A specific mutation in \textit{TBL1XR1} causes Pierpont syndrome

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ABSTRACT

Background The combination of developmental delay, facial characteristics, hearing loss and abnormal fat distribution in the distal limbs is known as Pierpont syndrome. The aim of the present study was to detect and study the cause of Pierpont syndrome.

Methods We used whole-exome sequencing to analyse four unrelated individuals with Pierpont syndrome, and Sanger sequencing in two other unrelated affected individuals. Expression of mRNA of the wild-type candidate gene was analysed in human postmortem brain specimens, adipose tissue, muscle and liver. Expression of RNA in lymphocytes in patients and controls was additionally analysed. The variant protein was expressed in, and purified from, HEK293 cells to assess its effect on protein folding and function.

Results We identified a single heterozygous missense variant, c.1337A>C (p.Tyr446Cys), in transducin \(\beta\)-like 1 X-linked receptor 1 (\textit{TBL1XR}) as disease-causing in all patients. \textit{TBL1XR1} mRNA expression was demonstrated in pituitary, hypothalamus, white and brown adipose tissue, muscle and liver. mRNA expression is lower in lymphocytes of two patients compared with the four controls. The mutant \textit{TBL1XR1} protein assembled correctly into the nuclear receptor corepressor (NCoR)/silencing mediator for retinoid and thyroid receptors (SMRT) complex, suggesting a dominant-negative mechanism. This contrasts with loss-of-function germline \textit{TBL1XR1} deletions and other \textit{TBL1XR1} mutations that have been implicated in autism. However, autism is not present in individuals with Pierpont syndrome.

Conclusions This study identifies a specific \textit{TBL1XR1} mutation as the cause of Pierpont syndrome. Deletions and other mutations in \textit{TBL1XR1} could cause autism. The marked differences between Pierpont patients with the p.Tyr446Cys mutation and individuals with other mutations and whole gene deletions indicate a specific, but as yet unknown, disease mechanism of the \textit{TBL1XR1} p.Tyr446Cys mutation.

INTRODUCTION

In 1998 Pierpont and coworkers described two unrelated boys with remarkably similar faces (high forehead, underdeveloped mid-face, narrow palpebral fssures and anteverted nares), short stature, hearing loss, developmental delay and distinctive palmar and plantar fat pads. Two similar patients were subsequently reported, including one with a choroid plexus papilloma, whereupon the condition was named Pierpont syndrome. While several patients resembling Pierpont syndrome have been reported, clinical re-evaluation and molecular analyses have shown that they had either Coffin–Siris or Wiedemann–Steiner syndrome (H. Brunner, personal communication 2013). Initially this caused uncertainty about the phenotype defining Pierpont syndrome, but the characteristics of both Wiedemann–Steiner syndrome and Coffin–Sirs syndrome are better known nowadays and allow easy differentiation from the phenotype in the reported patients with Pierpont syndrome. Until now, the cause of Pierpont syndrome has remained unknown. However, de novo autosomal-dominant mutations were suspected to be the most likely cause.

For the present study, we collected DNA from two newly identified and four earlier-reported patients with Pierpont syndrome. We performed whole-exome sequencing in four patients and in the parents of one of them, and identified identical de novo missense mutations in the transducin \(\beta\)-like 1 X-linked receptor 1 (\textit{TBL1XR1}) gene in all four patients. Sanger sequencing of the two newly diagnosed patients revealed the same mutation. \textit{TBL1XR1} is part of the nuclear receptor corepressor (NCoR) complex that plays an essential role in gene transcription.

METHODS

Study cohort

The study cohort consisted of six unrelated patients with Pierpont syndrome (table 1). The clinical diagnosis was based on the combination of the facial characteristics, palmar and plantar fat pads, and global developmental delay (figure 1). The description of patients 1–4 has been published. Blood samples were obtained from all patients and their (unaffected) parents. Informed consent for the study was obtained from the parents of all patients. The Medical Ethics Committee of the Academic Medical Centre in Amsterdam (NL45117.018.13) approved the study.

Molecular analysis

Targeted enrichment and massive parallel sequencing were performed on genomic DNA extracted from circulating leucocytes of four patients and the
parents of one of them. Enrichment of the whole exome was performed using the Nimblegen SeqCap EZ Library V3.0 (Roche). Each captured library was then loaded on a SOLiD5500xl platform (Applied Biosystems) (patient 20112226, 20121069 and 20121072). Paired-end and single-end sequence reads were aligned to hg19 using the Lifescope aligner (V2.5.1) (Applied Biosystems). Presumed PCR duplicates were discarded using Picard Tools (http://picard.sourceforge.net) and dbSNP (V.137), and predictions were made regarding probabilities of being disease causing. Only variants passing all applied GATK filters, predicted to be a de novo mutation within the trio and disease-causing by KGGSeq were retained.

### Protein characterisation

The structure of the WD40 domain of TBL1XR1 was obtained from the Protein Data Bank (PDB accession code 4LG9). For expression in mammalian cells, constructs of TBL1XR1, HDAC3 and GPS2-SMRT chimaera were cloned into the pcDNA3 vector. Transient transfections and protein purifications were performed as described elsewhere. For the TBL1XR1/HDAC3/GPS2-SMRT chimaera complex, the GPS2-SMRT chimaera contained an N-terminal 10×His-3×Flag tag and a tobacco etch virus (TEV) protease cleavage site. HEK293F cells (Invitrogen) were cotransfected with mixtures of both tagged and untagged constructs using polyethylenimine (PEI) (Sigma). To transfect 60 mL of cells, 60 μg DNA total was diluted in 6 mL of phosphate-buffered saline (PBS) (Sigma) and 100 μL of 0.5 mg/mL PEI was added, then vortexed briefly, 240 μL of 0.5 mg/mL PEI was added, then vortexed briefly, and incubated for 20 min at room temperature, then added to 60 mL cells (final density 1×10^6 cells/mL). Cells were harvested 48 h after transfection. For the interaction studies the cells were lysed by sonication in 50 mM TrisCl pH 7.5, 100 mM potassium acetate, 5% v/v glycerol, 0.3% v/v
Triton X-100 and Roche complete protease inhibitor (buffer A); insoluble material was removed by centrifugation. The complex was bound to Flag resin (Sigma), washed three times with buffer A, three times with buffer B (50 mM Tris/Cl pH 7.5, 300 mM potassium acetate, 5% v/v glycerol) and three times with buffer C (50 mM Tris/Cl pH 7.5, 50 mM potassium acetate, 5% v/v glycerol, 0.5 mM tris (carboxyethyl) phosphine (TCEP)). The complex was eluted from the resin by overnight cleavage at 4°C with TEV protease in buffer C.

mRNA expression
We analysed TBL1XR1 mRNA expression in brain tissue (hypothalamus; pituitary gland), in white and brown adipose tissue, in muscle tissue and in liver tissue. In addition we analysed TBL1XR1 RNA expression in lymphocytes of two patients (aged 13 and 20 years, respectively) and four controls (age between 25 and 30 years).

Tissues
Three hypothalami and pituitaries were obtained from the Netherlands Brain Bank in accordance with permission for brain autopsy and the use of human brain material and clinical information for research purposes. Three unfixed, frozen (−80°C) hypothalami–pituitary specimens were used for mRNA expression. The paraventricular nucleus (PVN) region was cut in serial, coronal 50 μm sections from unfixed frozen hypothalami on a
cryostat and the PVN area macroscopically dissected, collected, and stored at −80°C until processing, as previously reported.10 RNA was extracted from the PVN and from homogenised pituitaries using TriReagent (Sigma) per manufacturer’s instructions, followed by DNase treatment (Qiagen GmbH, Germany). cDNA was synthesised with an Applied Biosystem Kit. White adipose tissue cDNA was kindly provided by Drs M Serlie and M Kilicarslan (Department of Endocrinology, AMC, Amsterdam) and synthesised from RNA isolated from subcutaneous, periumbilical adipose tissue biopsies from healthy lean men under local anaesthesia (approved by the Medical Ethics Committee of the Academic Medical Centre in Amsterdam). Liver tissue cDNA was kindly provided by Drs M Serlie and P Gilijamse (Department of Endocrinology, AMC, Amsterdam) and synthesised from RNA isolated from liver tissue biopsies obtained during gastric bypass surgery (approved by the Medical Ethics Committee of the Academic Medical Centre in Amsterdam). RNA was isolated using TRIzol reagent (Invitrogen, Breda, the Netherlands) followed by the NucleoSpin RNA extraction kit (Macherey & Nagel GmbH, Duren) and DNase treatment (Ambion, Carlsbad, California, USA). cDNA was synthesised using Transcriptor First Strand cDNA Synthesis Kit (Roche) according to the manufacturer’s instructions. Brown adipose tissue biopsies were taken during thyroid surgery (approved by the Medical Ethics Committee of the University Medical Centre Maastricht) and the samples were kindly provided by Drs E Nascimento, E Broeders, N Bouvy, P Schrauwen and W van Marken Lichtenbelt (Maastricht University). RNA was isolated on the Magna Pure (Roche Molecular Biochemicals, Mannheim, Germany) using the Magna Pure LC mRNA tissue kit. The protocol and buffers supplied with the corresponding kit were applied. cDNA synthesis was performed using the Transcriptor cDNA Synthesis Kit for RT-PCR with oligo d(T) primers (Roche Molecular Biochemicals, Mannheim, Germany). Muscle cDNA was commercially available and obtained from Clontech, Takara (Mountain View, California, USA). RNA from whole blood of four healthy controls and two patients was isolated using the High Pure RNA Isolation Kit (Roche Molecular Biochemicals, Mannheim, Germany) according to the manufacturer’s protocol. cDNA synthesis was performed using the Transcriptor cDNA Synthesis Kit for RT-PCR with oligo d(T) primers (Roche Molecular Biochemicals, Mannheim, Germany). From every sample a –RT reaction was performed in order to check for genomic DNA contamination.

Figure 2 (A) Surface representation of the transducin β-like 1 X-linked receptor 1 (TBL1XR1) WD40 domain (PDB ID 4LG9), the mutated residue (Y446) is shown in cyan. (B) Comparison of Y446 in human TBL1XR1 (cyan) and f446 in yeast (purple). (C) Representation of the TBL1XR1/HDAC3/GPS2-SMRT chimaera complex. (D) Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS–PAGE) of the purification of the wild-type and mutant TBL1XR1/HDAC3/GPS2-SMRT chimaera complex.
wise had no signiﬁcant health problems. Devel-
oped pectus excavatum and thoracic scoliosis, but other-
body weight and little subcutaneous fat tissue. She gradually
decrease in height, a relatively large head, low
was estimated to be below 35 at age 18 years. She had increas-
control. Formal cognitive testing was not possible, but her IQ
to develop any speech and had no sphincter
diagnosed with bilateral talipes. Her development was markedly delayed from
early on: she never developed any speech and had no sphincter
problems were noticed at the age of 11 years. Both her unusual face and
and the abnormal creases of palms and soles were evident at birth.
She has always had mild fat pads anteromedial to both heels.

Patient 6 was the ﬁrst-born child of healthy, non-
consanguineous parents. She was remarkably hypotonic at birth.
At that time it was noticed that she had unusual facial morphology, broad thumbs, deep pillowing of palms and soles, and
bilateral talipes. Her development was markedly delayed from
early on: she never developed any speech and had no sphincter
formal cognitive testing was not possible, but her IQ
was estimated to be below 35 at age 18 years. She had in-
decreased growth in height, a relatively large head, low
body weight and little subcutaneous fat tissue. She gradually
developed pectus excavatum and thoracic scoliosis, but oth-
erwise had no signiﬁcant health problems.

Molecular analysis

Whole-exome sequencing yielded a single missense mutation
c.1337A>C in TBL1XR1 located at 3q26.32, resulting in the
amino acid substitution p.Tyr446Cys (Y446C) in all four
patients studied, but not in the parents of one of them (see
online supplementary table S1). No other potentially pathogenic
variant in the same gene was present in all four patients. Sanger
sequencing demonstrated the same mutation in the two other
patients. All other parents tested negative for the mutation using
Sanger sequencing, indicating de novo occurrence. The mutation
was at an evolutionary conserved position (ﬁgure 2A) and
absent in control populations (dbSNP 1000 genomes, NHBLI,
ESR, GoNL).

Stability of mutated complexes

TBL1XR1 is a highly conserved protein found in all eukaryotes
(see online supplementary ﬁgure S1). It contains two structured
domains: an amino-terminal domain that mediates tetramerisation
of the protein and a carboxy-terminal WD40 domain.

Figure 3 (A) Transducin β-like 1 X-linked receptor 1 (TBL1XR1) mRNA expression in human pituitary and hypothalamic PVN. (B) TBL1XR1 mRNA expression in human white and brown adipose tissue, liver and muscle tissue. TBL1XR1 transcript PCR product on 2% agarose gel. The expected product is 126 bp. BAT, brown adipose tissue; PIT, pituitary; PVN, paraventricular nucleus; WAT, white adipose tissue.

RESULTS

Study cohort

Patient 5 was the term, ﬁrst-born child of healthy, non-
consanguineous parents. She had intrauterine growth retard-
ation, was hypotonic at birth, and had bilateral hip dislocations.
She experienced feeding difﬁculties with gastrostomy placement
in infancy, and followed a markedly delayed motor and cogni-
tive development. She was able to walk with assistance, and had
no speech. Formal cognitive testing at age 7 years showed her
IQ to be 45. Hearing loss was detected in the ﬁrst year of life.
She gradually developed a progressive thoracolumbar scoliosis
requiring rod placement at age 10 years. Her postnatal growth
in height and of skull circumference was decreased. Onset of
menstrual cycles was at the age of 11 years. Both her unusual face and
the abnormal creases of palms and soles were evident at birth.

Patient 6 was the ﬁrst-born child of healthy, non-
consanguineous parents. She was remarkably hypotonic at birth.
At that time it was noticed that she had unusual facial morphology, broad thumbs, deep pillowing of palms and soles, and
bilateral talipes. Her development was markedly delayed from
early on: she never developed any speech and had no sphincter
control. Formal cognitive testing was not possible, but her IQ
was estimated to be below 35 at age 18 years. She had in-
decreasingly decreased growth in height, a relatively large head, low
body weight and little subcutaneous fat tissue. She gradually
developed pectus excavatum and thoracic scoliosis, but oth-
erwise had no signiﬁcant health problems.

The TBL1XR1 tyrosine-to-cysteine mutation identiﬁed here is
located in the WD40 domain on one side of the inner surface of
the WD40 ring (ﬁgure 2A). Y446 is largely exposed to solvent,
and mutation to cysteine would not be expected to signiﬁcantly
perturb the structure of the domain. A tyrosine in this position is
found in nearly all TBL1XR1 proteins, although the equivalent
residue is a phenylalanine in the homologous Sif2 protein from
Saccharomyces cerevisiae. The structure of the WD40 domain
from Sif2 has also been reported.12 Despite relatively low
sequence identity between TBL1XR1 and Sif2, the structures
of their WD40 rings itself are similar. Furthermore, the yeast
residue equivalent to Y446, f446, adopts a very similar conforma-
tion (ﬁgure 2B) suggesting a conserved function for this largely
non-polar amino acid. To conﬁrm that the Y446C mutation does
not grossly perturb the fold and behaviour of TBL1XR1 we
examined the ability of the TBL1XR1 to assemble correctly with
the GPS2:SMRT:HDAC3 complex. As predicted, the mutant
protein was readily expressed and puriﬁed and assembled cor-
rectly into the TBL1XR1:GPS2:SMRT:HDAC3 complex (ﬁgure
2C and D), suggesting that the molecular pathology of the
Y446C mutation is an impaired protein–protein interaction with
an as yet unidentified molecular partner rather than a failure to
fold correctly.

mRNA expression

TBL1XR1 mRNA expression was well visible in the pituitary
and the PVN area of the hypothalamus, as well as in liver and
muscle tissue and both white and brown adipose tissue, ﬁtting
the clinical symptomatology of Pierpont syndrome (ﬁgure 3A, B).

Figure 4 Relative expression of transducin β-like 1 X-linked receptor 1 (TBL1XR1) mRNA to hypoxanthine phosphoribosyl transferase (used as reference gene) in leucocytes of patients (closed circles) and controls (open circles). Individual values are depicted and mean values ±SD is represented by a solid line.
TBL1XR1 mRNA expression in whole blood was lower in patients compared with controls (figure 4). The small number of patients available for analysis precludes statistical analysis to determine whether this difference is significant.

DISCUSSION

In this study, we found a single TBL1XR1 missense mutation in six patients with Pierpont syndrome that was absent in their unaffected parents.

TBL1XR1, a member of the WD40 repeat-containing protein family, is composed of 18 exons.13 The product of TBL1XR1, TBL1XR1 (or TBLR1; 55 593 Da; 514 amino acids), contains a carboxy-terminal WD40 domain containing eight WD40 repeats and an amino-terminal LisH domain that mediates tetramerisation of the protein and its interactions with NCoR/SMRT and GPS2.13 14 TBL1XR1 is an essential component of the NCoR/SMRT corepressor complex (figure 2C), which interacts with nuclear hormone receptors, a family of ligand-dependent transcription factors involved in regulation of gene transcription (figure 5).15 When bound to unliganded nuclear hormone receptors, corepressors mediate silencing of gene transcription by recruiting chromatin-modifying enzymes. When a nuclear hormone receptor is liganded, corepressors dissociate to relieve repression of transcription. In negatively regulated target genes, corepressors are essential for activation of transcription.16 The WD40 repeats in TBL1XR1 are thought to be involved in the interaction of the corepressor complex with histones stabilising the association of the complex with the chromatin.13 17 TBL1XR1 also may play a regulatory role in the NF-κB pathway and Wnt-mediated transcription. NF-κB transcription requires IKKα to phosphorylate SMRT on chromatin, which recruits TBL1XR1 to the gene promoter. During depletion of TBL1XR1, NF-κB transcription and cell survival are compromised.17 18 TBL1XR1 also recruits β-catenin to the Wnt target-gene promoter. In the presence of TBL1XR1, β-catenin is able to remove corepressors from the promoter of Wnt target genes by competitive binding, thereby activating transcription.19

TBL1XR1 mutations have been implicated in several phenotypes. Recurrent TBL1XR1 mutations have been described in DNA of lymphatic malignancies, including primary central nervous system lymphomas,20 21 acute lymphoblastic leukaemia22 and Sézary syndrome.23 The precise mechanisms by which TBL1XR1 mutations contribute to tumourigenesis remain unclear, but it has been hypothesised that loss of TBL1XR1 could compromise the ability of corepressor complexes to inhibit receptor activity, leading to increased activation of receptor target genes.22 In addition, it has been suggested that TBL1XR1 might act as a tumour-suppressor gene in the lymphatic system,21 and upregulates VEGF-C inducing lymphangiogenesis in oesophageal squamous cell carcinoma.24 Contrarily, TBL1XR1 has been nominated as a novel breast cancer oncogene,25 indicating that any role of TBL1XR1 in tumourigenesis is tissue-specific.

Whole-exome sequencing of 209 children with autism spectrum disorder (ASD) and their parents showed a de novo p.Leu282Pro mutation in TBL1XR1 in one child, who also had intellectual disability.26 Subsequently, evaluation of 44 candidate genes in 2494 ASD cases identified two de novo TBL1XR1 mutations (p.Leu282Pro, p.Ile397SerfsX19).27 Apart from intellectual disability, however, these patients had no features in common with Pierpont syndrome (B O’Roak and E Eichler, personal communication 2013). Similarly, a non-dysmorphic patient with intellectual disability, autism and West syndrome was found to have a de novo p.Gly70Asp mutation in TBL1XR1.28 Three patients, including a mother and child, have been described with a deletion involving only TBL1XR1 in patients who had mild to moderate intellectual disability without autistic behaviour or manifestations of Pierpont syndrome.29 30 In addition, three cases with small deletions involving TBL1XR1 and other genes are included in the Decipher database (http://decipher.sanger.ac.uk/). All had intellectual disability, ASD or ASD-like behaviour but lacked physical signs of
Pierpont syndrome (Z Stark, M Decamp, B Dallapiccola, personal communications, 2014). In one additional published patient the phenotype was attributed to a 2.2 Mb deletion at 3q26.3 involving TBL1XR1, but an updated annotation showed that the deletion did not encompass TBL1XR1. This suggests that the phenotype of individuals with a microdeletion 3q26.3 is caused by a loss of function of TBL1XR1, and consists of intellectual disability and frequently ASD, and a phenotype that shows no resemblance to Pierpont syndrome. It remains at present uncertain whether the abundant hypothalamic and pituitary mRNA expression of wild-type TBL1XR1 reported here is related to the intellectual disability in individuals with deletions.

The differences in phenotype in subjects with the Y446C mutation compared with subjects with whole-gene deletions or other TBL1XR1 mutations suggest different pathogenic mechanisms. The Y446C mutation could act in a dominant negative way, in agreement with our finding that the mutant TBL1XR1 Y446C protein is able to assemble into the HDAC3 corepressor complex. Since TBL1XR1 Y446C can form hetero-tetramers with wild-type TBL1XR1, TBL1XR1 Y446C will likely be present in most HDAC3 corepressor complexes, and the impaired or inappropriate protein–protein interactions with an as yet unidentified molecular partner will likely be present ubiquitously.

In conclusion, one specific TBL1XR1 missense mutation is responsible for the phenotype in individuals with Pierpont syndrome. The difference in phenotype between non-ASD Pierpont patients with the Y446C mutation in TBL1XR1 and individuals with a complete deletion or other mutation of TBL1XR1 suggests mutation-specific mechanisms of pathogenesis for ASD. Further studies of the pathogenesis in individuals with deletions and mutations in TBL1XR1 could yield useful insights into the pathogenesis of ASD.

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Contributors CAH and RCH collected and analysed data, and wrote the manuscript. AJ, BR and RCH performed exome sequencing data validation and mutation analysis. PJW, AB, OB-S and JWR performed functional studies. FF, RH, RK, AHO, MEP, GB5, FS, ASPv1 and EF collected patient samples and analysed data. RCH conceived the project and supervised the experiments. All authors revised the manuscript critically and approved the final version for publication.

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REFERENCES


Correction
