Peroxisomal L-bifunctional enzyme (Ehhadh) is essential for the production of medium-chain dicarboxylic acids

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Abstract  L-bifunctional enzyme (Ehhadh) is part of the classical peroxisomal fatty acid β-oxidation pathway. This pathway is highly inducible via peroxisome proliferator-activated receptor α (PPARα) activation. However, no specific substrates or functions for Ehhadh are known, and Ehhadh knockout (KO) mice display no appreciable changes in lipid metabolism. To investigate Ehhadh functions, we used a bioinformatics approach and found that Ehhadh expression covaries with genes involved in the tricarboxylic acid cycle and in mitochondrial and peroxisomal fatty acid oxidation. Based on these findings and the regulation of Ehhadh’s expression by PPARα, we hypothesized that the phenotype of Ehhadh KO mice would become apparent after fasting. Ehhadh mice tolerated fasting well but displayed a marked deficiency in the fasting-induced production of the medium-chain dicarboxylic acids adipic and suberic acid and of the carnitine esters thereof. The decreased levels of adipic and suberic acid were not due to a deficient induction of o-oxidation upon fasting, as Cyp4a10 protein levels increased in wild-type and Ehhadh KO mice. We conclude that Ehhadh is indispensable for the production of medium-chain dicarboxylic acids, providing an explanation for the coordinated induction of mitochondrial and peroxisomal oxidative pathways during fasting.—Houten, S. M., S. Denis, C. A. Argmann, Y. Jia, S. Ferdinandusse, J. K. Reddy, and R. J. A. Wanders. Peroxisomal L-bifunctional enzyme (Ehhadh) is essential for the production of medium-chain dicarboxylic acids. J. Lipid Res. 2012. 53: 1296–1303.

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Mitochondria and peroxisomes both perform fatty acid β-oxidation, but they have different roles in metabolism (1–3). Mitochondria oxidize the bulk of long-chain fatty acids present in our diet and fat stores, whereas peroxisomes oxidize specific carboxylic acids such as very long-chain fatty acids, branched-chain fatty acids, bile acids, and fatty dicarboxylic acids (DCAs) (1–3). Both organelles harbor multiple sets of different enzymes that function in β-oxidation. As such, peroxisomal enzymes differ in their ability to handle the specific peroxisomal carboxylic acid substrates. This knowledge has been derived from experiments with purified enzymes and from analysis of material from patients with single peroxisomal enzyme deficiencies and peroxisomal enzyme knockout (KO) mouse models (1–3).

There are four enzymatic steps in each cycle of peroxisomal β-oxidation: oxidation, hydration, dehydrogenation, and thiolytic cleavage (1–3). Rat and mouse peroxisomes have three acyl-CoA oxidases that perform the first step in β-oxidation. Acox1 handles the straight-chain substrates such as the very long-chain fatty acids and long-chain DCAs, Acox2 is active with the bile acid intermediates and the branched-chain fatty acids, and Acox3 accepts the branched-chain fatty acids (4). For the fourth step, rodents also have three different thiolases, including the 3-ketoacyl-CoA thiolases A (Acaa1a) and B (Acaa1b), and the sterol carrier protein x (Scpx or Scp2). Scp2 is active toward the 3-ketoacyl-CoA species of all peroxisomal substrates. In contrast, no specific substrates are known for Acaa1a and Acaa1b, although they are active toward the 3-ketoacyl-CoA esters of straight-chain fatty acids (5, 6).

For the second and third step of β-oxidation, the hydroxylase and 3-hydroxyacyl-CoA dehydrogenase activity, peroxisomes harbor D-bifunctional enzyme (Hsd17b4, also known as D-PBE, MFP2, or DBP) and L-bifunctional enzyme (Ehhadh, also known as L-PBE, MFP1, or LBP). Previous studies indicated that Ehhadh KO mice display no appreciable changes in lipid metabolism, and thus

Abbreviations:  Crot, carnitine octanoyltransferase; DCA, dicarboxylic acid; Ehhadh, L-bifunctional enzyme; GO, Gene Ontology; KO, knockout; PPARα, peroxisome proliferator-activated receptor α; Scp, sterol carrier protein.

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Hsd17b4 seems to be able to handle all peroxisomal sub- 
strates (7), which is in line with earlier biochemical studies
using purified enzymes (8–12). Indeed, HSD17B4-defi- 
cient patients and Hsd17b4 KO mice accumulate very 
long-chain as well as branched-chain fatty acids and bile 
acid intermediates (13, 14). Thus, no specific substrates 
for Ehhadh have been identified, although the enzyme is 
active toward the enoyl-CoA esters of straight-chain fatty 
acids (15, 16).

DCAs destined for peroxisomal β-oxidation are prod-
ucts of fatty acid ω-oxidation. Long-chain fatty acid ω-
oxidation is initiated by microsomal cytochrome P450 
enzymes of the Cyp4a family, producing an ω-hydroxyl 
group that is further metabolized into an ω-carboxyl group by 
the successive action of an alcohol and aldehyde dehy-
drogenase. DCA β-oxidation ends with the production of 
medium-chain DCAs such as adipic (C6-DCA) and suberic 
acid (C8-DCA). Available evidence suggests that Ehhadh 
might play a role in the β-oxidation of DCAs (17–19), 
based on observations that DCA β-oxidation is not de-
cient in HSD17B4-deficient fibroblasts and that in vitro 
Hsd17b4 and Ehhadh handle these substrates with com-
parable efficiency (18). Moreover, in vitro the β-oxidation 
of the DCAs of long-chain and polyunsaturated fatty acids is 
impaired in Ehhadh KO hepatocytes but not in Hsd17b4 
KO hepatocytes (17, 19).

It has been known for decades that the peroxisomal en-
zymes Acox1, Ehhadh, and Acaa1b, often referred to as 
the classical β-oxidation pathway, are highly inducible by 
phthalate esters and drugs such as fibrates and Wy-14,643 
(20). In the liver, this effect is mediated by peroxisome 
proliferator-activated receptor α (PPARα), a nuclear hor-
monoreceptor activated by these compounds. In normal 
physiology, PPARα is most likely activated by lipolysis-in-
duced elevated levels of free fatty acids. PPARα mediates 
the adaptive response to fasting by increasing mitochon-
drial β-oxidation, ketogenesis, and microsomal ω-oxidation 
(21, 22). The function of the parallel induction of peroxi-
somal fatty acid β-oxidation is less well understood.

We used a bioinformatics approach to shed light on the 
physiological role of the classical peroxisomal β-oxidation 
pathway. This analysis positions Ehhadh in processes 
that generate energy from fatty acids. Combined with the fact 
that Ehhadh is PPAR inducible, we hypothesized that the 
phenotype of Ehhadh KO mice would become apparent 
after an overnight fast. Consequently, we measured me-
tabolites in Ehhadh KO mice after fasting and show that 
Ehhadh is crucial for the formation of medium-chain 
DCAs such as C6-DCA and thus β-oxidation of the major 
long-chain DCAs produced during fasting.

MATERIALS AND METHODS

Generation of liver Ehhadh gene coexpression 
subnetworks

GeneNetwork (www.genenetwork.org) is a depository of data-
sets and tools for use in complex systems biology approaches in 
or order to generate or predict higher order gene function (23, 24).

We selected liver microarray data from three independently gen-
erated panels of genetically heterogeneous mice, an F2 intercross 
between C57BL/6 and BTBR mouse strains in which all cases are 
homezygous for the obese mutation in the leptin gene (the 
B6BTBRF2 cross; n = 41) (25), an intercross between C57BL/6 
and DBA/2J (the Bxd genetic reference population; n = 60 male 
mice) (26, 27), and an F2 intercross with C57BL/6j x C3H/HeJ 
on an ApoE null background (BHF2) (28). We used the (B6 x 
BTBR)F2-ob/ob Liver mRNA M430 RMA, UNC Agilent G4121A 
Liver ORIG LOWESS Stanford (male mice), and UCLA BHF2 
Liver Male miRlatio datasets, respectively. The sole Ehhadh probe 
on each of the liver databases was selected and the top ~500 Eh-
hadh covariates from each experiment were compared. The 
strongest Ehhadh liver covariates from each experiment (~45 
genes per cross) were used to construct coexpression subnet-
works, which were subsequently merged using cytoscape (see 
Fig. 1 for the cutoff Pearson correlation coefficients used for the 
different crosses) (29). To determine which Gene Ontology (GO)
terms were significantly overrepresented in the sets of Ehhadh 
covariates, the cytoscape plug-in Bingo (Biological Networks 
Gene Ontology tool) was used (30). Correlations between Eh-
hadh liver expression and various clinical phenotypes were deter-
mined in the B6BTBRF2 cross database using GeneNetwork.

Animals

The generation of Ehhadh−/− (Ehhadh KO) mice has been de-
scribed previously (7). Male WT (129S2/Hsd) and Ehhadh KO 
(129 background) were kept on regular chow and analyzed at 
2 months of age. All mice were euthanized at 3:00 PM after 0, 6, or 
20 h of fasting (n = 3 animals per time point). At this time, mice 
were anesthetized using pentobarbital, followed by blood, urine, 
and organ collection. All experiments were approved by the insti-
tutional review boards for animal experiments at the Academic 
Medical Center, Amsterdam, and the Northwestern University 
Feinberg School of Medicine, Chicago. All animals received hu-
man care in conformity with the Public Health Service Policy on 
Human Care and Use of Laboratory Animals.

Metabolite measurements

Glucose and β-hydroxybutyrate were measured in perchloric 
ad acid deproteinized blood using established methods. Insulin 
(Ultra sensitive mouse insulin ELISA; Crystal Chem Inc., Downers 
Grove, IL) and acylcarnitines were measured in EDTA-plasma. 
Plasma, urine, and tissue acylcarnitines were measured on a tan-
dem mass spectrometer (Waters Quattro Premier XE) using meth-
ods as described previously (31, 32). Urinary organic acids were 
measured using methoxyamine. After acidification, the orga-
nic acids were extracted twice using ethyl acetate/diethyl ether 
(1:1) and derivatized with N,O-Bis(trimethylsilyl)trifluoroacet-
amide with 1% Trimethylchlorosilane (BSTFA + TMCS; Thermo 
Scientific). The methoxime trimethylsilyl esters were analyzed by 
GC/MS (Agilent HP 5973 mass spectrometer) and GC-flame ion-
ization detection (Agilent 6890 Series GC) using CP-Sil 5 (Chrom-
pack 7441) and CP-Sil 19 (Chrompack 7712) capillary columns. 
Creatinine was measured in urine using ultraperformance liquid 
chromatography-tandem MS with multiple reaction monitoring in 
positive electrospray ionization mode (Waters Quattro Premier 
XE). Heptfluorobutyric acid was used as an ion pair agent for the 
reverse-phase ultraperformance liquid chromatography. Stable 
isotope internal standards were used for quantification.

Immunoblot analysis

Liver homogenates were prepared in PBS using a dispersion tool 
followed by sonication. Samples were further prepared according 
to the instructions for electrophoresis of NuPAGE Bis-Tris mini gels

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search for clues on the role of Ehhadh, we generated gene coexpression subnetworks using published liver microarray data. We selected three independent mouse experiments: an F₂ intercross between C57BL/6 and BTBR mouse strains in which all cases are homozygous for the obese mutation in the leptin gene (the B6BTBRF₂ cross; triangles), an intercross between C57BL/6 and DBA/2J (the BxD genetic reference population; diamonds), and an F₂ intercross with C57BL/6/J x C3H/HeJ on an ApoE null background (BHF₂; hexagons). Nodes shared by more than one cross are shown as circles. The gene-gene interactions (edges) are indicated as color-coded correlation coefficients. Gene products known to localize in mitochondria are blue nodes, peroxisomal gene products are yellow nodes, and the microsomal Cyp4a gene products are pink nodes. Gene products with a dual peroxisomal and mitochondrial localization are purple nodes.

Fig. 1. The hepatic Ehhadh gene coexpression subnetwork. The merged Ehhadh gene subnetwork for an F₂ intercross between C57BL/6 and BTBR mouse strains in which all cases are homozygous for the obese mutation in the leptin gene (the B6BTBRF₂ cross; triangles), an intercross between C57BL/6 and DBA/2J (the BxD genetic reference population; diamonds), and an F₂ intercross with C57BL/6/J x C3H/HeJ on an ApoE null background (BHF₂; hexagons). Nodes shared by more than one cross are shown as circles. The gene-gene interactions (edges) are indicated as color-coded correlation coefficients. Gene products known to localize in mitochondria are blue nodes, peroxisomal gene products are yellow nodes, and the microsomal Cyp4a gene products are pink nodes. Gene products with a dual peroxisomal and mitochondrial localization are purple nodes.

(4–12%; Life Technologies). Cyp4a10 was detected using goat anti-rat Cyp4a1 (Daichi Pure Chemicals, Tokyo, Japan). Acox1 was detected with an antibody specific for the 50 kDa rat protein (gift of P. van Veldhoven, Katholieke Universiteit Leuven, Belgium). Ehhadh was detected using an IgG fraction against the rat protein (gift of T. Hashimoto, Shinshu University School of Medicine, Matsumoto, Nagano, Japan). Hsd17b4 was detected using an IgG fraction against human Hsd17b4 (gift of T. Hashimoto). Rabbit anti-Abcd3 (or PMP70) was raised against a 21 amino acid synthetic rat peptide (Zymed, Carlsbad, CA). Antibodies were visualized using the Odyssey Infrared Imaging System (Li-Cor Biosciences).

Statistical analysis

The six groups of mice were compared using the nonparametric Kruskal-Wallis (ANOVA) test followed by Dunn’s multiple comparison test to determine statistical significance between the WT and Ehhadh KO samples after 20 h of fasting.

RESULTS

The Ehhadh gene coexpression subnetwork indicates a role in the generation of energy

Genes that participate in a similar biochemical process or physiological function often have coregulated expression. To
coexpression subnetworks, which were subsequently merged into one network and analyzed further by GO enrichment (Fig. 1). Overall, the combined network contained several established PPARα target genes (e.g., Acadm and Hdhb) and was significantly enriched for GO terms such as fatty acid oxidation, tricarboxylic acid cycle, mitochondria, and peroxisomes (Supplementary Fig. IIIB–D). The merged gene expression subnetwork also contained Cyp4a10 and Cyp4a14. These genes encode members of the cytochrome P450 family that perform the first rate-limiting step in the ω-oxidation of long-chain fatty acids. Thus, these coexpression subnetworks are consistent with a function of Ehhadh in the generation of energy from fatty acids.

To demonstrate that genetic variation in Ehhadh could be related to variation in metabolic traits, we queried GeneNetwork to determine if Ehhadh liver expression correlated with clinical endpoints, which had been archived in the B6BTBRF2 cross database (25). This analysis revealed a significant and negative correlation of hepatic Ehhadh expression with fasting plasma glucose in this population of mice, suggesting that variation in expression of Ehhadh and its partners in the coexpression network could affect glucose metabolism possibly via its effects on generation of energy from fatty acids (Supplementary Fig. III).

**Decreased medium-chain dicarboxylic acid levels in Ehhadh KO mice upon fasting**

Ehhadh is a well-established PPARα target gene (33, 34). Its expression is induced during fasting. In combination with our finding that genes involved in the generation of energy from fatty acids are in the gene coexpression subnetwork of Ehhadh, we reasoned that fasting would reveal a phenotype in Ehhadh KO mice. We fasted WT and Ehhadh KO and analyzed metabolites after 0 (fed), 6 (postabsorptive), and 20 h (fasted) of fasting. Blood glucose and plasma insulin decreased with time of fasting, whereas blood β-hydroxybutyrate levels increased (Fig. 2A). Although blood glucose and β-hydroxybutyrate levels were slightly lower in Ehhadh KO animals, the ketogenic response upon fasting appeared adequate.

Next we determined the plasma acylcarnitine profile. Changes in the plasma acylcarnitine profile are thought to reflect tissue acyl-CoA levels. The induction of ω-oxidation after an overnight fast is reflected in an increase in plasma C6-DCA- and C8-DCA-carnitine in WT mice. In contrast, this increase was virtually absent in Ehhadh KO mice. Other long-chain acylcarnitines, such as C18:1-carnitine, increased upon fasting in WT and Ehhadh KO mice (Fig. 2A). Acylcarnitine analysis in tissues of WT mice revealed that liver, but not heart (data not shown), displayed an increase in C6-DCA- and C8-DCA-carnitine upon fasting. Again, this increase was virtually absent in Ehhadh KO mice (Fig. 2B).

In addition to the acylcarnitine profiles, we also measured the organic acids in urine because the urinary excretion of free C6-DCA and C8-DCA is quantitatively greater than their excretion as acylcarnitines. As expected, urinary C6-DCA and C8-DCA levels were higher in fasted WT mice. In Ehhadh KO mice, however, C6-DCA and C8-DCA levels did not increase after fasting (Fig. 2C). We conclude that the increase in the formation of medium-chain DCAs upon fasting is virtually absent in Ehhadh KO mice suggesting that the peroxisomal β-oxidation of long-chain DCAs is disturbed.

**Fasting induces PPARα targets in WT as well as Ehhadh KO mice**

To verify whether the defect in the production of medium-chain DCAs in Ehhadh KO mice was not caused by a failure to induce genes involved in ω-oxidation, we analyzed expression of selected PPARα target genes using immunoblot analysis (Fig. 3A). Fasting induced a marked increase in the expression of Cyp4a10 in WT and Ehhadh KO mice. Ehhadh protein was also highly induced upon fasting in WT mice and, as expected, was absent in the Ehhadh KO mouse. Hsd17b4, which theoretically could compensate for Ehhadh deficiency, was slightly induced by fasting in WT and Ehhadh KO mice, which is consistent with its induction by PPARα agonists (35). An induction was also observed for Acox1, most notably for the 72 kDa full-length protein. Abcd3 (Pmp70) levels did not respond to fasting. Thus, the PPARα response upon fasting does not seem to be disturbed in Ehhadh KO mice.

**DISCUSSION**

In this study, we combined prior knowledge with gene coexpression subnetworks and mouse experiments to elucidate the role of Ehhadh in metabolism. Ehhadh belongs to the so-called classical peroxisomal β-oxidation pathway, together with Acox1 and Acaal1b. In the liver, this pathway is induced by peroxisome proliferators in a mechanism that depends on PPARα. A similar response is elicited by fasting, a stress that leads to physiologic PPARα activation. In addition to peroxisomal β-oxidation, PPARα induces mitochondrial β-oxidation, ketogenesis, and microsomal ω-oxidation, among many other pathways (36). We found that hepatic Ehhadh coexpression subnetworks were composed of genes involved in the tricarboxylic acid cycle and mitochondrial and peroxisomal fatty acid oxidation, which is consistent with a function in the generation of energy from fatty acids. We were able to demonstrate that, during fasting, Ehhadh plays an indispensable role in the formation of the medium-chain DCAs adipic and suberic acid and their carnitine esters. Our results offer an explanation for the coordinated induction of mitochondrial and peroxisomal oxidative pathways during fasting.

Medium-chain DCAs are the final products of microsomal ω-oxidation of long-chain fatty acids and the subsequent peroxisomal β-oxidation of long-chain DCAs (Fig. 3B). The Ehhadh coexpression subnetwork contained at least three genes involved in this process: Cyp4a10, Cyp4a14, and Aldh3a2 (Fig. 1; Supplementary Fig. IIA). Previous biochemical studies have indicated that peroxisomes are important for the β-oxidation of long-chain DCAs (37–42).
hypothesized to perform this role based on preliminary reports on the Abcd3 KO mice (45). Indeed, Abcd3 was present in our gene coexpression subnetwork. For the individual \( \beta \)-oxidation steps of long-chain DCAs, it has been demonstrated that ACOX1 is crucial for the first step in humans (18). The last step in the \( \beta \)-oxidation of DCAs can be performed by multiple thiolases (Acaa1a, Acaa1b, and Scp2). Based on our results, it seems reasonable to speculate that the inducible Acaa1b is crucial. Indeed, Acaa1b was present in the gene coexpression subnetwork. On the other hand, fibroblasts of patients with rhizomelic chondrodysplasia punctata type 1, in which the mature 41 kDa form of ACAA1 is absent, have normal \( \beta \)-oxidation of long-chain DCAs, suggesting this was confirmed in vitro using peroxisome-deficient cells. Oxidation of hexadecanedioic acid (C16-DCA) was strongly reduced in fibroblasts of patients with a peroxisome biogenesis disorder (18). The use of a KO mouse model revealed a similar picture with deficient C14-DCA oxidation in hepatocytes devoid of Pex5 (17). Before peroxisomal \( \beta \)-oxidation, long-chain DCAs are activated to their CoA ester by a microsomal acyl-CoA synthetase (42, 43), the molecular identity of which is unknown. Acsl1, which is present in the gene coexpression subnetwork, is a candidate gene for this function (44). The resulting long-chain DCA-CoA is subsequently transported across the peroxisomal membrane probably by one of the three peroxisomal ABC half-transporters (Fig. 3B). Abcd3 has been hypothesized to perform this role based on preliminary reports on the Abcd3 KO mice (45). Indeed, Abcd3 was present in our gene coexpression subnetwork.

For the individual \( \beta \)-oxidation steps of long-chain DCAs, it has been demonstrated that ACOX1 is crucial for the first step in humans (18). The last step in the \( \beta \)-oxidation of DCAs can be performed by multiple thiolases (Acaa1a, Acaa1b, and Scp2). Based on our results, it seems reasonable to speculate that the inducible Acaa1b is crucial. Indeed, Acaa1b was present in the gene coexpression subnetwork. On the other hand, fibroblasts of patients with rhizomelic chondrodysplasia punctata type 1, in which the mature 41 kDa form of ACAA1 is absent, have normal \( \beta \)-oxidation of long-chain DCAs, suggesting

Fig. 2. Metabolites in WT and Ehhadh KO mice. A: Blood and plasma metabolites. B: Liver C6-DCA and C8-DCA acylcarnitine. C: Urinary C6-DCA and C8-DCA and their acylcarnitine esters. Values were obtained in pooled urine samples and determined in duplicate. Statistical significance in the Dunn’s multiple comparison test is indicated as follows: * \( P < 0.05 \). The error bars indicate the SEM.
that, at least in humans, ACAA1 in not crucial (18). The role of Acaa1b in the β-oxidation of long-chain DCAs could be investigated in the Acaa1b KO mouse model during fasting (46). Fibroblasts from patients with HSD17B4 deficiency had normal oxidation of C16-DCA, suggesting that Ehhadh has a role in performing the second and third step of long-chain DCA β-oxidation (18). Indeed, recombinant Hsd17b4 and Ehhadh handle long-chain DCA substrates with comparable efficiency (18). Moreover, oxidation of C14-DCA was reduced in Ehhadh-deficient hepatocytes, whereas it was elevated in Hsd17b4 KO hepatocytes (17). The fact that the oxidation of C14-DCA was more deficient in Pex5 KO hepatocytes when compared with Ehhadh KO hepatocytes hindered concluding that Ehhadh is essential for oxidation of long-chain DCAs. In addition, Hsd17b4 is inducible by PPARγ (35) and thus could theoretically compensate for Ehhadh deficiency also during fasting. Moreover, Hsd17b4 expression correlated significantly with Ehhadh in the B6BTBRF2 and BHF2 crosses (data not shown). Indeed, we observed a small increase in the protein levels of Hsd17b4 upon fasting in Ehhadh KO mice, but production of medium-chain DCAs was deficient, from which we concluded that Hsd17b4 is unable to compensate for Ehhadh deficiency. Therefore, we provide the first in vivo evidence that Ehhadh is essential for the generation of medium-chain DCAs.

The final steps in the peroxisomal metabolism of DCAs are poorly understood. The thiolytic cleavage of the CoA esters is achieved by acyl-CoA thioesterases (Fig. 3B). In mice and humans, Acot4 or Acot8 are most likely involved in the metabolism of medium-chain DCAs (47), and, indeed, Acot4 and cytosolic Acot1 are present in our Ehhadh coexpression subnetworks. Alternatively, the CoA ester can be converted into a carnitine ester by carnitine octanoyltransferase (Crot). Whether a DCA is converted to an organic acid or an acylcarnitine probably depends on the relative expression levels of Crot versus the thioesterases (48). Expression of Crot in liver is high (48), which is in accordance with the fact that we could measure the formation of C6-DCA-carnitine in liver but not in heart.

**Fig. 3.** Immunoblots of ω- and β-oxidation proteins in WT and Ehhadh KO mice. A: Approximately 10 µg of total liver protein was used for electrophoresis and subsequently blotted onto nitrocellulose. B: Schematic representation of long-chain fatty acid ω-oxidation and subsequent peroxisomal long-chain DCA β-oxidation.
ω-Oxidation contributes significantly to the oxidation of fatty acids. Increased medium-chain DC aciduria is observed during conditions characterized by increased fatty acid oxidation, such as fasting and diabetic ketosis. In addition, ω-oxidation is increased in patients with an inborn error of mitochondrial β-oxidation. In these cases, ω-oxidation followed by peroxisomal β-oxidation seems to function as a sink for fatty acids overflowing from the mitochondrial β-oxidation system. We hypothesize that this function is the explanation for the coordinate induction of mitochondrial and peroxisomal β-oxidation after PPARα activation. The Ehhadh KO mouse is the first model with a clear deficiency in the peroxisomal β-oxidation of long-chain DCAs and can therefore be used to understand the physiological role of this pathway. We did not find evidence for additional defects in peroxisomal functions upon fasting. After the overnight fast, there was no accumulation of bile acid precursors or very long-chain fatty acids (data not shown).

Besides this role in the peroxisomal β-oxidation of DCAs, recent studies suggest additional functions for Ehhadh in humans. A systematic genetic analysis of cytochrome P450 enzyme activities in human liver revealed EHHADH as a novel regulatory gene for the P450 system (49). In a bioinformatics study, EHHADH was selected as a candidate gene for nonalcoholic fatty liver disease. Subsequent genetic analysis revealed SNPs in EHHADH that associated with fasting insulin levels (50). This coincides with our observation that in the B6BTBRF2 cross, hepatic Ehhadh expression and characterization.

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