A novel mutation in the thiamine responsive megaloblastic anaemia gene SLC19A2 in a patient with deficiency of respiratory chain complex I

Curt Scharfe, Michael Hauschild, Thomas Klopstock, Antoon J M Janssen, Peter H Heidemann, Thomas Meitinger, Michaela Jaksch

Abstract

The thiamine transporter gene SLC19A2 was recently found to be mutated in thiamine responsive megaloblastic anaemia with diabetes and deafness (TRMA, Rogers syndrome), an early onset autosomal recessive disorder. We now report a novel G1074A transition mutation in exon 4 of the SLC19A2 gene, predicting a Trp358 to ter change, in a girl with consanguineous parents. In addition to the typical triad of Rogers syndrome, the girl presented with short stature, hepatosplenomegaly, retinal degeneration, and a brain MRI lesion. Both muscle and skin biopsies were obtained before high dose thiamine supplementation. While no mitochondrial abnormalities were seen on morphological examination of muscle, biochemical analysis showed a severe deficiency of pyruvate dehydrogenase and complex I of the respiratory chain. In the patient’s fibroblasts, the supplementation with high doses of thiamine resulted in restoration of complex I activity. In conclusion, we provide evidence that thiamine deficiency affects complex I activity. The clinical features of TRMA, resembling in part those found in typical mitochondrial disorders with complex I deficiency, may be caused by a secondary defect in mitochondrial energy production.

Keywords: TRMA syndrome; SLC19A2 gene; complex I deficiency

The first description of thiamine responsive megaloblastic anaemia syndrome (TRMA, OMIM 249270) is attributed to Rogers et al in 1969, who reported an 11 year old girl with megaloblastic anaemia, diabetes mellitus, and sensorineural deafness. Further reports on TRMA described congenital heart disease, arrhythmias, abnormalities of the retina and optic nerve, aminoaciduria, situs inversus, and stroke-like episodes in addition to the characteristic triad. Thiamine treatment results in improvement of haematological and endocrine function, while neurological symptoms do not respond as well. Recently, the TRMA disease locus was localised to a 1.4 cM region on chromosome 1q23.3. Three studies identified loss of function mutations in the TRMA causing gene SLC19A2 in affected subjects in a total of nine families. SLC19A2 encodes a putative transmembrane protein of 497 amino acids, with homology to members of the solute carrier family (fig 1). Functional characterisation indicates that this protein is a high affinity saturable transporter of thiamine. Intra- cellular thiamine deficiency in TRMA leads to decreased activity of enzymes dependent on thiamine pyrophosphate (TPP), the active form of thiamine: the pentose phosphate shunt enzyme transketolase (TK) and three mitochondrial enzyme complexes, the pyruvate dehydrogenase complex (PDHC), alpha-ketoglutarate dehydrogenase (KGDH), and branched chain ketoacid dehydrogenase (BCKD). Here we report a patient with TRMA carrying a novel homozygous stop mutation in the SLC19A2 gene, who presented with additional clinical features compared to those previously described and a severe complex I deficiency in addition to PDHC deficiency.

Patient and methods

CASE REPORT

The 14 year old girl was born to first degree cousins of Turkish descent (fig 2). The parents and three older brothers are healthy. After an uneventful pregnancy she developed macrocytic anaemia and thrombocytopenia at 5 months. The megaloblastic anaemia was confirmed by bone marrow biopsy showing ringed sideroblasts up to 50%. She was found to be deaf at 18 months and diabetes mellitus presented at the age of 3 years. Additional findings were retinal degeneration, short stature (~2.6 standard deviation score, SDS), incomplete right bundle branch block of the heart, mild hepatomegaly, and a homogeneous enlargement of the spleen (12.3 cm in length). Brain MRI at 12 years showed a lesion of about 2 cm (area of left middle cerebral artery in the parietal lobe) but without any neurological correlates. Lactate levels were increased in serum (3.55 mmol/l, reference range <1.8 mmol/l) and in cerebrospinal fluid (2.3 mmol/l, reference range <1.8 mmol/l). The lactate/pyruvate ratio was increased twofold. Thiamine levels in plasma were in the normal range, whereas intracellular TPP (20.1 ng/ml, reference range 30-90 ng/ml) and TPP synthase activity of erythrocytes (7.5 nmol/h/g Hb, reference range 10-20 nmol/h/g Hb) were reduced. Automatic scanning of blood cells showed a mean MCV of 96.1 fl (reference range 80-94 fl), a low Hb concentration of 89

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g/l (reference range 120-160 g/l), and a low reticulocyte index of 2.4 per 1000. A manual differential showed anisocytosis with micro- and macrocytes. Morphological and ultrastructural examination of skeletal muscle showed mild lipidosis and increased subsarcolemmal NADH reductase activity but no definite mitochondrial abnormalities. After one week of high dose thiamine supplementation (2 × 100 mg/day thiamine-HCL), reticulocytosis was observed (114 per 1000) followed by an almost complete resolution of anaemia within four weeks (2.6 reticulocytes per 1000, Hb 11.3 g/l, MCV 100.1 fl). TPP and TPP synthase activity were not verified after treatment. Insulin dosage could be reduced in the following six months from 1.8 to 0.7 U/kg/day. The serum lactate level dropped to 1.36 mmol/l. Retinal degeneration, deafness, and splenomegaly remained unchanged.

MUTATION DETECTION
DNA was extracted from skeletal muscle, skin fibroblasts, and leucocytes according to standard purification protocols (Qiagen, Hilden, Germany). Polymerase chain reaction (PCR), Southern blot analysis, and single strand conformational polymorphism (SSCP) analysis for exclusion of mtDNA mutations were performed as previously described. The entire SLC19A2 coding sequence (GenBank AF135488), consisting of six exons, was amplified in the index patient with the forward and backward intronic primers as previously described. Cycle sequencing of gel purified fragments was performed using the Perkin-Elmer ABI PRISM Big Dye Termination kit. Sequences were determined with a Perkin-Elmer Applied Biosystems 377 automated sequencer. Restriction fragment length polymorphism analysis (RFLP) was done using exon 4 primers as previously described and BclI as restriction enzyme. Resulting fragments were separated on a 3% agarose gel and analysed after ethidium bromide staining.

SKIN FIBROBLAST CELL CULTURE AND THIAMINE SUPPLEMENTATION
Fibroblasts from skin were grown in high glucose Dulbecco’s modified Eagle’s medium.
A novel mutation in SLC19A1

Results

Marker enzyme citrate synthase. Activities were related to the mitochondrial measured by addition of 0.2 mmol/l NADH.

RFLP SSCP analysis. No major mitochondrial cephalomyopathies were excluded by standard mutations associated with mitochondrial en-
family members by RFLP analysis using exon 4 site, we confirmed the sequencing results in all was homozygous for the wild type (fig 2). As zygous for the mutation and one brother (II.2) and two brothers (II.1 and II.3) were hetero-
protein at codon 358. The parents (I.1 and I.2) 4, predicting a premature truncation of the termination mutation at position 1074 in exon patient showed a novel homozygous G to A with normal control chromosomes. Analysis of obtained from the family members were her healthy sibs, and their parents. Sequences was measured by addition of 0.2 mmol/l NADH. Activities were related to the mitochondrial marker enzyme citrate synthase.

BIOCHEMISTRY

Activities of PDHC, complexes I (rotenone sensitive NADH ubiquinone oxidoreductase), II + III (succinate cytochrome-c oxidoreductase), and IV (cytochrome-c oxidase) of the mitochondrial respiratory chain were deter-
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MUTATION DETECTION

We performed genotyping of the affected girl, her healthy sibs, and their parents. Sequences obtained from the family members were compared with the SLC19A2 sequence and with normal control chromosomes. Analysis of the complete SLC19A2 gene in the index patient showed a novel homozygous G to A termination mutation at position 1074 in exon 4, predicting a premature truncation of the protein at codon 358. The parents (I.1 and I.2) and two brothers (II.1 and II.3) were hetero-
zymous for the mutation and one brother (II.2) was homozygous for the wild type (fig 2). As the G1074A mutation creates a BclI restriction site, we confirmed the sequencing results in all family members by RFLP analysis using exon 4 primers (data not shown). Frequent mtDNA mutations associated with mitochondrial en-
ccephalomyopathies were excluded by standard RFLP SSCP analysis. No major mitochondrial rearrangements were found by Southern blot analysis.

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Skeletal muscle and skin fibroblast biochemical analyses were performed before thiamine treatment. Respiratory chain activities showed marked deficiency of complex I with a residual activity of 35% in skeletal muscle. PDHC activity was reduced to 50% of the lower refer-
ence range in muscle tissue (table 1). Complexes II and III showed a minor reduction of about 10% only, and complex IV had normal activity. In order to investigate whether the decreased complex I activity was influenced by the thiamine deficiency, the patient’s fibro-
blasts were cultured with and without thiamine. We found that supplementation with a high concentration of thiamine (3 μmol/l) resulted in a 2.5 fold increase in complex I activity compared to fibroblasts cultured without thiamine. Similarly, PDHC activity was within the normal range after thiamine supplement-

Discussion

We have identified a novel loss of function mutation in the high affinity thiamine trans-
porter gene SLC19A2 in a child with TRMA. Biochemical measurement of muscle and fibroblasts before thiamine supplementation showed not only the expected deficiency of PDHC, but also a marked deficiency of complex I of the mitochondrial respiratory chain, which normalised after thiamine supplement-
ction. Clinically, anaemia and diabetes improved within two weeks after thiamine supple-
mentation. Thiamine is an ubiquitously occurring co-

Table 1  Biochemical analysis of respiratory chain complexes I, II+III, and IV, and PDHC in muscle tissue

<table>
<thead>
<tr>
<th>Activity (mU/U CS)</th>
<th>Patient</th>
<th>Control range</th>
</tr>
</thead>
<tbody>
<tr>
<td>PDHC</td>
<td>9.3</td>
<td>20–53</td>
</tr>
<tr>
<td>NADH-QO1 oxidoreductase (CI)</td>
<td>60</td>
<td>170–560</td>
</tr>
<tr>
<td>Succinate-cyt C oxidoreductase</td>
<td>70</td>
<td>80–450</td>
</tr>
<tr>
<td>(CII+III)</td>
<td>1370</td>
<td>900–4700</td>
</tr>
<tr>
<td>Cytochrome C oxidase (CIV)</td>
<td>1370</td>
<td>900–4700</td>
</tr>
<tr>
<td>Citrate synthase</td>
<td>75.0</td>
<td>45–105*</td>
</tr>
</tbody>
</table>

*Citrate synthase (CS) in U/g NCP.

(DMEM, GIBCO BRL), supplemented with 10% fetal bovine serum (FBS, GIBCO BRL), with and without 3 μmol/l thiamine as previously described and incubated for at least 14 days.

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We performed genotyping of the affected girl, her healthy sibs, and their parents. Sequences obtained from the family members were compared with the SLC19A2 sequence and with normal control chromosomes. Analysis of the complete SLC19A2 gene in the index patient showed a novel homozygous G to A termination mutation at position 1074 in exon 4, predicting a premature truncation of the protein at codon 358. The parents (I.1 and I.2) and two brothers (II.1 and II.3) were hetero-
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Y

Factor of four important enzymes (TK, PDHC, KGDH, and BCKD) of carbohydrate metabol-
ism. Studies on human intestinal and erythro-

cyte thiamine absorption suggest that two uptake pathways exist, transport by a high affinity, low capacity carrier and passive intake by a low affinity/high capacity system. Functional characterisation of the SLC19A2 protein indicates that it is a high affinity, saturable transporter showing an amino acid identity of 55% with the reduced folate transporter RFC1 and the major part of thiamine is presumably absorbed via this pathway. Labeling studies using H-thiamine indicate that TRMA fibroblasts take up only 5-10% of wild type amounts.

Correspondingly, thiamine responsive diseases may be classified as acquired diseases because of thiamine deficiency, inherited diseases because of defects of thiamine transport, and inherited diseases because of defects of thiamine dependent enzymes (table 2). Beri-
beri (Indonesian for sheep, because of the characteristic gait of the patients) is a sensori-
motor neuropathy still endemic in Asia result-
ning from the low thiamine content of polished rice. The most common cause for thiamine deficiency in Europe and North America is chronic alcoholism with malnutrition, less common are anorexia nervosa, parenteral nutrition, or chronic intestinal diseases. While alcoholic neuropathy is caused by the deficiency of several vitamins, Wernicke’s enceph-

apathy and Korsakow’s syndrome are mainly the result of thiamine deficiency alone, thus responding well to thiamine therapy. Leigh disease (sub-
acute necrotising encephalomyelopathy) re-
sembles Wernicke’s encephalopathy clinically, radiologically, and pathologically. The patho-
biochemical link to thiamine metabolism is that about 15-20% of Leigh cases are caused by PDHC deficiency leading to decreased mito-
chondrial energy production. There may be several other clinical presentations of PDHC

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Table 2  Thiamine responsive diseases

<table>
<thead>
<tr>
<th>Pathogenesis</th>
<th>Neurological symptoms</th>
<th>Other symptoms</th>
</tr>
</thead>
<tbody>
<tr>
<td>Acquired diseases resulting from thiamine deficiency</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Beriberi</td>
<td>Endemic in Asia, owing to the low thiamine content of polished rice</td>
<td>Sensorimotor neuropathy, hypacusis, optic neuritis, cranial nerve lesions</td>
</tr>
<tr>
<td>Neuropathy</td>
<td>Chronic alcoholism with malnutrition, anorexia nervosa, parenteral nutrition, intestinal diseases</td>
<td>Eye muscle and gaze paresis, nystagmus, papillary dysfunction, vegetative dysregulation, seizures, confusion, apathy, coma</td>
</tr>
<tr>
<td>Wernicke’s encephalopathy</td>
<td>Chronic alcoholism with malnutrition, anorexia nervosa, parenteral nutrition, intestinal diseases</td>
<td>Loss of short term and long term memory</td>
</tr>
<tr>
<td>Korsakow’s syndrome</td>
<td>Chronic alcoholism with malnutrition, anorexia nervosa, parenteral nutrition, intestinal diseases</td>
<td></td>
</tr>
</tbody>
</table>

Inherited diseases resulting from defects of thiamine transport

<table>
<thead>
<tr>
<th>Pathogenesis</th>
<th>Neurological symptoms</th>
<th>Other symptoms</th>
</tr>
</thead>
<tbody>
<tr>
<td>TRMA</td>
<td>Autosomal recessive; mutations in the thiamine transporter gene</td>
<td>Megaloblastic anaemia, diabetes and deafness, abnormalities of the retina and the optic nerve, stroke-like episodes</td>
</tr>
</tbody>
</table>

Inherited diseases resulting from defects of thiamine dependent enzymes

<table>
<thead>
<tr>
<th>Pathogenesis</th>
<th>Neurological symptoms</th>
<th>Other symptoms</th>
</tr>
</thead>
<tbody>
<tr>
<td>Leigh syndrome (subgroup)</td>
<td>Mutations in PDHC genes</td>
<td>Ophthalmoplegia, nystagmus, ataxia, dystonia, optic atrophy, seizures, myoclonus, neuropathy, psychomotor retardation</td>
</tr>
<tr>
<td>Maple syrup urine disease (subgroup)</td>
<td>Mutations in BCKD genes</td>
<td>Acute episodes with vomiting, lethargy or coma, seizures, mental and physical retardation</td>
</tr>
<tr>
<td>KGDH deficiency</td>
<td>Mutations in KGDH genes</td>
<td>Hypotonia and neurological deterioration, death in childhood</td>
</tr>
<tr>
<td>Predisposition to Wernicke’s encephalopathy</td>
<td>Mutations in TK genes</td>
<td></td>
</tr>
</tbody>
</table>

PDHC = pyruvate dehydrogenase complex.
BCKD = branched chain alpha ketoacid dehydrogenase.
KGDH = ketoglutarate dehydrogenase.
TK = transketolase.

Deficiency as well.\(^{22}\) Mutations in BCKD are associated with a thiamine responsive variant of maple syrup urine disease (MUSD),\(^{23}\) while mutations in the tricarboxylic acid cycle enzyme KGDH lead to an early fatal neurodevelopmental disease, KGDH deficiency.\(^{22}\) TK mutations, finally, may cause a genetic predisposition to the development of Wernicke’s and Korsakow’s syndrome.\(^{24}\)

In TRMA, congenital heart disease, arrhythmias, abnormalities of the retina and the optic nerve, aminoaciduria, situs inversus, and stroke-like episodes have been described in single cases in addition to megaloblastic anaemia, diabetes, and deafness. The patient presented here suffers from the typical triad and additional findings were retinal degeneration, short stature, incomplete right bundle branch block of the heart, and splenomegaly. Thus, we have expanded the clinical spectrum of TRMA by the symptoms short stature and splenomegaly. Moreover, brain MRI at 12 years of age showed a left parietal cortical lesion without clinical correlate. There is one published report of a cerebral infarction in TRMA.\(^{25}\) In our patient, the lesion may represent a metabolic decompensation of the energy dependent cortex, as is seen in MELAS syndrome.\(^{26}\)

Combining our data with results from other reports,\(^{8-11}\) eight loss of function mutations and one missense mutation have now been described in the coding region of SLC19A12 (fig 1). The nonsense mutation at position 1074 in our patient leads to a premature truncation of the protein at codon 358 in the predicted transmembrane domain 7. Thus, we can conclude that among the small number of patients examined there is no clustering of mutations.

Biochemically, we found not only the expected PDHC deficiency, but also a hitherto unreported severe complex I deficiency. Complex I of the mitochondrial respiratory chain is well known to catalyse the transfer of electrons from NADH to ubiquinone and couples this reaction to proton translocation across the inner mitochondrial membrane.\(^{27}\) The mechanism of the deficiency in TRMA is obscure. In humans, neither thiamine related proteins nor thiamine itself are known to be associated with the function of complex I. The only known cofactors of complex I are FMN, Fe/S clusters, and NADPH.\(^{28}\) A pleiotropic effect resulting from deficiencies of PDHC and KGDH is also unlikely, since complex I was measured by addition of NADH. In the yeast Saccharomyces cerevisiae, 11 thiamine diphosphate dependent enzymes are known and none of them is related to the respiratory chain.\(^{29}\) However, if Pda1p, a subunit of PDHC, is knocked out in yeast, respiratory deficient mutations are generated at high frequency. The reason for the instability of the mitochondrial genome in these mutants is not understood.\(^{30}\) Frequent mtDNA mutations have been excluded in our TRMA patient as the cause for complex I deficiency. Moreover, a secondary mtDNA mutation is unlikely in view of normalisation of complex I activity after thiamine supplementation. However, we cannot exclude a second nuclear mutation affecting complex I in this single consanguineous patient with TRMA syndrome. One other report of respiratory chain activities in two independent TRMA patients showed normal activities, but thiamine was discontinued only one week before biopsy.\(^{31}\)

In general, combined defects of the mitochondrial enzymes PDHC and complexes of the respiratory chain have been found in 5-10% of patients with impaired mitochondrial energy production in muscle tissue when examined systematically.\(^{11}\) The molecular basis is not clear. Disturbed import or misassembly
of cytosolic synthesised mitochondrial proteins could be excluded by immunoblotting. From a theoretical point of view, respiratory chain defects may lead to decreased activity of PDHC via increased levels of citric acid cycle substrates and acetyl-CoA, while there is no evidence that PDHC mutations can cause respiratory chain defects.

The importance of thiamine to the activity of complex I or associated proteins involved in function or assembly of the respiratory chain has not been reported previously. In addition to deficiencies of thiamine dependent mitochondrial enzymes, a defect of complex I of the respiratory chain would further impair mitochondrial energy production. The main symptoms of TRMA, sideroblastic anemia, diabetes, and deafness, as well as many of the additional symptoms described here and by others, are frequently found in diseases with respiratory chain deficiency. It cannot be decided phenomenologically if they result from the PDHC defect, the complex I defect, or another consequence of the TRMA mutations. To address these questions, respiratory chain activities should be determined in other TRMA patients and correlations between genotype, biochemistry, and phenotype should be established.

We thank the patient and her family for their participation in this study. We thank Professor D Pongratz and Prof Dr W Müllner-Felber for morphological examination of patient muscle biopsies. The excellent technical assistance of K Schulte is also greatly appreciated. This work was supported by the German Federal Ministry for Education, Research and Technology (BMBF01KW90/05) and by the Deutsche Forschungsgemeinschaft (Ja 8021/2-1).