chromatography-tandem mass spectrometry. For additional information, see Supplemental Table S2.

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$^a$Ratio of mean spot volume on ethe1-1 gels to mean spot volume on wild-type gels.

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leaves compared with short-day conditions, resulting in a significantly higher total amino acid concentration in mutant than in wild-type plants (65.3 ± 7.9 versus 47.6 ± 8.8 nmol mg⁻¹ fresh weight). Surprisingly, there were no significant differences in the contents of sulfide, thiosulfate, or sulfite between wild-type and mutant plants upon extended dark treatment (Supplemental Table S6).

To better characterize the effect of ETHE1 knockdown on energy metabolism, we analyzed leaf carbohydrate and adenylate levels (Fig. 5D; Supplemental Table S5). As expected, starch was almost completely depleted after 7 d of darkness in wild-type and mutant plants, and concentrations of Suc as well as several monosaccharides also decreased significantly. Differences in metabolite contents between ethe1-1 and the wild type were again most pronounced in the dark-treated plants. Levels of starch, Suc, Glc, and Fru as well as total adenylate concentrations (ATP, ADP, and AMP) were elevated in ethe1-1 compared with wild-type leaves. However, the AMP-ATP ratio, an indicator of low cellular energy status, was also significantly higher in ethe1-1 than in wild-type plants under short-day conditions and extended darkness (Fig. 5D).

Together with the strong phenotypic effects, the changes in the metabolite profile of mutant plants point toward a pivotal role of ETHE1 during dark-induced carbohydrate starvation. In agreement with this, the transcript amount of ETHE1 was 6.5-fold higher in rosette leaves of wild-type plants subjected to extended darkness compared with leaves of plants grown under long- or short-day conditions (Fig. 5E).

DISCUSSION

Plant ETHE1 has recently been identified as an SDO localized in the mitochondria with an essential but as yet undefined function in early embryo development (Holdorf et al., 2012). Here, we describe the physiological role of ETHE1 in the catabolism of sulfur-containing amino acids and BCAA based on the analysis of three Arabidopsis knockdown mutants. T-DNA insertion into the 5’ untranslated region in ethe1-1 resulted in a strong decrease in enzyme activity to about 1% of wild-type levels, which was sufficient for plant viability but led to pronounced growth defects throughout the life cycle. A decrease in SDO activity by about 50% in ethe1-2 and ethe1-3 was tolerated by the plants without any obvious phenotypic effects.

The Biochemical Function of ETHE1: Sulfur Oxidation during Cys Catabolism

Increased concentrations of Cys, Met, and GSH in ethe1 knockdown plants indicate a function of ETHE1
in sulfur amino acid metabolism. We performed biochemical studies on plants, isolated mitochondria, and recombinant ETHE1 enzyme to investigate details of this function. Our results identified a new mitochondrial pathway catalyzing the detoxification of sulfide or reduced sulfur species derived from Cys catabolism by oxidation to thiosulfate (Fig. 6).

In plants, free sulfide is normally rapidly incorporated into Cys by the different OAS (thiol) lyase isoforms (Hell and Wirtz, 2011). However, an alternative route is required for the degradation of sulfur-containing amino acids. Exposure of Arabidopsis plants to environmental sulfur derived from Cys catabolism by oxidation to thiosulfate (Fig. 6).

Several lines of evidence indicate that, in addition to its role in Cys catabolism, ETHE1 is probably involved in energy metabolism and the use of amino acids as alternative respiratory substrates during carbohydrate starvation. Under conditions of low sugar availability such as extended darkness, drought, or extreme temperatures, fatty acids are oxidized by peroxisomal β-oxidation, and in addition, cellular proteins and entire organelles are degraded by autophagy to produce amino acids as an energy source (Araújo et al., 2011). Especially BCAA, aromatic amino acids, and Lys have a key function as substrates for ATP production (Izumi et al., 2013). The pathways oxidizing these amino acids are localized in the mitochondria and transfer electrons into the respiratory chain via the ETF/ETFQO complex (Taylor et al., 2004; Araújo et al., 2010).

Coexpression analysis as well as mitochondrial proteomics clearly placed ETHE1 in the functional context of carbohydrate starvation, and ETHE1 expression was indeed induced by extended darkness. In agreement with these results, phenotypic defects of ETHE1 knockout plants were more pronounced under light-limiting conditions. Plants developed starvation-induced chlorosis, which is similar to the phenotype produced by defects in autophagy or the ETF/ETFQO system and associated dehydrogenases (Ishizaki et al., 2005, 2006; Araújo et al., 2010; Izumi et al., 2013). The amino acid profile of ethel1 mutants, which in addition to an accumulation of sulfur amino acids revealed an increase in BCAA characteristic for alternative respiration defects, suggests a specific role of ETHE1 in this pathway. Although premature chlorosis...
and leaf senescence clearly indicate an energy shortage, depletion of starch, sugar, and ATP was not accelerated in ethel1-1 plants. Similar findings from previous studies demonstrate that metabolic adaptations to energy deprivation in plants can be complex. Low concentrations of malate and fumarate lead to accelerated dark-induced senescence in a malic enzyme-overexpressing Arabidopsis line, while sugar levels are high (Fahnenstich et al., 2007). Down-regulation of different respiratory chain complexes restricts growth despite unchanged or even increased steady-state ATP levels (Szal et al., 2008; Robison et al., 2009; Geisler et al., 2012). The high AMP-ATP ratio in ethel1-1 plants could induce a broad transcriptional response to stress and energy deprivation mediated by AMP-activated protein kinases such as KIN10 (AT3G01090), which is coexpressed with ETHE1 (Baena-González et al., 2007).

The amino acid profile of young ethel1-1 seeds is again strikingly similar to defects in isovaleryl-CoA dehydrogenase, which is involved in the degradation of BCAA (Gu et al., 2010). In contrast to knockout mutants for Lys-ketoglutarate reductase/saccharopine dehydrogenase or Thr aldolase, which very specifically accumulate Lys or Thr in the seeds (Zhu et al., 2001; Jander et al., 2004), isovaleryl-CoA dehydrogenase deficiency leads to a general increase in free amino acids similar to ETHE1 deficiency (Gu et al., 2010). Thus, BCAA catabolism plays an important role in regulating amino acid levels in seeds, and inhibition of this pathway in ethel1 mutants might interfere with the nutrient supply to the developing embryo. However, since defects in embryogenesis are not described for any of the mutants related to autophagy or the use of amino acids as respiratory substrates (Ishizaki et al., 2005, 2006; Araújo et al., 2010; Gu et al., 2010; Izumi et al., 2013), the severe consequences of ETHE1 deficiency indicate additional problems. Lack of the mitochondrial sulfurtransferase STR1, which we suggest is involved in the same pathway as ETHE1, also impairs embryogenesis (Mao et al., 2011). Thus, seed abortion seems to be an immediate consequence of the block in sulfur catabolism, possibly caused by an increase in toxic intermediates such as sulfide or reactive persulfide compounds. This hypothesis will have to be tested (e.g. with ethel1/str1 double mutants). In humans suffering from ethylmalonic encephalopathy, C4 and C5 acylcarnitines and acylglycines accumulate in the bloodstream, indicating a block in fatty acid and BCAA oxidation at the level of acyl-CoA. Indeed, H$_2$S has been shown to inhibit short-chain acyl-CoA dehydrogenase in vitro, so that the increase in tissue sulfide concentrations caused by ETHE1 deficiency is thought to be responsible for the metabolite profile of the patients (Tiranti et al., 2009). However, sulfide concentrations were normal in ethel1-1 leaves. Another possible explanation is the inhibition of acyl-CoA dehydrogenases by CoA persulfides (Shaw and Engel, 1987), which are likely to accumulate when high concentrations of reduced sulfur are present. The increased intensity of NBT staining in ethel1-1 leaves without changes in H$_2$O$_2$ production indicate that the block in persulfide oxidation probably leads to an accumulation of reactive sulfur species. Indirect pleiotropic effects such as a decrease in respiratory chain activity and inactivation of additional enzymes by increased ROS levels could also play a role. Proteome studies in ETHE1-deficient mice have further indicated a possible regulatory effect via posttranslational protein modifications (Hildebrandt et al., 2013). Thus, our results clearly demonstrate the central function of Arabidopsis ETHE1 in metabolic adaptation to prolonged darkness. Additional experiments will be necessary to clarify mechanistic aspects and distinguish between a direct role of ETHE1 in BCAA catabolism versus general effects on energy homeostasis.

**CONCLUSION**

In summary, this study identified the physiological role of ETHE1, which is in amino acid catabolism. The SDO detoxifies reactive intermediates in the degradation of sulfur-containing amino acids and strongly affects the oxidation of BCAA as alternative respiratory substrates in situations of carbohydrate starvation. Therefore, ETHE1 is expected to be relevant for plant productivity during seed production as well as for stress tolerance against drought or shading.

**MATERIALS AND METHODS**

**Plant Material and Growth Conditions**

All Arabidopsis (Arabidopsis thaliana) plants used for this study were of the Columbia ecotype. Plants were grown in climate chambers under long-day conditions (16 h of light/8 h of dark) or short-day conditions (8 h of light/16 h of dark) at 22°C, 65 μmol m$^{-2}$ s$^{-1}$ light, and 65% humidity. The T-DNA insertion lines SALK_021573 (ethel1-1), SALK_091996 (ethel1-2), and SALK_127065 (ethel1-3) for the gene ATIG53580 were obtained from the Nottingham Arabidopsis Stock Centre (University of Nottingham).

Plants for fumigation experiments were germinated and grown on soil under short-day conditions. Three-week-old plants were transferred into fumigation cabinets to allow acclimatization for 1 week. Subsequently, plants were exposed to sulfate (1 ppm H$_2$S) for 12 d according to Buchner et al. (2004).

For dark treatment, plants were grown under short-day conditions for 7 weeks and then transferred to darkness for 7 d. Before and after the dark treatment, complete rosettes of five wild-type and mutant plants were harvested and used for metabolite analysis.

**Isolation of T-DNA Insertion Mutants and Genotype Characterization**

Homozygous mutant lines were identified by genomic PCR using gene-specific primers (5’-TGGAATTCGGGTATATGGTG-3’ and 5’-CGGATCAACAATCCATCCCATC-3’ for ethel1-1, 5’-TGGAATTCGGGTATATGGTG-3’ and 5’-CCCATGTTACAAATCTCCAT-3’ for ethel1-2, and 5’-CATGATGTGATTGATACCG-3’ and 5’-GGATCAACAATCCATCCTCC-3’ for ethel1-3) and the T-DNA left border primer Lb17 (5’-TTTTGCGGATTTCGAAA-3’). PCR products were sequenced by Seqlab to determine the exact T-DNA insertion sites. ETHE1 expression was analyzed by quantitative reverse transcription (RT)-PCR as described by Niessen et al. (2012). Primer combinations were 5’-AAGGTGTACGCGTTG-3’ and 5’-CTTGGAGAAAGCCATCTTGTTAC-3’ for ETHE1 and 5’-GGGATGGAAGCCAAAATGAAGG-3’ and 5’-TTGTCACCAAGC-AAAGTCG-3’ for glyceraldehyde-3-phosphate dehydrogenase (GAPDH; AT1G3340).

**Expression and Purification of ETHE1**

The coding sequence of AT1G33580 was cloned into the pET28a(+) expression vector in frame with a C-terminal 6× His tag using the primes...

DAB staining solution (1 mg mL⁻¹) was added, followed by incubation at 38°C overnight with shaking. Cell-free lyase in 50 mM NaPO₄, 300 mM NaCl, and 10 mM imidazole, pH 8.0, was applied to a 1-mL HisTrap HP column (GE Healthcare) and eluted with a 10 to 250 mM imidazole gradient. ETHE1 purified as a single peak (Supplemental Fig. S1A). We obtained a high yield of soluble protein with an electrophoretic mobility of 28 kD, which is in agreement with the calculated molecular mass of 28,008 D for the monomer (Supplemental Fig. S1A). The purified protein contained 0.5 atoms of Fe²⁺ per monomer, as reported previously (McCoy et al., 2006; Krüstel et al., 2009). Preincubation of the enzyme with 1 mM equivalent of Fe and addition of 2.5 mM ascorbate did not increase SDO activity.

The plasmid containing human ETHE1 was generously provided by Valeria Tiranti and Massimo Zeviani (The Foundation of the Carlo Besta Neurological Institute) and expressed in the same way as Arabidopsis ETHE1.

**SDO Activity Test**

SDO activity was measured at 25°C in a Clarke-type oxygen electrode (Orbecos Oxygraph and Hansatech DW1 Oxygraph) following the procedure described by Hildebrandt and Grieshaber (2008). The reaction contained 1 to 2 μg mL⁻¹ of purified enzyme or 150 to 300 μg mL⁻¹ of mitochondrial protein in 0.1 mM KH₂PO₄, pH 7.4. For the standard activity test, 1 mM GSH (final concentration) was added, followed by 15 μL mL⁻¹ of a saturated elemental sulfur solution in acetone. Acetone did not inhibit enzyme activity. Rates were measured during the linear phase of oxygen depletion, which occurred in the first 2 to 3 min.

**Phenotype Analysis**

For general phenotype analysis, a modified version of the procedure described by Boyes et al. (2001) was used. Plants were grown under long-day conditions, and growth parameters were measured three times per week. Embryo morphology was analyzed with a microscope equipped with Nomarski optics. Silica was clearly expressed in Hosier’s solution (15 mL of distilled water, 3.75 g of gum arabic, 2.5 mL of glycerine, and 50 g of chloral hydrate) overnight before seeds were dissected.

**Histochemical Detection of H₂O₂ and Superoxide**

Histochemical detection of H₂O₂ was performed as described by Therdal-Christensen et al. (1997) with slight modifications. Rosette leaves were incubated in DAB staining solution (1 mg mL⁻¹ DAB, 0.05% [v/v] Tween 20, and 10 mM Na₂HPO₄) for 7 h. Superoxide was detected by formazan staining for 5 h in 0.1 mM MgCl₂ and 25 mM HEPS, pH 7.6. After DAB or NBT staining, chlorophyll was removed by boiling the leaves in bleaching solution (ethanol:acetic acid:glycerol, 3:1:1) for 15 min. The reaction contained 1 to 2 μg mL⁻¹ of mitochondrial protein in 0.1M KPO₄, pH 7.4.

**Metabolite Analysis**

Products of the SDO reaction were analyzed by HPLC (Hildebrandt and Grieshaber, 2008). Hydrophilic metabolites were extracted from 50 mg of leaf material as described by Wirtz and Hell (2003). Derivatization, separation, and quantification of thiols, OAs, amino acids, and sugars were performed as described by Heeg et al. (2008). Sulfite, sulfide, and thiosulfate were determined according to Birke et al. (2012). Soluble sugars were extracted from powdered plant material (50 mg) by incubation with 0.5 mL of 80% (v/v) ethanol for 45 min at 80°C. Cell debris and insoluble starch were removed by centrifugation for 10 min at 25,000g and 4°C. Soluble sugars of the resulting supernatant were separated with a gradient of 15 to 300 mM NaOH on a CarboPac PA1 column connected to an ICS-3000 system (Dionex) and quantified by high-performance anion-exchange chromatography-pulsed amperometric detection. Data acquisition and quantification were performed with Chromelon 6.7 ( Dionex). For the quantification of starch, the sediment of soluble sugar extraction was washed twice with 80% ethanol and resuspended in 0.2 mL of 0.2 M KOH. Starch was partially hydrolyzed by incubation at 95°C for 1 h and subsequently digested in 25 mM sodium acetate, pH 5.2, with 0.1 unit of amyloglucosidase for 16 h at 37°C. The resulting Glc was quantified by high-performance anion-exchange chromatography-pulsed amperometric detection as described above.

Adenylates were quantified as described by Burstebinder et al. (2010).

**Cell Suspension Cultures and Isolation of Mitochondria**

Arabidopsis cell suspension cultures were established and maintained as described by May and Leaver (1993) and Sunderhaus et al. (2006). Briefly, Arabidopsis seedlings were surface sterilized, plated on solid Murashige and Skoog medium (0.44% [w/v] Murashige and Skoog medium and [Duchefa], 0.2% [w/v] Suc, and 1% [w/v] agar, pH 5.7), and grown for 10 d under long-day conditions. Callus formation was induced by incubating stem explants on solid callus induction medium (0.316% [w/v] Gamborg’s B5 medium [Duchefa], 3% [w/v] Suc, 1% [w/v] agar, 0.5 mg L⁻¹ 2,4-dichlorophenoxyacetic acid, and 0.05 mg L⁻¹ kinetin, pH 5.7) at 25°C in the dark. Suspension cultures were grown in 500-mL flasks containing 100 mL of liquid B5 medium (callus induction medium without agar) at 25°C and 90 rpm in the dark. Cells were transferred into fresh medium every 7 d. There were no significant differences between growth rates of wild-type cells and the ethel1 mutants. Mitochondria were prepared according to the procedure described by Wernerh et al. (2001). The high purity of mitochondria prepared according to this method has been demonstrated by proteome analysis (Kr üstel et al., 2003).

Mitochondria from cell culture were used to identify the general biochemical function of ETHE1. SDO activity was also measured in mitochondria prepared from rosette leaves of 8-week-old wild-type Arabidopsis plants grown under short-day conditions following the protocol described by Keech et al. (2005).

**Proteomics**

One-dimensional SDS-PAGE and protein-blot analysis were carried out following standard methods. Antibodies against purified 6× His-ETH1E were produced by Biogenes, and antibodies against OAS (thiol) lyase, which recognize the three major isoforms of the protein, were used as published (Heeg et al., 2008).

Mitochondrial proteins from wild-type and ethel1 cell culture were separated by two-dimensional IEF/SDS-PAGE as described by Hildebrandt et al. (2013) with some modifications: 0.5 mg of mitochondrial protein from each sample was solubilized by shaking in 450 μL of rehydration buffer (6 mM urea, 2 mM thiourea, 50 mM dithiothreitol, 2% [v/v] CHAPS, 5% [v/v] immobilized pH gradient buffer 3-11NL, 12 μL mL⁻¹ DeStreak reagent, and a trace of bromophenol blue) for 60 min at room temperature. IEF was carried out on Immobiline DryStrips gels (24 cm, nonlinear gradient pH 3-11) using the Ettan IEFphor 3 system (GE Healthcare). For the second dimension, the High Performance Electrophoresis FlatTop Tower System (Serva Electrophoresis) was used with precast Tris-Gly gels (12.5% polyacrylamide, 24 × 20 cm). Gel image analysis and protein identification by mass spectrometry were carried out as described by Hildebrandt et al. (2013). Briefly, spots were cut from the two-dimensional gels with a manual spot picker (Genetix), washed in 0.1 M ammonium bicarbonate, and dehydrated with acetonitrile. After tryptic digestion, peptides were extracted by successive incubation with 50% (v/v) acetonitrile plus 5% (v/v) formic acid, 50% (v/v) acetonitrile plus 1% (v/v) formic acid, 50% (v/v) acetonitrile plus 1% (v/v) formic acid, and 100% acetonitrile. Nano-HPLC electrospray ionization quadrupole time of flight mass spectrometry analyses were carried out using the Easy-nLC system (Proxeon) coupled to a microTOF-QII mass spectrometer (Bruker Daltonics). Liquid chromatography separation was achieved with a C18 reverse-phase column (Proxeon EASY-Column [length = 10 cm, i.d. = 75 μm]; ReproSil-Pur C18-AQ, 3 μm, 120 A) coupled to a Proxeon EASY-PreColumn (length = 2 cm, i.d. = 100 μm; ReproSil-Pur C18-AQ, 5 μm, 120 A) using an acetonitrile/formic acid gradient (Klodmann et al., 2011). Tandem mass spectrometry fragmentation was carried out automatically. Proteins were identified using the Mascot search algorithm against The Arabidopsis Information Resource 10 (www.arabidopsis.org).

**Miscellaneous Methods**

A coexpression analysis based on a manually curated database of 40,000 microarrays was performed with Genetigator (www.genetigator.com; Hruz et al., 2008). Genes that are coregulated with AT5G3580 under relevant conditions were called coexpressed.
conditions were identified following a two-step workflow. First, experiments with a significant change (P < 0.05) of at least 1.5-fold in ETHE1 expression were selected using the perturbations tool. The 100 genes with the most similar expression patterns in these experiments were then identified with the coexpression tool using the Pearson correlation coefficient as the measure of similarity.

Protein was quantified using the Bio-Rad Protein Assay reagent, and iron was quantified using the colorimetric chelator ferene (Hennessy et al., 1984).

Supplemental Data

The following materials are available in the online version of this article.

Supplemental Figure S1. Purification, pH, and temperature optima of Arabidopsis and human ETHE1.

Supplemental Figure S2. Growth parameters of ethel-1 and wild-type rosettes under long-day conditions.

Supplemental Figure S3. Identification of proteins with altered abundance in mitochondria of ethel-1 compared with the wild type.

Supplemental Figure S4. Leaf senescence in wild-type and ethel-1 plants under long- and short-day growth conditions.

Supplemental Figure S5. Histochemical detection of ROS and reactive sulfur species in leaves of wild-type and ethel-1 plants.

Supplemental Table S1. Identification of substrates for recombinant ETHE1 and the SDO reaction in Arabidopsis mitochondria.

Supplemental Table S2. Identification of proteins with altered abundance in mitochondria of ethel-1 compared with the wild type.

Supplemental Table S3. Genes that are coexpressed with ETHE1 in Arabidopsis under relevant conditions.

Supplemental Table S4. Amino acid and GSH contents of wild-type and ethel-1 seeds at 4 to 5 d after pollination.

Supplemental Table S5. Metabolite contents of wild-type and ethel-1 rosette leaves under long- and short-day growth conditions as well as after extended darkness.

Supplemental Table S6. Contents of sulfi te, thiosulfate, and sulfide in wild-type and ethel-1 mutant rosette leaves after 7 d of extended darkness.

ACKNOWLEDGMENTS

We thank Valeria Tiranti and Massimo Zeviani for providing the plasmid for the expression of human ETHE1, Christoph Peterhansel and Stefanie Fromm for assistance with PCR experiments, Herbert Geyer and Jens-Peter Barth for taking care of the plants, Traud Winkelmann for support with the microscope, Mascha Brinkötter for taking part in histochemical ROS detection, and Lorna Jackson for optimizing the immunodetection of the ETHE1 protein. We thank the Metabolomics Core Technology Platform of the Excellence cluster CellNetworks (University of Heidelberg) for support with HPLC-based metabolite quantification.

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LITERATURE CITED


Hildebrandt TM, Griesshaber MK (2008) Three enzymatic activities catalyze the oxidation of sulfi de to thiosulfate in mammalian and invertebrate mitochondria. FEBS J 275: 3352–3361

