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Molecular Basis of Hepatic Carnitine Palmitoyltransferase I Deficiency

Lodewijk IJlst,* Hanna Mandel,§ Wendy Oosthein,* Jos P.N. Ruiter,* Alisa Gutman,† and Ronald J.A. Wanders*†

*Department of Clinical Chemistry and †Department of Pediatrics, University of Amsterdam, Academic Medical Center, 1100 D E Amsterdam, The Netherlands; ‡Department of Pediatrics, Rambam Medical Center, Haifa 31096, Israel; and †Department of Clinical Biochemistry, Hadassah University Hospital, Jerusalem 9120, Israel

Abstract

Mitochondrial fatty acid β-oxidation is important for energy production, which is stressed by the different defects found in this pathway. Most of the enzyme deficiencies causing these defects are well characterized at both the protein and genomic levels. One exception is carnitine palmitoyltransferase I (CPT I) deficiency, of which until now no mutations have been reported although the defect is enzymatically well characterized. CPT I is the key enzyme in the carnitine-dependent transport across the mitochondrial inner membrane and its deficiency results in a decreased rate of fatty acid β-oxidation. Here we report the first delineation of the molecular basis of hepatic CPT I deficiency in a new case. cDNA analysis revealed that this patient was homozygous for a missense mutation (D454G). The effect of the identified mutation was investigated by heterologous expression in yeast. The expressed mutant CPT IA displayed only 2% of the activity of the expressed wild-type CPT IA, indicating that the D454G mutation is the disease-causing mutation. Furthermore, in patient’s fibroblasts the CPT IA protein was markedly reduced on immunoblot, suggesting that the mutation renders the protein unstable. (J. Clin. Invest. 1998. 102:527–531.) Key words: carnitine palmitoyltransferase • fatty acid • Mendelian disorder • hereditary disease • gene expression

Introduction

The mitochondrial β-oxidation of long-chain fatty acids is a major source of energy, especially in the heart. Before their catabolism, long-chain fatty acids are activated to their CoA esters in the extramitochondrial space by long-chain acyl-CoA synthetases localized in the mitochondrial outer membrane as well as the peroxisomal and endoplasmic reticulum membrane. Transport of long-chain acyl-CoA esters across the mitochondrial inner membrane requires carnitine and three proteins including carnitine palmitoyltransferase I (CPT I),† the carnitine acylcarnitine carrier (CAC), and CPT II. The first enzyme (CPT I) is localized in the outer-mitochondrial membrane and converts the fatty acyl-CoA ester to its carnitine ester. This carnitine ester is subsequently transported across the mitochondrial inner membrane by CAC which belongs to the mitochondrial carrier family. Once inside the mitochondrial lumen, CPT II reconverts the carnitine ester to the CoA ester which can then serve as a substrate for β-oxidation. CPT II is bound to the mitochondrial inner membrane facing the mitochondrial matrix. The relationship between CPT I and CPT II has long remained an enigma. However, recent studies notably by McGarry and co-workers have clearly established that CPT I and CPT II are distinct enzyme proteins encoded by different genes (for review see reference 1). There is only a single form of CPT II expressed in all tissues. On the other hand, two different isoforms of CPT I have been described with distinct tissue distributions. These two forms are called the hepatic (CPT IA) and muscle form (CPT IB) and are encoded by different genes localized on chromosome 11q13.1-13.5 and 22q13.31-13.32, respectively (2).

Clinically, three different phenotypes can be distinguished as characterized by muscular (3), hepatic (4), or hepatocardiomyoskeletal symptoms, respectively (5). In the hepatic type, CPT I is deficient, whereas CPT II is normally active. In the other types of CPT deficiency, CPT II is deficient to different extents with normal CPT I activity. After the first report on CPT I deficiency in 1981 (4) at least 11 cases with CPT I deficiency have been described (for overview see reference 6) presenting with coma, seizures, hepatomegaly, and hypoketotic hypoglycemia, usually after a period of fasting or after a viral infection. When appropriately treated, patients suffering from hepatic CPT I deficiency may survive normally. Remarkably, patients suffering from CPT I deficiency do not display chronic muscle weakness and/or cardiomyopathy, which is in marked contrast to other inherited deficiencies in the oxidation of long-chain fatty acids including CPT II deficiency.

The molecular basis of CPT I deficiency has so far remained unresolved although the cloning of human CPT IA was reported in 1995 (7). We now report the resolution of the molecular defect in a patient with enzymatically proven CPT I deficiency.

Methods

Case. Patient S.I. is the second child of consanguineous parents (2nd–3rd degree cousins). She presented at 15 mo of age with diarrhea and feeding difficulties. On admission she was severely hypotonic and lethargic. Physical examination revealed hepatomegaly, normal heart sounds and rhythm, and decreased tendon reflexes.

At time of admission she suffered from hypoketotic hypoglycemia (glucose 1.6 mmol/liter). Further laboratory findings in her blood were (normal values between parentheses): pH 7.2, HCO3, 11 mmol/
liter, base excess 12 mmol/liter, aspartate aminotransferase 438 IU/liter (< 40 IU/liter), alanine aminotransferase 148 IU/liter (< 40 IU/liter). The urinary excretion of dicarboxylic acids (adipic, suberic, sebacic, 3-hydroxy-sebacic, dodecenedioic, decadienedioic, decenedioic, 3-hydroxy-dodecenedioic acids) was slightly elevated during this episode. This mild dicarboxylic aciduria is not a common feature of CPT I deficiency, although it has been reported twice before (6, 8).

Since the child was diagnosed, she had several episodes of hypoglycemia and (mild) metabolic acidosis, which occurred during acute viral infection and/or because of feeding problems, necessitating administration of intravenous glucose and bicarbonate.

At 18 mo of age she started to walk. Now at 30 mo she is slightly hypotonic and falls frequently. Before her diagnosis she had several encephalopathic episodes lasting for 5 to 10 d, which may have been caused by hypoglycemia due to the CPT I deficiency. The hypotonicity as well as the motor retardation are probably caused by these hypoglycemic episodes.

Cell culture conditions. Cell culture conditions were exactly as described previously (9).

Fatty acid β-oxidation. Fatty acid β-oxidation of [9,10-3H]-myristate and palmitate in fibroblasts was performed essentially as described by Manning and co-workers (10). To this end fibroblasts were harvested with trypsin-EDTA according to standard procedures and suspended in Ham’s F10 medium. The cell density of the fibroblast suspension was estimated by light scattering (OD490 = 0.14 corresponding to ~ 0.05 mg/ml protein). From this suspension, 0.4 ml (20 μg protein) was seeded in 1-cm² glass vials and the cells were allowed to attach overnight. After washing the cells with PBS, 200 μl of RPMI medium (without glucose) was added containing 20 mM Hepes, pH 7.4, 100 μM fatty acid (myristic or palmitic acid), 200,000 dpm tritium labeled fatty acid ([9,10-3H]-myristic or [9,10-3H]-palmitic acid) obtained from Amersham (Arlington Heights, IL), and 1 mg/ml BSA (essentially fatty acid free) (Sigma Chemical Co., St. Louis, MO). The reaction was stopped by rapid cooling on ice-water after 2 h of incubation at 37°C and the labeled product ([3H]-water) was measured as described (11). The remaining cells were homogenized in Triton/PBS (1 g/liter) by sonication and protein content was measured using the BCA kit from Sigma Chemical Co. (12).

Enzyme assays. Enzyme assays were performed as described before (13).

CPT activity. CPT activity was measured essentially as described by Demaureg and co-workers (5) with some modifications. The assay mixture (500 μl final volume) contained 50 mM Hepes, pH 7.4, 150 mM KCl, 1 mM EDTA, 1 mM DTT, 1.3 μg/ml BSA (essentially fatty acid free), 0.5 mM L-carnitine (Sigma Chemical Co.), and 200,000 dpm [1-14C]-L-carnitine (New England Nuclear Life Science, Boston, MA), 0.1 μM palmityl-CoA (Boehringer Mannheim, Mannheim, Germany). Reactions were started by adding fibroblasts (300 μg protein) or yeast homogenate (10–20 μg protein) and incubated for 10 min at 37°C with (CPT II activity) or without (CPT I + CPT II activity) 0.2 mM malonyl-CoA, which is a specific inhibitor of CPT I but not of CPT II. Reactions were terminated by addition of 0.5 ml 0.5 M HCl and the labeled product palmityl-carnitine was extracted with n-hexanol as described (14).

Immunoblot analysis. Fibroblast homogenates were subjected to SDS-PAGE on a 7.5% acrylamide gel. CPT IA protein was visualized with 5′-aaa gag gaa aca gct atg acc agt TAC GTG AGC GAC-3′ and 1596CPT1rM13 5′-cag gaa aca get atg ace GGT CCT TAT AAC CTC TTG AC-3′; fragment C: 1460CPT1f-21M13 5′-tgaatt aac aag aeg gcc gct AGC TCA TGT CCA TTG AGC ACA GC-3′ and 2351CPT1rM13rev 5′-cag gaa aca get atg ace CGT TTG CCT TCC CAG CAG CTC-3′.

Sequence analysis of these PCR fragments using fluorescent labeled M13 primers (Amersham) was performed on an Applied Biosystems 377A automated DNA sequencer following the manufacturer’s protocols.

Construction of expression plasmids. Two expression plasmids were constructed for expression of CPTI-454D (wild-type) and CPTI-454G (mutant) in Saccharomyces cerevisiae. The complete open reading frame of the gene coding for CPT IA was amplified in a PCR reaction using the following primer set: sense 5′-aaa aag ctt aaa ATG GCA GAA GCT CAC CAA GC-3′ and antisense 5′-aaa gaa ttc CTG CCC AGC AGC TCC AGT GG-3′. The PCR products amplified from control and patient’s cDNA were first inserted into pGEM-T (Promega Corp., Madison, WI). The cloned PCR products were sequenced to assess the integrity of the PCR process.

Plasmid pYES2 (Invitrogen Corp., Carlsbad, CA) was used to create pYCPTI-454D and pYCPTI-454G by cloning the ORF of control and mutant CPT IA, respectively, into the HindIII and EcoRI sites downstream of the GAL1 promoter.

Yeast culture and expression. Wild-type S. cerevisiae (INVSc2: MATα, his3-D200, ura3-167 obtained from Invitrogen) and the transformed strains were grown to OD600 = 0.2 in a medium composed of 0.67 g/liter yeast nitrogen base without amino acids (Difco Laboratories Inc., Detroit, MI) and 20 g/liter lactate, supplemented with the appropriate amino acids. Overnight induction was initiated by the addition of galactose to a final concentration of 2 g/liter. The cells were harvested and spheroplasts were prepared according to standard procedures (17). Spheroplasts were homogenized by sonication in a buffer containing 10 mM Mops, pH 7.4, 160 mM KCl 1 mM EDTA, and 1 mM PMSF. The homogenates were centrifuged at 10,000 g for 30 s and the supernatants were used for enzyme activity measurements.

Results

Fatty acid oxidation and enzyme analysis. The organic acid profile in urine of the index patient suggested a fatty acid oxidation defect. This was confirmed by initial β-oxidation measurements in lymphocytes. Biochemical studies in fibroblasts from the index patient showed that the oxidation of the long-chain fatty acids myristate and palmitate was markedly decreased (Table I). To exclude that this was due to a defect in either very-long chain acyl-CoA dehydrogenase or mito-

<table>
<thead>
<tr>
<th>Parameter measured</th>
<th>Patient</th>
<th>Controls</th>
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</thead>
<tbody>
<tr>
<td>Overall β-oxidation activity</td>
<td>Myristic acid (nmol/h/mg)</td>
<td>1.4</td>
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<tr>
<td></td>
<td>Palmitic acid (nmol/h/mg)</td>
<td>0.5</td>
</tr>
<tr>
<td>Enzyme activity measured</td>
<td>CPT I (nmol/min/mg)</td>
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<tr>
<td></td>
<td>CPT II (nmol/min/mg)</td>
<td>0.70</td>
</tr>
<tr>
<td>Immunoblot analysis</td>
<td>88-kD cross-reactive material</td>
<td>Virtually absent (n = 2)</td>
</tr>
</tbody>
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In two controls we found two differences when compared with the reported sequence: an A1435C and an A1702G changing the glutamine at position 479 to a proline and the threonine at position 568 into an alanine, respectively. Since these fibroblasts were found to contain normal CPT I activity, these differences likely represent polymorphisms.

Figure 1. Electropherogram of a control subject, the index patient, and both parents showing the sequence surrounding the A1361G mutation (indicated by an arrow) in CPT IA.

Discussion

sequence analysis. To study CPT IA at the protein level, we first performed immunoblot experiments using an antibody raised against CPT IA. In control fibroblasts the CPT IA protein was found to be clearly present, whereas the signal was very weak in the patient’s fibroblasts (Table I). Earlier studies have shown that fibroblasts express CPT IA but not CPT IB (7) which led us to study CPT IA in more detail.

Expression studies. The aspartate at position 454 is located in a region which is highly conserved among 17 reported carnitine acyltransferases (Fig. 2). To investigate the effect of the mutation on the enzyme activity we expressed in the yeast S. cerevisiae both the wild-type and the mutant CPT I. S. cerevisiae is not only easy to manipulate genetically but is particularly suited for this study because yeast lacks endogenous CPT activity. Homogenates of transformed cells (derived from four to six independent transformants) as well as untransformed cells were prepared and CPT activity was measured (Fig. 3). In agreement with literature data, wild-type yeast and yeast transformed with the expression vector (pYES2) only did not display any CPT activity. On the other hand, cell homogenates from transformants with pYCPTI-454D (wild-type CPT IA) were found to contain high CPT IA activity. The specific activity was ~ 10-fold higher than observed in fibroblasts. In contrast, transformants with pYCPTI-454G (mutant CPT IA) displayed only 2% of the expressed wild-type CPT IA. These data show that the D454G substitution causes loss of CPT IA activity and is responsible for the hepatic CPT I deficiency in this patient.

Figure 2. Comparison of different acyltransferases from different species: CPT IA from human and rat; CPT IB from human and rat; CPT II from human and rat; carnitine octanoyltransferase (COT) from bovine and rat; carnitine acetyltransferase (CAT) from human; choline acetyltransferase (ChAT) from human and rat; and Drosophila melanogaster. The consensus pattern is: [NDV]-R-[WF]-X(0,1)-[LIVMFY]-X(2)-[DN]-[GSA]-X(2)-[GA]-X(3)-[ED]-[H][X]-[DE]-[AG] with the active histidine residue in bold.

So far 11 patients with CPT I deficiency have been reported in literature. The patient described in this report showed many of the clinical abnormalities described in other patients with CPT I deficiency including hepatomegaly and periods of muscle weakness and fainting due to hypoglycemia. Our observation using cDNA obtained from fibroblasts of control subjects and the index patient.

Analysis of the patient’s cDNA revealed the A1435C polymorphism, a silent G963A mutation, and an A1361G missense mutation (Fig. 1). As a consequence of this mutation the aspartate at position 454 is changed into a glycine (D454G). The finding of the A1361G mutation in a heterozygous form in both parents (Fig. 1) indicates that the patient is truly homozygous for this mutation.
that fibroblasts of this patient were deficient in CPT I activity indicated that the patient is deficient in CPT IA, which is the only CPT I isoform expressed in fibroblasts (7). Molecular analysis of CPT IA cDNA of this patient revealed a homozygous A1361G missense mutation changing the aspartate at position 454 into a glycine. This mutation was associated with a dramatic decrease in CPT activity as demonstrated by expression studies in S. cerevisiae, mutant CPT IA (454G) displayed only 2% of the activity of expressed wild-type CPT IA (454D). These data show that the D454G mutation is the disease-causing mutation.

Alignment of different reported carnitine acyltransferases reveals structural sequences shared within this transferase family. The histidine at position 473 is thought to be the active residue (18–20) and are conserved among all transferases indicative for an important role. Indeed, the role of an aspartate as part of a "catalytic triad" has been suggested by Brown et al. (20). To test this hypothesis, they performed site-directed mutagenesis of CPT II and changed the aspartate at position 353 (homologous to the aspartate at position 454 in CPT IA) into an alanine. When expressed in yeast, the resulting mutant CPT II was unstable as judged by immunoblots and the lysate contained < 1% of the CPT activity of yeast-expressed wild-type CPT II. They concluded that the majority of the synthesized protein became misfolded and subsequently degraded and that only a small portion of the translated protein achieved the correct conformation having normal activity.

The finding that CPT IA protein was hardly detectable in the patient’s fibroblasts upon immunoblot analysis suggests that the D454G mutation also renders the CPT IA protein unstable, thus explaining the deficient CPT I activity in our patient.

Acknowledgments

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References


