A recurrent mitochondrial p.Trp22Arg NDUFB3 variant causes a distinctive facial appearance, short stature and a mild biochemical and clinical phenotype

DOI:
10.1136/jmedgenet-2015-103576

Citation for published version (APA):

Published in:
Journal of Medical Genetics

Citing this paper
Please note that where the full-text provided on Manchester Research Explorer is the Author Accepted Manuscript or Proof version this may differ from the final Published version. If citing, it is advised that you check and use the publisher's definitive version.

General rights
Copyright and moral rights for the publications made accessible in the Research Explorer are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

Takedown policy
If you believe that this document breaches copyright please refer to the University of Manchester’s Takedown Procedures [http://man.ac.uk/04Y6Bo] or contact uml.scholarlycommunications@manchester.ac.uk providing relevant details, so we can investigate your claim.
SHORT REPORT

A recurrent mitochondrial p.Trp22Arg NDUF B3 variant causes a distinctive facial appearance, short stature and a mild biochemical and clinical phenotype

Charlotte L Alston, Caoimhe Howard, Monika Oláhová, Steven A Hardy, Langping He, Philip G Murray, Siobhan O’Sullivan, Gary Doherty, Julian P H Shield, Iain P Hargreaves, Ardeshr A Monavari, Ina Knerr, Peter McCarthy, Andrew A M Morris, David R Thorburn, Holger Prokisch, Peter E Clayton, Robert McFarland, Joanne Hughes, Ellen Crushell, Robert W Taylor

ABSTRACT

Background Isolated Complex I deficiency is the most common paediatric mitochondrial disease presentation, associated with poor prognosis and high mortality. Complex I comprises 44 structural subunits with at least 10 ancillary proteins; mutations in 29 of these have so far been associated with mitochondrial disease but there are limited genotype-phenotype correlations to guide clinicians to the correct genetic diagnosis.

Methods Patients were analysed by whole-exome sequencing, targeted capture or candidate gene sequencing. Clinical phenotyping of affected individuals was performed.

Results We identified a cohort of 10 patients from 8 families (7 families are of unrelated Irish ancestry) all of whom have short stature (<9th centile) and similar facial features including a prominent forehead, smooth philtrum and deep-set eyes associated with a recurrent homozygous c.64T>C, p.Trp22Arg NDUF B3 variant. Two sibs presented with primary short stature without obvious metabolic dysfunction. Analysis of skeletal muscle from three patients confirmed a defect in Complex I assembly.

Conclusions Our report highlights that the long-term prognosis related to the p.Trp22Arg NDUF B3 mutation can be good, even for some patients presenting in acute metabolic crisis with evidence of an isolated Complex I deficiency in muscle. Recognition of the distinctive facial features—particularly when associated with markers of mitochondrial dysfunction and/or Irish ancestry—should suggest screening for the p.Trp22Arg NDUF B3 mutation to establish a genetic diagnosis, circumventing the requirement of muscle biopsy to direct genetic investigations.

INTRODUCTION

Mitochondrial respiratory chain disease is a significant cause of human disease with a population prevalence of approximately 1 in 5000 in adults and children. Symptoms can manifest in the neonatal period but onset is often later in infancy, early childhood or even delayed to adulthood. Patients may present with disease affecting a single organ or have a multisystemic disorder typical of conditions such as Leigh syndrome. Approximately 70% of paediatric mitochondrial disease cases are caused by nuclear gene variants, while ~30% harbour defects involving mitochondrially encoded (mtDNA) genes. Conversely, mtDNA mutations more often underlie adult mitochondrial disease presentations.

Investigation of isolated Complex I deficiency is particularly amenable to an NGS-based strategy given the number of genes implicated in its pathogenesis, with 44 structural subunits and at least 10 ancillary proteins required for enzyme assembly. It is the most common paediatric mitochondrial respiratory chain deficiency and mutations have been described in at least 29 genes to date, almost all being associated with a poor clinical course and bleak prognosis. Here we report the clinical and molecular genetic investigation of 10 patients from 8 unrelated families who all harbour an identical homozygous c.64T>C, p.Trp22Arg NDUF B3 mutation, affecting a Complex I accessory subunit, previously reported in association with severe neurological presentations. Most of our patients had considerably milder presentations despite harbouring the same variant. Recognition of mild dysmorphic facial features common to our initial patients prompted screening for the p.Trp22Arg NDUF B3 variant in similar patients, leading to five further genetic diagnoses. This report demonstrates that the c.64T>C, p.Trp22Arg NDUF B3 mutation can be associated with good long-term prognosis and that recognition of a cluster of physical
Subject and methods

All patient samples were referred to the nationally commissioned ‘Highly Specialised Mitochondrial Diagnostic Laboratory’ in Newcastle upon Tyne for investigation of a putative mitochondrial defect. A clinical summary for each patient is given in table 1; detailed case reports are provided as online supplementary information. Informed parental consent was obtained.

Histochemical and biochemical analyses

Enzymatic activities of individual mitochondrial respiratory chain complexes were determined in patient muscle biopsies as previously described.11

Targeted next-generation sequencing

A custom 84.38 Kb Ampliseq panel was designed using the Ion Ampliseq Designer V2.2.1 (http://www.ampliseq.com) to target 49 genes implicated in Complex I deficiency (see online supplementary table S1). To generate the barcoded Ampliseq target library using the Ion AmpliSeq Library Kit 2.0 and Ion Xpress Barcode Adapter 1–96 Kit, 40 ng patient DNA was used. Libraries were quantified using an Agilent 2100 Bioanalyzer and pooled at 100 pM for emulsion PCR and enrichment using the Ion OneTouch2 and Enrichment system. Sequencing using the Ion PGM 200 Sequencing Kit was performed using 316 chips on an Ion PGM Sequencer, all according to the manufacturer’s protocol. Torrent Suite V4.2.1 was used to align reads against the human genome (hg19). The Variant Caller plugin was used to identify sequence variants that were annotated using wANNOVAR.12

Whole-exome sequencing

Targeted enrichment and sequencing was performed using 3 μg patient DNA. Enrichment was performed using the Illumina HiSeq SureSelect All Exon v5 Enrichment Kit, and sequencing was performed on an Illumina HiSeq 2500 sequencer, all as directed. Sequence data were mapped with BWA software to the human genome (hg19). Variants were called using GATK V2.4.7 software and annotated using Ensembl V72. Ensembl’s ‘defined consequence hierarchically’ system retained the highest impacting gene variant. Filtering removed variants with ≤5× coverage, a minor allele frequency (MAF)>1%, those predicted to be non-functional, and those reported in dbSNP138 (unless seen in a minor allele frequency (MAF)>1%, those predicted to be non-functional, and those reported in dbSNP138 (unless seen in a minor allele frequency (MAF)>1%, those predicted to be non-functional, and those reported in dbSNP138 (unless seen in a minor allele frequency (MAF)>1%, those predicted to be non-functional, and those reported in dbSNP138 (unless seen in the Human Gene Mutation Database (HGMD)) or an in-house database (n=647 exomes).

Mutation screening, confirmation and carrier testing

The c.64T>C, p.Trp22Arg NDUFB3 sequence variant was screened and confirmed using M13-tagged amplicons and Sanger sequencing with BigDye V3.1 kit (Life Technologies). Capillary electrophoresis was performed using an ABI3130xl. Familial screening for the c.64T>C, p.Trp22Arg NDUFB3 sequence variant was undertaken using parental and sibling DNA samples where available and appropriate.

Haplotype analysis

A putative founder effect was investigated by genotyping two proximal (D2S2309 and D2S2214) and two distal (D2S116 and D2S2309), short tandem repeat (STR) markers flanking the NDUFB3 gene. Corresponding PCR primers are listed on Ensembl. Mapping distance was calculated using MAP-O-MAT.13

Identification of a common underlying genetic defect

All patients in the cohort were found to harbour an identical homozygous c.64T>C, p.Trp22Arg NDUFB3 sequence variant (table 1). Each of the three patients analysed by targeted NGS harboured between 54 and 57 genomic variants which were filtered to exclude those with a MAF >1% and variants outside the coding region ±10 bp of the intron/exon boundaries. For cases identified by whole exome sequencing (WES), from the 526 candidate variants compatible with autosomal recessive inheritance only a single, homozygous variant in NDUFB3, c.64T>C, p.Trp22Arg remained after filtering. All NGS-based strategies were confirmed by conventional Sanger sequencing.

The c.64T>C (chr2(hg38):g.201078946T>C) variant is referenced on dbSNP (rs142609245) and variant frequencies are recorded on ESP6500 (European: 14/8586 alleles (0.16%);
<table>
<thead>
<tr>
<th>Patient (sex)</th>
<th>Ancestry</th>
<th>Clinical Presentation</th>
<th>Gestational age and birth weight (centile)</th>
<th>Age at latest review</th>
<th>Height at review (centile)</th>
<th>Lactate</th>
<th>Short stature</th>
<th>Prominent forehead</th>
<th>Long/thin philtrum</th>
<th>Residual CI activity*</th>
<th>Identified by</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 (M) English</td>
<td>RSV+ acute respiratory collapse and hypoglycaemia aged 8 weeks requiring intubation for 8 days. Pulmonary hypertension on echocardiogram. Maximum-recorded lactate 14 mmol/L. Discharged after 18 days. Normal cardiac function and morphology at 13 months.</td>
<td>Term &lt;0.4th</td>
<td>9.5 years</td>
<td>&lt;0.4th</td>
<td>+++</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>35%</td>
<td>Targeted NGS panel.</td>
<td></td>
</tr>
<tr>
<td>2 (F) Irish</td>
<td>IUGR. Acute life-threatening event, age 20 days, required intubation. Hypertrophic cardiomyopathy.</td>
<td>30weeks 2nd</td>
<td>6 years</td>
<td>2nd</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>33%</td>
<td>Targeted NGS panel.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3 (F) Irish</td>
<td>IUGR and oligohydramnios, FTT, mild hypertrophic cardiomyopathy.</td>
<td>34weeks 2nd–9th</td>
<td>3.5 years</td>
<td>0.4th–2nd</td>
<td>++</td>
<td>+</td>
<td>+</td>
<td>32%</td>
<td>Targeted NGS panel.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4 (F) Irish</td>
<td>Growth restriction. Ketotic hypoglycaemia following vomiting illness. Short stature prompted endocrinology referral. Growth hormone therapy. MRI: high signal in periventricular white matter and dentate nuclei.</td>
<td>39weeks 0.4th–2nd</td>
<td>8 years</td>
<td>n.d.</td>
<td>++</td>
<td>+</td>
<td>+</td>
<td>24%</td>
<td>Mutation screen.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>5 (M) Irish</td>
<td>IUGR. Poor feeding. Congenital hypothyroidism (strong paternal family history). Developmental delay, growth failure, FTT, learning difficulties. Endocrinology review for short stature.</td>
<td>37weeks 0.4th–2nd</td>
<td>10 years</td>
<td>0.4th</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>35%</td>
<td>Mutation screen.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>6 (F) Irish</td>
<td>Oligohydramnios. IUGR. Poor feeding at birth. MRI brain and echocardiogram normal. Age-appropriate skills. Family history of previous neonatal death.</td>
<td>37weeks &lt;0.4th</td>
<td>2.5 years</td>
<td>2nd–9th</td>
<td>+++</td>
<td>+</td>
<td>+</td>
<td>35%</td>
<td>Mutation screen.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>9 (F) Irish</td>
<td>Sib of P6. IUGR. Growth hormone therapy. Normal MRI brain, echocardiogram and ECG.</td>
<td>Term &lt;0.4th</td>
<td>8 years</td>
<td>2nd</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>n.d.</td>
<td>Whole-exome sequencing; endocrinology.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>10 (M) Irish</td>
<td>IUGR, chronic lung disease, growth restriction and weight faltering. Dysmorphic with partial agenesis of corpus callosum. Acute collapse with rhinovirus bronchiolitis, severe pulmonary hypertension at 5.5 months. Elevated lactates with intercurrent illnesses.</td>
<td>31weeks &lt;0.4th</td>
<td>11 months</td>
<td>&lt;0.4th</td>
<td>+++</td>
<td>+</td>
<td>+</td>
<td>36%</td>
<td>Mutation screen.</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Residual Complex I activities, normalised to the activity of the matrix marker enzyme citrate synthase, are expressed as a percentage of mean control values.
FTT, failure to thrive; IUGR, intrauterine growth restriction; N.D., not determined; NGS, next-generation sequencing; RSV, respiratory syncytial virus.
African-American: 2/4404 alleles (0.05%) and ExAC (Non-Finnish Europeans: 69/66 604 alleles (0.1%); African: 2/ 10 390 alleles (0.02%); Latino: 1/11 568 alleles (0.01%); South Asian: 9/16 484 alleles (0.05%)). There are no homozygous cases recorded on either ESP650015 or ExAC16 databases. Although the highest prevalence is recorded in European populations, the presence of the c.64T>C, p.Trp22Arg NDUFB3 variant in non-European populations suggests other independent occurrences of this pathogenic mutation.

Carrier testing
With the exception of patients 4 and 5, where familial samples were unavailable, parental carrier testing confirmed recessive inheritance. Analysis of samples from the unaffected twin of

Figure 1  Clinical presentation associated with homozygous NDUFB3 variant (A) Clinical photographs of eight patients harbouring a homozygous pathogenic c.64T>C, p.Trp22Arg NDUFB3 variant. Patient 1 is of English descent, whereas the remaining cases are all of Irish heritage. Patients 6/7 and 8/9 are clinically affected sibling pairs. All have characteristic physical features including a prominent forehead, smooth philtrum, deep-set eyes and low-set ears. (B) Clinical photographs of patient 10, the youngest case within our cohort, illustrating the characteristic physical features associated with the p.Trp22Arg NDUFB3 variant.
patient 1 and the three unaffected siblings of patients 8 and 9 confirmed the homozygous genotype segregates with a clinically affected status.

Haplotype analysis
Analysis of the NDUFB3-flanking STR markers across 0.5cM support multiple, independent occurrences of the c.64T>C, p.Trp22Arg variant (see online supplementary figure). Analysis of the markers most proximal to the NDUFB3 gene (D2S309 and D2S309), those most likely to be in linkage disequilibrium, shows three discrete haplotypes (1-1, 2-1 and 1-2). When including the distal STR markers in the analysis, this increases to seven haplotypes (α/β, plus #). There is one particularly prevalent haplotype (α#) in the patient cohort that is present in the heterozygous state in 8/10 cases and homozygous for 1/10 cases, supporting a founder allele. Additionally, the ‘b’ and ‘c’ haplotypes are present in two unrelated families. Haplotype analysis of the two previously reported cases shows the variants are also on the background of either the ‘α’ or ‘β’ haplotypes, suggesting a shared founder. We infer that the ‘#’ haplotype corresponds to the allele harbouring the truncating NDUFB3 mutation reported by Haack et al, as patient RC1 harboured a p.Trp22Arg variant in compound heterozygosity with p.Gly70*.

Steady-state levels of respiratory chain components and complexes
The p.Trp22Arg variant affects an evolutionarily conserved amino acid residue (figure 2A). We investigated the steady-state protein levels of OXPHOS subunits in muscle available from three patients harbouring a homozygous p.Trp22Arg NDUFB3 variant by SDS-PAGE and immunoblotting. The steady-state levels of Complex I subunit proteins NDUFB8 and NDUFA9 were decreased in all three patients while levels of protein components of Complexes II, III, IV and V were normal (figure 2B). Analysis of the assembly of OXPHOS complex subunits into mitochondrial respiratory chain complexes was undertaken by BN-PAGE, showing a decrease of fully assembled Complex I in P6, P2 and P3 muscle—correlating with the recorded biochemical defect—while the assembly profile of Complexes II, III, IV and V were all normal (figure 2C). Immunoblotting with NDUFB8 appeared to show partially assembled Complex I intermediates of ~650 kDa in patient muscle, consistent with other defects involving subcomplex Iβ of the hydrophobic membrane arm, of which NDUFB3 and NDUFB8 are both integral components.17−19

DISCUSSION
Mitochondrial disease presentations are frequently heterogeneous, with a paucity of genotype-phenotype correlations to direct molecular genetic testing even with a known biochemical diagnosis. We present a cohort of 10 patients from 8 non-consanguineous families who harbour a homozygous c.64T>C, p.Trp22Arg NDUFB3 variant; together these patients represent a distinct clinical presentation. The majority of patients presented with intrauterine growth restriction (IUGR) and share characteristic facial features including a prominent forehead, smooth philtrum, deep-set eyes and low-set ears. All patients are short (height <9th centile) and while short stature is not uncommon in mitochondrial disorders, dysmorphic features are rare with the exception of PUS120 and FBXL421 mutations. NDUFB3 encodes a structural Complex I subunit, and contrary to reported Complex I-deficient cases there were surprisingly few persistent features of mitochondrial disease; blood lactate levels were typically normal, although transient acidotic events were reported following illness leading, in some cases, to hospital admission before recovery. There were no seizures, ataxia or other neurological deficit noted; patients 2 and 3 had hypertrophic cardiomyopathy on echocardiography, but this resolved with time. All patients are reported to be well, with good levels of energy, attaining developmental milestones and making good progress at school (where appropriate). Patient 10 (<1 year of age) is much younger than the rest of our patient cohort, but is making excellent developmental progress (see online supplementary case reports).

With the exception of one patient (patient 1), all are reported to be of Irish ancestry. Interestingly, analysis of the NDUFB3-flanking STR markers supports multiple, independent occurrences of the c.64T>C, p.Trp22Arg variant, despite its prevalence in the Irish population. Across the 0.5cM region analysed, there are six different p.Trp22Arg alleles; given that this region is not a recognised recombination hot spot, it is likely that the mutation has arisen independently and recurrently although our data suggest a common founder for some cases and cannot fully exclude recombination as a contributory factor.

The c.64T>C, p.Trp22Arg NDUFB3 variant is represented on the ExAC server (0/81/121214 (homozygous/heterozygous/alleles); MAF=6.6×10−6) and has been reported in the literature twice previously, once in compound with a nonsense mutation and once as a homozygote; functional complementation experiments confirmed NDUFB3 as the causative gene defect in both cases.9,10 The homozygous case reported by Calvo et al9 had IUGR (weight <3rd centile) and presented with hypotonia...
and lactic acidosis, required ventilation and died at 4 months of age. The other reported case was born at 35 weeks gestation with low birth weight (3rd centile), with severe lactic acidosis and ketosis developing by day 2. Despite an initially severe presentation, her symptoms ameliorated and she is reported to remain of short stature but suffers illness-induced bouts of lactic acidosis. An older sibling of patients 6 and 7 in our series died on day 2 of life with profound lactic acidosis and multiorgan failure. No underlying cause was identified but a metabolic disorder was suspected, prompting early metabolic investigation of subsequent siblings.

Functional investigation of available patient muscle biopsy revealed a marked decrease in steady state levels of Complex I structural subunits, and although BN-PAGE analysis showed a marked decrease in Complex I subunits (NDUF8 and NDUF9) in patient samples compared with controls. The assembly of Complexes I–V was normal in all three patient samples when compared with age-matched controls. The lower panel suggests a presence of additional, partially assembled Complex I intermediates in both control and patient samples; the upper band (indicated by *) is likely to represent the ~650 kDa Iβ subcomplex of the hydrophobic membrane arm while the lower band (indicated by ***) represents partially assembled intermediates which are only visible in patient samples. These were detected by probing with an antibody raised against NDUF8 and are in agreement with published studies.17 In (B) and (C), SDHA (Complex II) was used as loading control.

![Figure 2](Figure2.png)

**Figure 2** Analysis of OXPHOS complex assembly and protein expression levels (A) Clustal Omega sequence alignment shows the evolutionary conservation of the p.Trp22 residue (marked with asterix), based on the human sequence (amino acids 1–43). (B) Immunoblot analysis of steady state levels of OXPHOS subunits in mitochondrial lysates isolated from control (C1, C2) and patient skeletal muscle samples (P6, P3, P2). OXPHOS subunit-specific antibodies against the indicated proteins showed a marked decrease in Complex I subunits (NDUFB8 and NDUFA9) in patient samples compared with controls. (C) One-dimensional blue native polyacrylamide gel electrophoresis (PAGE) (4–16% gradient) analysis showing a defect in the assembly of Complex I in patients with the homozygous *NDUFB3* variant. Individual OXPHOS complexes were detected by immunoblotting using subunit-specific antibodies (Complex I (NDUFB8), Complex II (SDHA), Complex III (UQCRC2), Complex IV (COX1) and Complex V (ATP5A)). The assembly of Complexes II–V was normal in all three patient samples when compared with age-matched controls. The lower panel suggests a presence of additional, partially assembled Complex I intermediates in both control and patient samples; the upper band (indicated by *) is likely to represent the ~650 kDa Iβ subcomplex of the hydrophobic membrane arm while the lower band (indicated by ***) represents partially assembled intermediates which are only visible in patient samples. These were detected by probing with an antibody raised against NDUF8 and are in agreement with published studies.17 In (B) and (C), SDHA (Complex II) was used as loading control.
screening was performed, revealing Wolff–Parkinson–White (WPW) syndrome in patient 8, a rare cardiac conduction defect which is over-represented in patients with mitochondrial disease.

The initial manifestation of WPW syndrome can be sudden death and the diagnosis might facilitate interventions including non-invasive risk stratification and/or therapeutic ablation.

Many cases of isolated Complex I deficiency associated with nuclear gene mutations are discrete entities and no common variant accounts for more than a few apparently unrelated cases. We present 10 patients from 8 families who harbour the same homozygous NDUFB3 variant and share a plethora of uni-fying physical features, an unprecedented finding in association with isolated Complex I deficiency. Recognition of the distinctive facial features in combination with short stature should suggest screening for the c.64T>C, p.Trp22Arg NDUFB3 mutation, even in the absence of ‘classic’ metabolic symptoms, and particularly when Irish ancestry is involved.

Author affiliations
1Wellcome Trust Centre for Mitochondrial Research, Institute of Neuroscience, Newcastle University, Newcastle upon Tyne, UK
2National Centre for Inherited Metabolic Disorders, Temple Street Children’s University Hospital, Dublin, Ireland
3Centre for Paediatrics and Child Health, Institute of Human Development, Faculty of Medical & Human Sciences, University of Manchester, & Manchester Academic Health Science Centre, Manchester, UK
4Department of Metabolic Paediatrics, Royal Hospital for Sick Children, Belfast, UK
5University of Bristol and Bristol Royal Hospital for Children, Bristol, UK
6Neurometabolic Unit, National Hospital for Neurology and Neurosurgery, London, UK
7Manchester Centre for Genomic Medicine, Central Manchester University Hospitals NHS Foundation Trust, Manchester Academic Health Science Centre, Manchester, UK
8Department of Paediatrics, The Royal Children’s Hospital, Murdoch Children’s Research Institute, University of Melbourne, Parkville, Australia
9Institute of Human Genetics, Helmholtz Zentrum München, German Research Center for Environmental Health, Munich, Germany

Acknowledgements
The authors thank James O’Sullivan, Beverly Anderson and Simon Williams from the Manchester Centre for Genomic Medicine for their support.

Contributors
CLA, RM, MO and RWT contributed to the project design, analysis of the data and/or the drafting of the manuscript. CH, PGM, SO’S, GD, JHPS, AAM, IK, PM, AAMM, DRT, HP, PEC, JC and EC recruited patients and family members and phenotypically characterised the families. CLA, MO, SAH, LH and IPH performed the biochemical and molecular genetic studies. All authors critically revised the manuscript text. RWT supervised the study.

Funding
This work was supported by grants (to RWT and RM) from The Wellcome Trust for Mitochondrial Research (096919/11/Z), the Medical Research Council (UK) Centre for Translational Muscle Disease Research (G0601943), The Lily Foundation and the UK NHS Highly Specialised Commissioners which funds the “Rare Mitochondrial Disorders of Adults and Children” Diagnostic Service in Newcastle upon Tyne (http://www.newcastle-mitochondria.com). HP was supported by the German Bundesministerium für Bildung und Forschung (BMBF) through the German Network for mitochondrial disorders (mitoNET, 01GM1113C) and the E-Rare project GENOMIT (01GM1207). This work was supported by an Early Career Grant from the Society for Endocrinology to PGM. CLA is the recipient of a National Institute for Health Research (NIHR) doctoral fellowship (NIHRHCS-D12-03-04).

Disclaimer
The views expressed are those of the authors and not necessarily those of the NHS, the NIHR or the Department of Health.

Competing interests
None declared.

Patient consent
Obtained.

Ethics approval
Not commissioned.

Open Access
This is an Open Access article distributed in accordance with the terms of the Creative Commons Attribution (CC BY 4.0) license, which permits others to distribute, remix, adapt and build upon this work, for commercial use, provided the original work is properly cited. See: http://creativecommons.org/licenses/by/4.0/.

REFERENCES
Genotype-phenotype correlations


A recurrent mitochondrial p.Trp22Arg NDUFB3 variant causes a distinctive facial appearance, short stature and a mild biochemical and clinical phenotype

Charlotte L Alston, Caoimhe Howard, Monika Oláhová, Steven A Hardy, Langping He, Philip G Murray, Siobhan O'Sullivan, Gary Doherty, Julian P H Shield, Iain P Hargreaves, Ardeshr A Monavari, Ina Knerr, Peter McCarthy, Andrew A M Morris, David R Thorburn, Holger Prokisch, Peter E Clayton, Robert McFarland, Joanne Hughes, Ellen Crushell and Robert W Taylor

*J Med Genet* published online April 18, 2016

Updated information and services can be found at:
http://jmg.bmj.com/content/early/2016/04/18/jmedgenet-2015-103576

These include:

**References**
This article cites 23 articles, 12 of which you can access for free at:
http://jmg.bmj.com/content/early/2016/04/18/jmedgenet-2015-103576#BIBL

**Open Access**
This is an Open Access article distributed in accordance with the terms of the Creative Commons Attribution (CC BY 4.0) license, which permits others to distribute, remix, adapt and build upon this work, for commercial use, provided the original work is properly cited. See:
http://creativecommons.org/licenses/by/4.0/

**Email alerting service**
Receive free email alerts when new articles cite this article. Sign up in the box at the top right corner of the online article.

**Topic Collections**
Articles on similar topics can be found in the following collections

- Open access (159)
- Epidemiology (620)
- Clinical diagnostic tests (350)
- Genetic screening / counselling (865)
- Metabolic disorders (319)
- Muscle disease (142)
- Neuromuscular disease (251)
- Surgery (105)
- Surgical diagnostic tests (105)

To request permissions go to:
http://group.bmj.com/group/rights-licensing/permissions

To order reprints go to:
http://journals.bmj.com/cgi/reprintform

To subscribe to BMJ go to:
http://group.bmj.com/subscribe/