POMT2 mutations cause α-dystroglycan hypoglycosylation and Walker-Warburg syndrome

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Background: Walker-Warburg syndrome (WWS) is an autosomal recessive condition characterised by congenital muscular dystrophy, structural brain defects, and eye malformations. Typical brain abnormalities are hydrocephalus, lissencephaly, agenesis of the corpus callosum, fusion of the hemispheres, cerebellar hypoplasia, and neuronal overmigration, which causes a cobblestone cortex. Ocular abnormalities include cataract, microphthalmia, buphthalmos, and Peters anomaly. WWS patients show defective O-glycosylation of α-dystroglycan (α-DG), which plays a key role in bridging the cytoskeleton of muscle and CNS cells with extracellular matrix proteins, important for muscle integrity and neuronal migration. In 20% of the WWS patients, hypoglycosylation results from mutations in either the protein O-mannosyltransferase 1 (POMT1), fukutin, or fukutin related protein (FKRP) genes. The other genes for this highly heterogeneous disorder remain to be identified.

Objective: To look for mutations in POMT2 as a cause of WWS, as both POMT1 and POMT2 are required to achieve protein O-mannosyltransferase activity.

Methods: A candidate gene approach combined with homozygosity mapping.

Results: Homozygosity was found for the POMT2 locus at 14q24.3 in four of 11 consanguineous WWS families. Homozygous POMT2 mutations were present in two of these families as well as in one patient from another cohort of six WWS families. Immunohistochemistry in muscle showed severely reduced levels of glycosylated α-DG, which is consistent with the postulated role for POMT2 in the O-mannosylation pathway.

Conclusions: A fourth causative gene for WWS was uncovered. These genes account for approximately one third of the WWS cases. Several more genes are anticipated, which are likely to play a role in glycosylation of α-DG.

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Walker-Warburg syndrome (WWS) is a congenital disorder characterised by multiple anomalies of the brain, muscle, and eye. This combination of malformations is also found in muscle-eye-brain disease (MEB) and in Fukuyama congenital muscular dystrophy (FCMD). The most severe anomalies are seen in WWS patients, especially with regard to the brain malformations. Brain malformations typical of WWS are agyria, agenesis of the corpus callosum, cerebellar vermis and septum, and occasional occipital encephalocele. The pathogenesis underlying WWS, MEB, FCMD, and other congenital muscular dystrophies (CMD) such as congenital muscular dystrophy 1C (MDC1C) and 1D (MDC1D) involves functional disruption of α-dystroglycan (α-DG) by mutations in genes that are involved in O-mannosylation of this protein. The O-linked carbohydrate chains of α-DG are an important component of the dystrophin glycoprotein complex which mediates the interaction between the extracellular matrix and the cytoskeleton of muscle cells and neurons. A common O-mannosyl glycan structure found on α-DG is NeuAcα2-3Galβ1-4GlcNAcβ1-2Man-Ser/Thr. The first step in the synthesis of this glycan structure takes place in the endoplasmic reticulum by one or more proteins from a family of well conserved protein O-mannosyltransferases (PMTs). These proteins catalyse the transfer of a mannose from dolichyl phosphate activated mannose to serine or threonine residues of secretory proteins. In yeast, a family of seven PMTs (Pmt1p to Pmt7p) are known. Double and triple mutants of the PMTs in yeast indicate that proper O-mannosylation is required for its cell wall rigidity and cell integrity. In Drosophila and human there are only two orthologues: POMT1 and POMT2. RNAi knockdown of either POMT1 or POMT2 in Drosophila causes a rotation of the abdomen by 30–60°, demonstrating the requirement of both POMT1 and POMT2 for normal muscle development in the fly. No embryonic nervous system or eye abnormalities were observed for POMT1 knockouts. In addition, it has been shown that in humans POMT1 and POMT2 are also both required for O-mannosyltransferase activity. Previously we have shown that mutations in either POMT1, FCMD, or FKRP result in hypoglycosylation of α-DG, giving rise to the autosomal recessive disorder WWS. The phenotypic similarity seen in the fly knockdown of POMT1 and POMT2 and the simultaneous requirement for both proteins to obtain O-mannosyltransferase in fly as well as human made us reconsider POMT2 as candidate gene for WWS. In this study we show that POMT2 mutations also cause WWS.

METHODS

Genetic analysis

Using standard methods we extracted DNA from peripheral blood lymphocytes. Genome-wide homozygosity mapping was carried out at our linkage facility using the 10 cM spaced

Abbreviations: α-DG, α-dystroglycan; CMD, congenital muscular dystrophy; FCMD, Fukuyama congenital muscular dystrophy; MEB, muscle-eye-brain disease; PMT, protein O-mannosyltransferase; WWS, Walker-Warburg syndrome
microsatellite marker set from Applied Biosystems (ABI Prism linkage mapping set version 2, Applied Biosystems, Foster City, California, USA) and at MRC geneservice in Cambridge with use of the GeneChip Mapping 10K 2.0 array from Affymetrix (Santa Clara, California, USA). Additional homozygosity mapping for POMT2 was undertaken by polymerase chain reaction (PCR) of the flanking microsatellite markers D14S279, D14S983, and D14S59, which were subsequently resolved on 8% polyacrylamide sequencing gels and developed by silver staining.

**Mutation analysis**

All 21 exons of the POMT2 gene were amplified using specific primers for the 5'- and 3'-flanking intron sequences. Primers and PCR conditions are given in table 1. After purification from agarose gels, the PCR products were used for direct sequencing using the BigDye terminator kit (Perkin Elmer Applied Biosystems, Norwalk, Connecticut, USA), which were analysed on an ABI3700 capillary sequencer. The presence of the identified mutations in the normal population was tested by restriction enzyme analysis in chromosomes from control individuals. For this, the relevant amplicon was digested with TaqI (c.1912C>T), HpyCH4 IV (c.1005+1G>A), and NciI (c.1261delC) (New England Biolabs, Beverly, Massachusetts, USA).

**Immunohistochemistry**

Muscle biopsies from control and WWS patients were obtained after informed consent of patients and approval of the ethics commission. Myoblast cell cultures were established by enzymatic and mechanical treatment of muscle biopsies and by plating in Dulbecco’s modified Eagle’s

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**Table 1** Primer sequences and conditions for PCR reaction

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medium plus fetal calf serum (FCS), penicillin, streptomycin, and amphotericin B (Sigma, Poole, Dorset, UK). Myotubes were obtained by confluent myoblast cultures allowed to differentiate for seven days in cultures medium. Samples for immunohistochemical analysis were fixed in 2% paraformaldehyde in phosphate buffer saline (PBS) and incubated overnight with an anti-α-dystroglycan monoclonal antibody (VIA4-1, Upstate Biotechnology, Lake Placid, New York, USA) diluted 1/50, washed with PBS and then with an anti-mouse IgG TRITC conjugated antibody (Dako, Glostrup, Denmark). The same sample was then incubated with a polyclonal anti-caveolin 3 antibody (Santa Cruz Biotechnology, Santa Cruz, California, USA) diluted 1/50 followed by FITC conjugated anti-goat antibody. The sample was washed in PBS, mounted in Pro-long anti-fade reagent (Molecular Probes, Eugene, Oregon, USA), and examined with a Nikon epifluorescence microscope at a magnification of ×100.

Immunohistochemistry on muscle biopsies was carried out as described by Jimenez-Mallebrera et al.26 In Brief, frozen 8 μm sections were incubated with primary monoclonal antibodies to β-DG (NCL-b-DG, Novocastra Laboratories, Newcastle upon Tyne, UK), α-DG (IIH6, Upstate Biotechnology), and sheep polyclonal antibody recognising the core protein of α-DG.27 These were than revealed with an appropriate biotinylated secondary antibody (Amersham 1:200; Amersham Life Sciences, Amersham, UK) followed incubation with streptavidin conjugated to Alexa 594 (Molecular Probes) and visualised by epifluorescence microscopy.

**RESULTS**

**Direct linkage mapping of candidate genes using genome-wide homozygosity data**

We carried out genome-wide homozygosity mapping of 12 WWS patients from 11 unrelated consanguineous families in which linkage to the known WWS loci (POMT1, Fukutin, and FKRP) has been excluded. Depending on the amount of DNA available we used the 10 cM spaced microsatellite marker set (ABI Prism linkage mapping set version 2) or the GeneChip Mapping 10K 2.0 Array (Affymetrix). As can be expected from the genetic heterogeneity of WWS, these homozygosity mapping results of mostly singletons failed to point to a single WWS locus and indeed indicated further genetic heterogeneity. Although we failed to detect POMT2 mutations in an earlier study of 24 WWS families,22 we targeted POMT2 as a candidate gene based on the premise that all three previously identified WWS genes—POMT1, Fukutin and FKRP—are involved in O-mannosyl glycan synthesis. A similar function is likely for POMT2, based on the overlapping expression profiles and homologous amino acid composition compared with POMT1. In addition, recent reports indicate that POMT2 is required for the enzymatic activity of POMT1 in human as well as *Drosophila*.19 21 Our new mapping data indicated possible linkage to the POMT2 locus in four of 11 unrelated WWS families.

**Mutation analysis of POMT2**

Mutation analysis in all four families led to the identification of mutations in two of these, a nonsense mutation (c.1912C→T, p.R638X) in patient 1 and a splice site mutation (c.1912G→A, p.R638X) in patient 2.
both found in homozygosity. Both mutations result in the disruption of a restriction site for Taq1 and HpyCH4 IV, in exon 19 and exon 8, respectively. These disruptions were not observed in control individuals digested with Taq1 (170 chromosomes) and HpyCH4 IV (290 chromosomes). No mutations were detected in the POMT2 exons in the other two families that showed linkage to the POMT2 locus. Reasons for this could be that their linkage was a fortuitous finding or that a mutation resides in parts of the POMT2 gene such as an intron or regulatory elements that have not been analysed. An additional six consanguineous WWS families were then tested for homozygosity at the POMT2 locus. In two of these WWS families the data were consistent with linkage to POMT2. In the other four families the data were inconsistent with linkage to POMT2.

**Clinical description WWS patients with POMT2 mutations**

Patient 1 is a girl born to uncle-niece consanguineous Moroccan parents. A prenatal ultrasound indicated hydrocephalus which was confirmed by magnetic resonance imaging, which also showed type II lissencephaly (fig 2, panels A and B). At birth at 37 weeks gestation, weight was 3150 grams, and head circumference 36 cm. The child was severely hypotonic. Ophthalmological examination showed bilateral Peters anomaly with cataracts, left sided microphthalmia, and right sided buphthalmos. The creatine kinase was greatly raised at 12 144 U/l. MRI of the brain documented hydrocephalus, cobblestone lissencephaly, and aplasia of the corpus callosum.

Patient 2 is a male child born to first cousin Pakistani parents. Severe hydrocephalus was diagnosed prenatally on ultrasound and the child was delivered by caesarean section. A left sided cleft lip and palate was diagnosed. Imaging of the brain by MRI revealed aplasia of the posterior vermis, hypoplasia of the pons and cerebellum, and severe hydrocephalus and cobblestone cortex (fig 2, panels C and D). Ophthalmological investigation documented bilateral cataracts and persistent pupillary membrane. The retina could not be visualised. A muscle biopsy was consistent with a diagnosis of congenital muscular dystrophy. There was increased variability of fibre diameter, increased endomysial fibrosis, and basophilic regeneration. External genitalia were normal. The child died at the age of six months.

Patient 3 is a male infant referred at the age of two months and one week because of severe neonatal hypotonia, developmental delay, and poor visual behaviour, as previously reported.

He was the third child of a consanguineous Bengali family. His older siblings were healthy. Congenital hydrocephalus required a shunt at two weeks of age. Serum creatine kinase was markedly raised. Ophthalmological examination showed bilateral lamellar cataracts, and buphthalmos caused by anterior chamber anomalies. He had no head control and no apparent response to visuo-coustical stimuli. Brain MRI at the age of five weeks showed severe hydrocephalus with a thin and smooth cortical mantle. The patient died at eight months of age during a respiratory infection.

A further sibling was diagnosed prenatally with severe hydrocephalus at 18 weeks’ gestation. This pregnancy was subsequently terminated.

**Histopathology of WWS muscle tissue**

Immunolabelling of the glycoepitope of α-DG with the VIA4-1 antibody in cultured myotubes from patient 2 showed severely reduced staining compared with control myotubes (fig 3, panels A and B). Control labelling with anti-caveolin3, a marker of muscle differentiation, showed that α-DG

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(c.1005+1G→A) in patient 2, both found in homozygosity. For Taq1 and HpyCH4 IV, in exon 19 and exon 8, respectively. These disruptions were not observed in control individuals digested with Taq1 (170 chromosomes) and HpyCH4 IV (290 chromosomes). No mutations were detected in the POMT2 exons in the other two families that showed linkage to the POMT2 locus. Reasons for this could be that their linkage was a fortuitous finding or that a mutation resides in parts of the POMT2 gene such as an intron or regulatory elements that have not been analysed. An additional six consanguineous WWS families were then tested for homozygosity at the POMT2 locus. In two of these WWS families the data were consistent with linkage to POMT2. We identified a homozygous 1 base pair (bp) deletion (c.1261delC) in one of these families. This mutation introduces a premature stop codon (p.T433X). The mutation was also homozygously present in an affected sibling and disrupts one of the two restriction sites for NciI in exon 12, which was used to verify the absence of this mutation in 140 control chromosomes from the normal population. Pedigrees and DNA sequencing results of the three POMT2 mutated families are shown in fig 1.

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co-localises with caveolin3 at the sarcolemma of myotubes derived from a control individual (fig 3C). Similar normal staining was observed in myotubes derived from patient 2 (fig 3D). Reduced staining of α-DG was also observed in patient 3 by immunolabelling of the core and glyco-epitope of α-DG (fig 4, panels D and F). Normal staining was observed for α-DG in control muscle (fig 4, panels C and E). β-DG staining was normal in the patient as well as in the control (fig 4, panels A and B). Reduction of immunolabelling of α-DG and a mild reduction of laminin-α2 in muscle tissue from patient 3 were described previously by Jimenez-Mallebrera et al.26 No muscle tissue was available for patient 1.

**DISCUSSION**

We have detected three homozygous mutations in POMT2 in three families with typical WWS. The mutations included a nonsense mutation resulting in a premature stop codon, a splice site mutation, and a 1 bp deletion leading to a premature stop codon. All mutations were homozygous in the patients (fig 1). The phenotype seen in these WWS patients is indistinguishable from that of patients with POMT1, FCMD, or FKRP mutations. One of the sibpair from family 3 who carries a homozygous 1 bp deletion mutation was described earlier, and hypoglycosylation of α-DG (fig 4) and a possible reduction of laminin-α2 in muscle tissue was documented.26 Absence of glycosylated α-DG was also seen in a muscle biopsy from patient 2 in the present study (fig 3). This is consistent with the postulated role of O-glycosylation in normal neuromuscular, brain, and eye development.11 29

Although previously no enzymatic activity of POMT1 and POMT2 was determined in vertebrates, the involvement of POMT1 in WWS, the high amino acid identity between the two paralogues, and the overlapping expression pattern was reason to hypothesise that mutations in POMT2 also give rise to WWS.26 For this reason we previously undertook mutation analysis of POMT2 in 24 unrelated patients but no causative mutations were detected.22 In this study, 17 additional families were investigated, of which six showed possible linkage to the POMT2 locus. We found POMT2 mutations in three of these (fig 1), resulting in a frequency of 7% (3 of 41 families). Thus the incidence of POMT2 mutations appears to be in the same range as that of POMT1. POMT1 mutations were previously detected at a frequency of 20% and 7% in two large samples of WWS patients.22 31 This is in accordance with the requirement of both proteins to obtain O-mannosyl-transferase activity.19 21 So far, mutations in POMT1, POMT2, fukutin, and FKRP together explain almost one third of the WWS patients in our cohort. The majority of WWS cases remain unexplained and further genetic heterogeneity is likely from our genome-wide homozygosity data.

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Competing interests: none declared

REFERENCES


