Mutations in the SPG7 gene cause chronic progressive external ophthalmoplegia through disordered mitochondrial DNA maintenance

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Despite being a canonical presenting feature of mitochondrial disease, the genetic basis of progressive external ophthalmoplegia remains unknown in a large proportion of patients. Here we show that mutations in SPG7 are a novel cause of progressive external ophthalmoplegia associated with multiple mitochondrial DNA deletions. After excluding known causes, whole exome sequencing, targeted Sanger sequencing and multiplex ligation-dependent probe amplification analysis were used to study 68 adult patients with progressive external ophthalmoplegia either with or without multiple mitochondrial DNA deletions in skeletal muscle. Nine patients (eight probands) were found to carry compound heterozygous SPG7 mutations, including three novel mutations: two missense mutations c.2221G>A; p.(Glu741Lys), c.2224G>A; p.(Asp742Asn), a truncating mutation c.861dupT; p.Asn288*, and seven previously reported mutations. We identified a further six patients with single heterozygous mutations in SPG7, including two further novel mutations: c.184-3C>T (predicted to remove a splice site before exon 2) and c.1067C>T;
p.(Thr356Met). The clinical phenotype typically developed in mid-adult life with either progressive external ophthalmoplegia/ptosis and spastic ataxia, or a progressive ataxic disorder. Dysphagia and proximal myopathy were common, but urinary symptoms were rare, despite the spasticity. Functional studies included transcript analysis, proteomics, mitochondrial network analysis, single fibre mitochondrial DNA analysis and deep re-sequencing of mitochondrial DNA. SPG7 mutations caused increased mitochondrial biogenesis in patient muscle, and mitochondrial fusion in patient fibroblasts associated with the clonal expansion of mitochondrial DNA mutations. In conclusion, the SPG7 gene should be screened in patients in whom a disorder of mitochondrial DNA maintenance is suspected when spastic ataxia is prominent. The complex neurological phenotype is likely a result of the clonal expansion of secondary mitochondrial DNA mutations modulating the phenotype, driven by compensatory mitochondrial biogenesis.

Keywords: chronic progressive external ophthalmoplegia; hereditary spastic paraplegia; paraplegin; mtDNA maintenance; SPG7

Abbreviations: COX = cytochrome c oxidase; PEO = progressive external ophthalmoplegia; SDH = succinate dehydrogenase

Introduction

Progressive external ophthalmoplegia (PEO) is a classical presenting feature of mitochondrial disease, but the primary genetic basis has yet to be defined in a substantial proportion of patients. PEO and ptosis often occur in isolation, sometimes causing transient diplopia and significant field defects when severe, but in some patients PEO is part of a complex disorder involving both neurological and non-neurological features (Laforêt et al., 1995). A skeletal muscle biopsy remains a central clinical investigation, with a mosaic pattern of cytochrome c oxidase (COX)-deficient fibres and ragged-red fibres (indicative of mitochondrial sub-sarcolemmal accumulation) being key diagnostic features in most, but not all cases (Taylor et al., 2004).

In many patients with PEO, the underlying molecular defect is either a point mutation or a single, large-scale rearrangement of mitochondrial DNA (Moraes et al., 1989). However, a large proportion of patients harbour multiple mitochondrial DNA deletions in skeletal muscle which accumulate throughout life and cause the disorder (Zeviani et al., 1989; Moslemi et al., 1996). Several nuclear-encoded mitochondrial genes have been shown to cause these secondary defects of mitochondrial DNA (Copeland, 2008), but the underlying nuclear gene defect is not known in ∼50% of cases. Defining the molecular aetiology of this group will have direct implications for clinical management and genetic counseling, and also lead to novel mechanistic insights.

Here we show that mutations in the spastic paraplegia 7 gene (SPG7), which codes for the protein paraplegin (Casari et al., 1998), are an important cause of sporadic PEO with multiple mitochondrial DNA deletions presenting in mid-adult life. We demonstrate increased mitochondrial mass and hyperfused mitochondria in affected individuals, and accelerated clonal expansion of mitochondrial DNA mutations contributing to a complex neurological phenotype.

Materials and methods

Subjects

Whole exome sequencing was performed on eight subjects with PEO and no relevant family history who had >2% COX-deficient fibres, multiple deletions of mitochondrial DNA in skeletal muscle, and no mutation in POLG1, POLG2, SLC25A4, C10orf2, RRM2B, TK2, OPA1 and exons 5 and 13 of DNA2 (Ronchi et al., 2013). Following our initial findings, SPG7 was sequenced in a further 60 patients with unexplained PEO and/or multiple mitochondrial DNA deletions. Clinical details of patients with mutations are listed in Table 1. This study was approved and performed under the ethical guidelines issued by each of our institutions and complied with the Declaration of Helsinki.

Exome sequencing

Whole blood genomic DNA was fragmented to 150–200 bp by Adaptive Focused Acoustics (Covaris), end-paired, adenylated and ligated to adapters. Exonic sequences were enriched using Agilent SureSelect Target Enrichment (Agilent SureSelect Human All Exon 50 Mb kit). The captured fragments were purified and sequenced on a GAIIx platform using 75 bp paired-end reads. Bioinformatic analysis was performed using an in-house algorithm based on published tools. Sequence was aligned to the human reference genome (UCSC hg19), using NovoAlign (www.novocraft.com). The aligned sequence files were reformatted using SAMtools and duplicate sequence reads were removed using Picard. Single base variants were identified using Varscan (v2.2) and indels were identified using Dindel (v1.01). The raw lists of variants were filtered to include variants within the Sequence Capture target regions (±500 bp). On target variants were annotated using wAnnovar and common variants with a minor allele frequency >0.02 that were present in the 1000 Genomes (February 2012 data release), the NHLBI-5400 Exome Sequencing Project and 191 unrelated in-house exomes were excluded. Rare, protein altering, homozygous and compound heterozygous variants that fitted the recessive disease model were identified.

Sanger sequencing and multiplex ligation-dependent probe amplification analysis

Sanger sequencing of SPG7 was performed in the entire cohort of 68 patients using custom-designed primers (http://frodo.wi.mit.edu), PCR amplification with Immolase (Bioline), and Sanger sequencing with BigDye® Terminator v3.1 (Life Technologies) according to the manufacturer’s protocol on a 3130XL Genetic Analyzer (Life Technologies), addressing regions of poor exome coverage in the eight original subjects. Exon deletions of SPG7 were assessed by...
Table 1 Clinical features and diagnostic results of patients with mutations in SPG7

<table>
<thead>
<tr>
<th>Patient #</th>
<th>Clinical features</th>
<th>Age at onset (years)</th>
<th>Current age (years)</th>
<th>Affected relatives</th>
<th>Skeletal muscle histochemistry</th>
<th>Multiple mitochondrial DNA deletions</th>
<th>Complementary DNA change</th>
<th>Amino acid change</th>
<th>Exon</th>
<th>Mitochondria DNA copy number status</th>
<th>Reference for this mutation</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 M</td>
<td>PEO, ptosis, proximal myopathy, mild dysphagia, ataxia, spasticity</td>
<td>51</td>
<td>66</td>
<td>None</td>
<td>30% COX-deficient / 6% RRF</td>
<td>LRPCR + ve</td>
<td>c.861dup</td>
<td>p.Asn288*</td>
<td>6</td>
<td>Normal</td>
<td>Novel</td>
</tr>
<tr>
<td>2 M</td>
<td>PEO, ptosis, ataxia, spasticity, dysphagia, bladder symptoms, cerebellar atrophy</td>
<td>Mid-40s</td>
<td>56</td>
<td>Brother of 8 M</td>
<td>4% COX-deficient / 2% RRF</td>
<td>LRPCR + ve</td>
<td>c.1192C &gt; T</td>
<td>p.Arg398*</td>
<td>9</td>
<td>Normal</td>
<td>Schmidt et al., 2011</td>
</tr>
<tr>
<td>3 M</td>
<td>Mild PEO, ptosis, eye movements restricted horizontally &gt; vertically, hypometric saccades, lower limb proximal muscle weakness, ataxia, spasticity, mild cerebellar atrophy, mild cognitive impairment (MOCA 22/30)</td>
<td>47</td>
<td>53</td>
<td>None</td>
<td>1-2% COX-deficient fibres</td>
<td>LRPCR + ve (minimal changes noted)</td>
<td>c.1529C &gt; T</td>
<td>p.Ala510Val</td>
<td>11</td>
<td>Normal</td>
<td>McDermott et al., 2001</td>
</tr>
<tr>
<td>4 F</td>
<td>PEO, ptosis, proximal myopathy, ataxia, spasticity, dysphagia, dysphonia, dysarthria, optic atrophy, cerebellar atrophy</td>
<td>49</td>
<td>65</td>
<td>Brother</td>
<td>2% COX-deficient / 2% RRF</td>
<td>LRPCR + ve</td>
<td>c.1454_1462del</td>
<td>p.(Glu485Glu487del)</td>
<td>17</td>
<td>Normal</td>
<td>Novel</td>
</tr>
<tr>
<td>5 M</td>
<td>Jerky pursuits, dysarthria, ataxia, spasticity, dysdiadochokinesias, acanthocytosis, bladder symptoms, cerebellar atrophy</td>
<td>Late 20s</td>
<td>59</td>
<td>Brother</td>
<td>None; occasional intermediate fibres</td>
<td>LRPCR + ve</td>
<td>c.1923C &gt; T</td>
<td>p.(Arg742Asn)</td>
<td>17</td>
<td>Normal</td>
<td>Novel</td>
</tr>
<tr>
<td>6 M</td>
<td>PEO, ptosis, ataxia, spasticity, dysarthria</td>
<td>u/k</td>
<td>66</td>
<td>None</td>
<td>3% COX—deficient / 1% RRF</td>
<td>LRPCR + ve</td>
<td>c.1222G &gt; A</td>
<td>(Arg572Glu)</td>
<td>17</td>
<td>Normal</td>
<td>Novel</td>
</tr>
<tr>
<td>7 F</td>
<td>PEO, ptosis, ataxia, spasticity, proximal myopathy, moderate dysarthria, bladder symptoms</td>
<td>Late 20s</td>
<td>59</td>
<td>None</td>
<td>8% COX-deficient / 1% RRF</td>
<td>LRPCR -ve</td>
<td>c.2228T &gt; C</td>
<td>p.(Ile743Thr)</td>
<td>17</td>
<td>Normal</td>
<td>Brugman, 2008</td>
</tr>
</tbody>
</table>

**GROUP B: Single heterozygous mutations**

<table>
<thead>
<tr>
<th>Patient #</th>
<th>Clinical features</th>
<th>Age at onset (years)</th>
<th>Current age (years)</th>
<th>Affected relatives</th>
<th>Skeletal muscle histochemistry</th>
<th>Multiple mitochondrial DNA deletions</th>
<th>Complementary DNA change</th>
<th>Amino acid change</th>
<th>Exon</th>
<th>Mitochondria DNA copy number status</th>
<th>Reference for this mutation</th>
</tr>
</thead>
<tbody>
<tr>
<td>10 F</td>
<td>Ataxia, spasticity, dysdiadochokinesias, cerebellar atrophy</td>
<td>50</td>
<td>63</td>
<td>None</td>
<td>Normal</td>
<td>LRPCR + ve</td>
<td>c.184-3C &gt; T</td>
<td>(splicing defect)</td>
<td></td>
<td></td>
<td>Novel</td>
</tr>
<tr>
<td>11 M</td>
<td>Isolated PEO</td>
<td>60s</td>
<td>74</td>
<td>None</td>
<td>COX- deficient and RRF present</td>
<td>LRPCR + ve</td>
<td>c.1457G &gt; A</td>
<td>(Arg486Gln)</td>
<td>11</td>
<td></td>
<td>McDermott et al., 2001</td>
</tr>
<tr>
<td>12 F</td>
<td>PEO, spastic ataxia</td>
<td>4</td>
<td>44</td>
<td>Yes</td>
<td>Normal</td>
<td>LRPCR + ve</td>
<td>c.1529C &gt; T</td>
<td>p.Ala510Val</td>
<td>11</td>
<td></td>
<td>McDermott et al., 2001</td>
</tr>
<tr>
<td>13 M</td>
<td>PEO, ataxia</td>
<td>28</td>
<td>90</td>
<td>None</td>
<td>3% COX—deficient fibres</td>
<td>LRPCR + ve</td>
<td>c.1529C &gt; T</td>
<td>p.Ala510Val</td>
<td>11</td>
<td></td>
<td>McDermott et al., 2001</td>
</tr>
<tr>
<td>14 M</td>
<td>Ataxia, spasticity</td>
<td>u/k</td>
<td>55</td>
<td>MS (maternal unde); mother-walking difficulties</td>
<td>1% COX—deficient fibres</td>
<td>LRPCR + ve</td>
<td>c.1067C &gt; T</td>
<td>p.(Thr356Met)</td>
<td>8</td>
<td></td>
<td>Novel</td>
</tr>
<tr>
<td>15 F</td>
<td>PEO</td>
<td>54</td>
<td>58</td>
<td>n.a.</td>
<td>n.a.</td>
<td>c.233T &gt; A</td>
<td>p.(Glu74Arg)</td>
<td>2</td>
<td></td>
<td>McDermott et al., 2001</td>
<td></td>
</tr>
</tbody>
</table>

**Note:** The protein alterations without RNA/protein level evidence are in brackets. RNA evidence for mutations p.288ins*, p.Arg398*, p.Ala510Val, and p.Lys588* are included in this report.

*This variant is designated as rs111475461, has a frequency in the population of 0.02, and is of unproven pathogenicity (McDermott et al., 2001; Klebe, 2012).
cells were pelleted and RNA extracted using RNeasy® protocols for RNeasy® (Qiagen). Quality of extracted RNA was measured by means of Bradford assay. Samples (20 μg protein) were separated through 4–15% Mini-PROTEAN® TGX™ precast gels (Bio-Rad) and transferred to polyvinylidene fluoride membranes using Trans-Blot® Turbo™ transfer system (Bio-Rad). Membranes were probed with antibodies specific to SPG7 (sc-135026, Santa Cruz Biotechnology), AFG3L2 (14631-1-AP, Proteintech), OPA1 (MS995, Mitosciences), SDHA (70kDa Complex II subunit) (MS204, Mitosciences), porin (MSA03, Mitosciences), HSP60 (GTX110089, GeneTex) and GAPDH (sc-25778HRP, Santa Cruz Biotechnology), followed by species-appropriate horseradish peroxidase-conjugated secondary antibodies (Dako), using standard protocols. Protein signal was detected with Pierce ECL2 Western Blotting substrate (Thermo Scientific) and Biospectrum 500 Imaging System (UVP) as per manufacturer’s instructions. Densitometric analysis was performed using ImageJ software (National Institute of Health). GAPDH was used to normalize the results and the ratios protein of interest/GAPDH were calculated. Data represent the mean of three independent replicates. Statistical analysis was performed in Microsoft Excel using F-test: two-sample test for variances, followed by t-test: two sample assuming equal or unequal variances. Statistical significance was considered when P two-tail < 0.05.

Mitochondrial network analysis

Cells from four SPG7 primary fibroblast cell lines (Patients 1–4) and three control cell lines were cultured on glass bottom dishes (Wilco, HBST-3522), and mitochondria were stained using MitoTracker Red CMXRos at 0.75 nM. Live cell imaging was performed using Nikon A1R inverted confocal microscope equipped with a ×60 objective (numerical aperture = 1.40), in culture medium without phenol red and supplemented with 25 mM HEPES. Acquisitions were performed at 3% laser power, at the frame size of 512 × 512 with perfect voxel settings (x, y, z, 0.12 μm). Sixty-nine z-planes across 8 μm were captured to allow for a 3D reconstruction of mitochondrial networks from individual cells. Deconvolution and mitochondrial network analysis was performed using Huygens Essentials software (SVI). Fifty cells were imaged per individual cell line.

Deep resequencing of mitochondrial DNA

PCR amplification of the mitochondrial DNA control region (MT-HV52) in muscle DNA from six patients (Patients 1, 2, 4, 5, 6 and 7) was performed with tagged primers and ultra deep sequencing achieved using a Roche 454 GS Titanium FLX platform as previously described (Payne et al., 2011). An analysis pipeline of Pyrobayes, Mosaic and a custom R library was used to call and align the sequences to the mitochondrial DNA reference along with a control cloned mitochondrial DNA sequence. For quality control purposes, only sites covered by more than 10000
reads in each direction were considered for analysis. Data were compared to muscle mitochondrial DNA from 22 in-house controls: seven healthy individuals undergoing orthopaedic surgery (with two being over 65 years of age), eight with recessive POLG mutations known to cause a high mutation burden, six with dominant OPA1 mutations known to cause a defect of mitochondrial fusion-fission and control cloned mitochondrial DNA. Data were analysed as described previously (Payne et al., 2013), with a 0.2% heteroplasmy detection threshold, based on the sequencing of a cloned mitochondrial DNA template.

Results

Molecular genetics

Eight patients with PEO, multiple mitochondrial DNA deletions and no known genetic defect were subjected to whole exome sequencing. After excluding common variants found in the NHLBI-5400 Exome Sequencing project, 1000 Genomes and 191 in-house disease control subjects, we identified one patient with compound heterozygous SPG7 mutations, one of which had not been previously reported (Patient 1) and another patient with a single heterozygous mutation within the SPG7 gene (Patient 12) (Table 1). This led us to sequence SPG7 in the remaining larger cohort. Nine patients from eight families were found to carry compound heterozygous SPG7 mutations, comprising three novel mutations: a stop-gain mutation, c.861dupT p.Asn288* (Patient 1); and two missense mutations c.2221G>A p.(Glu741Lys) and c.2224G>A p.(Asp742Asn) in Patient 4. Seven previously reported mutations were also identified: p.Ala510Val (six patients), p.Lys558* (two patients), p.(Leu78*) (one patient), p.Arg398* (two patients), p.(Ile743Thr) (one patient), p.(Gly352Argfs*44) (two patients) and p.(Arg485_Glu487del) (one patient). A single heterozygous SPG7 mutation was identified in six additional patients, comprising two further novel mutations: c.184-3C>T (g.19571C>T, predicted to remove a splice site before exon 2), and c.1067C>T; p.(Thr356Met); and two previously reported pathogenic mutations: p.Ala510Val (three patients), and p.(Leu78*) (one patient) (Table 1). The most common mutation was p.Ala510Val, identified in nine patients (eight probands) from our panel of 68 probands (Table 1). The most common mutation was p.Ala510Val, identified in nine patients (eight probands) from our panel of 68 probands (Table 1).

Clinical features of patients with SPG7 mutations

Compound heterozygous SPG7 mutations

The clinical features of nine patients with compound heterozygous SPG7 mutations are summarized in Table 1, Patients 1–9. Mean age at onset was ~40 years (range 28–65 years) with current age 61 years (range 51–71 years). The most frequent clinical features of our patients were spastic ataxia (all nine patients) with both PEO and ptosis in eight patients (Fig. 1). Additional features included a proximal muscle weakness (five patients) and swallowing difficulties (four patients) resulting in mild to moderate disability. Other symptoms typically associated with hereditary spastic paraparesis were less frequent, including bladder dysfunction (three patients), and optic atrophy (two patients) resulting in significant visual impairment (one patient). Dysarthria was common (four patients). Other central neurological features of mitochondrial disease were not seen, such as encephalopathy, epilepsy, or stroke-like events, and cognitive impairment was observed in only a single patient (Patient 3 had a Montreal Cognitive Assessment Tool score of 22/30, losing 5 points for recall and 3 points for visuospatial). Sensorineural hearing loss was not a feature. Cardiac involvement was not evident. Cerebellar atrophy was present in all those who underwent magnetic resonance imaging (five patients); this was marked in four patients and mild in one patient. Motor evoked potentials performed in two patients with compound heterozygous mutations showed electrophysiological evidence of a length dependent degenerative process affecting corticospinal tracts axons projecting to the lower limb motor neurons (Fig. 2), as classically described in hereditary spastic paraplegia (Lang et al., 2011).

Single heterozygous mutations

The clinical features of six patients with single heterozygous SPG7 mutations are summarized in Table 1, Patients 10–15. Mean age at onset was ~26 years (range 6–65 years) with current age 66 years (range 44–90 years). PEO (four patients) was the most common clinical feature in this group of patients and was the only finding in two patients (Patients 11 and 15). Ataxia (three patients) and other cerebellar features including nystagmus (one patient), dysdiadochokinesia (one patient) and cerebellar atrophy (one patient) were evident. Lower limb spasticity was present in three patients.

Muscle fatigue was the presenting feature in all of the patients, followed by a progressive gait ataxia with spasticity. Proximal weakness developed later in the disease course in some subjects, and PEO/ptosis was a late feature.

Muscle mitochondrial DNA analysis

Diagnostic histology and oxidative enzyme histochemistry of the patients’ skeletal muscle biopsies revealed evidence of mitochondrial respiratory chain deficiency, with sequential COX-SDH histochemistry confirming variation in the severity of the COX-mosaic defect (Table 1). These findings were particularly pronounced in Patient 1 in whom ~30% COX-deficient fibres were noted, together with typical ‘ragged-blue’ fibres indicating subsarcolemmal mitochondrial accumulation (Fig. 3A). Long-range PCR amplification of muscle DNA clearly showed the presence of multiple mitochondrial DNA deletions (Fig. 3B), indicative of a disorder of mitochondrial DNA maintenance. Real-time PCR analysis of individual, laser-captured COX-deficient fibres showed that the majority, but not all, of these fibres harboured high levels of clonally-expanded mitochondrial DNA deletion involving the MTND4 gene (Fig. 3C), a consistent observation in patients with genetically-proven multiple mitochondrial DNA deletion disorders (Longley et al., 2006; Hudson et al., 2008; Blakely et al., 2012; Pitceathly et al., 2012). Similar findings were also noted in Patients 2, 4, 6 and 7 (not shown). No major abnormality of mitochondrial DNA copy number was detected in muscle DNA from any of the patients with compound heterozygous SPG7 mutations (Table 1).
Transcript analysis

Sequencing of complementary DNA derived from fibroblasts in Patients 2 and 3 only revealed one mutated allele, consistent with the prediction that these two patients harboured one allele likely to cause nonsense mediated decay, and confirming that the heterozygous mutations were in trans (Fig. 4). In accordance with this, the transcript levels increased following emetine treatment in two of the patients with nonsense SPG7 mutations (Fig. 5), but not in the one cell line with two missense SPG7 mutations (Patient 4). These findings were confirmed by Sanger sequencing of complementary DNA with transcript-specific primers (Fig. 4).

Reverse-transcriptase quantitative PCR of complementary DNA derived from muscle demonstrated elevated expression of SPG7, AFG3L2 and OPA1 transcripts in patients compared with controls (Fig. 5). The transcript levels of POLG and SDHA did not differ significantly between patients and controls.

Western blot analysis

Western blot of skeletal muscle protein showed a generalized increase in mitochondrial protein levels in the SPG7 Patients 1, 2, 4, 5 and 7, including markers of mitochondrial mass (SDHA, porin, and HSP60) and SPG7. By contrast, AFG3L2 protein levels were reduced in patients compared to controls (Fig. 6).

Mitochondrial network analysis

Fibroblasts from SPG7 patients had fewer mitochondrial networks (41.42–53.90 compared with 88.66 for controls; Fig. 7), which were larger than controls. The average network length was...
significantly longer for \textit{SPG7} patients ($4.05\text{–}4.78\,\mu m$ compared with $3.39\,\mu m$ for control subjects; Fig. 7C) the average length of the longest network per cell was also significantly higher in \textit{SPG7} patients ($25.73\text{–}42.27\,\mu m$ compared with $19.92\,\mu m$ for control subjects; Fig. 7D), and \textit{SPG7} patients had a greater proportion of long networks ($>10\,\mu m$, $4.4\%$ for the controls compared with $6.8$ to $10.2\%$ for the \textit{SPG7} patients; Fig. 7A) when compared with control subjects. In addition, the average volume per mitochondrial network was greater in \textit{SPG7} patients, as was the average total volume of mitochondrial networks per cell (Fig. 7E and F). All of these findings were highly statistically significant ($P < 0.0001$) except for average maximum network length in Patient 4 ($P = 0.004$), and no significant difference for total mitochondrial network volume per cell in Patient 4. Representative images from control and \textit{SPG7} cell lines are presented in Fig. 8.

**Deep resequencing of mitochondrial DNA**

Analysis of FLX ultra-deep resequencing was performed on 375 positions that met our minimum criteria of $>10,000$-fold coverage, with 258 not associated with poly-mononucleotide repeats. Overall, the frequency of low-level mitochondrial DNA heteroplasmy ($<1\%$) in \textit{SPG7} patients mutations was similar to control subjects, aged controls, patients with \textit{OPA1} mutation and lower than \textit{POLG} patients (Fig. 9). However, the number of high-level heteroplasies ($>1\%$) appeared to be greater in the \textit{SPG7} patients compared with controls or \textit{OPA1} patients, in keeping with an increased rate of clonal expansion of mitochondrial DNA point mutations, although this difference was not statistically significant ($P = 0.07$).

**Discussion**

Using an unbiased exome sequencing approach we identified pathogenic compound heterozygous \textit{SPG7} mutations in patients...
with PEO and multiple mitochondrial DNA deletions in skeletal muscle, and confirmed these unexpected findings in a larger cohort of undiagnosed patients with multiple mitochondrial DNA deletions. The majority of the compound heterozygotes had at least one known pathogenic SPG7 mutation, and both transcript and western blot analyses support a pathogenic role for the other mutations (Table 1), including novel nonsense mutations causing nonsense-mediated decay. Although we are unable to provide proof of pathogenicity for the novel mutations in Patient 4, these were associated with near-identical clinical findings to the other SPG7 patients, and had similar abnormalities on western blot, reverse transcription quantitative PCR, and mitochondrial network imaging. Given that these mutations affect a critically important region of the protein (Bonn et al., 2010), they are highly likely to be pathogenic. The presence of compound heterozygous SPG7 mutations in these nine patients from a cohort of 68 PEO patients indicate that SPG7 mutations are a common cause of PEO and that this gene should be sequenced in PEO patients with unexplained multiple deletions of mitochondrial DNA.

**Clinical features in patients with compound heterozygote SPG7 mutations**

Given our ascertainment methods, it is not surprising that the majority of the patients with SPG7 mutations had PEO, usually associated with marked ptosis. Although this has been previously reported in association with SPG7 (van Gassen et al., 2012), it was so uncommon that it was considered possibly a coincidental finding not related to the disorder. Our findings show that PEO and ptosis fall within the spectrum of complex SPG7 phenotypes, and
the presence of multiple mitochondrial DNA deletions provides the likely mechanism. Bladder dysfunction was seen in three patients, which has been reported in ~50% of patients with SPG7-related hereditary spastic paraplegia (van Gassen et al., 2012). Optic atrophy, recognized as part of a more severe SPG7 complex phenotype (van Gassen et al., 2012), was seen in two patients in our cohort resulting in significant visual impairment. Although cerebellar ataxia was a feature of all of the patients with compound heterozygous SPG7 mutations, cortical manifestations associated with other forms of mitochondrial disease such as cognitive impairment, epilepsy, encephalopathy and/or stroke-like events were not observed. Motor evoked potentials performed in two patients showed electrophysiological abnormalities classical of hereditary spastic paraplegia, which has infrequently been reported in patients harbouring OPA1 mutations (Yu-Wai-Man et al., 2010; Baker et al., 2011). This provides further evidence of corticospinal tract dysfunction and indicates that spasticity is not as rare in mitochondrial disorders as was previously thought.

Patients with single heterozygous SPG7 mutations

Although it is possible that a second recessive SPG7 variant is present in an area outside our analysis, perhaps in a regulatory region of the gene, dominant SPG7 mutations have been described (Sanchez-Ferrero et al., 2013), and diffusion tensor imaging demonstrated abnormalities in an asymptomatic heterozygote SPG7 mutation carrier (Warnecke et al., 2010). Furthermore, even after excluding the

Figure 5 Transcript level measurement with reverse transcription quantitative PCR. (A) SPG7 transcript analysis in Patients 1–4, using RNA from cultured fibroblasts. For Patients 1–3 who have one or more nonsense mutations in SPG7, treatment of fibroblasts with emetine (dark bars) (an inhibitor of nonsense-mediated messenger RNA decay) compared with normal conditions (light bars), resulted in significantly increased SPG7 messenger RNA in Patients 1 and 2 (*P < 0.05). Patient 4 who has 2 missense SPG7 mutations does not have alteration in SPG7 expression with emetine (nor do control; data not shown). (B) Transcript quantitation in complementary DNA derived from muscle, in Patients 1–4 (red bands), compared with three control muscle samples (blue bands). Levels of SPG7, AFG3L2, and OPA1 transcripts are elevated in patients compared with controls (*P < 0.02). Levels of POLG and SDHA did not differ significantly.

Figure 6 Western blot of muscle tissue. (A–C) Representative blots used in the quantification of protein expression of muscle tissue from five patients with compound heterozygous SPG7 mutations and three control subjects. Testing was performed in triplicate and quantification of aggregate mean with SD (normalized to GAPDH) are represented in D. Markers of mitochondrial mass, including SDHA, porin, and HSP60 are significantly increased in SPG7 patients compared with controls. SPG7 and OPA1 were also significantly elevated in SPG7 patients compared with controls. AFG3L2 was decreased compared with controls. All the above were statistically significant to *P < 0.01.
compound heterozygotes from our study, \textit{SPG7} mutations remain significantly enriched in the remaining 60 patients: the common p.Ala510Val mutation is present in 3 of 118 chromosomes (2.5%) but among regionally-matched controls only 1 in 192 chromosomes (0.5%). Given that the majority of the patients with single heterozygous mutations in \textit{SPG7} had a similar phenotype to the patients with compound heterozygous mutations, the heterozygous mutations are likely to be involved in the pathogenesis of the disorder in these patients. Although only one of six heterozygotes we studied reported a relevant family history, incomplete penetrance for presumed dominant \textit{SPG7} mutations has been reported previously (Sanchez Ferrero \textit{et al.}, 2013). Further familial segregation studies are warranted to definitely determine the inheritance pattern for the presumed dominant \textit{SPG7} mutations described here.

\section*{Novel mutations in \textit{SPG7}}

We demonstrate evidence of pathogenicity for three mutations (p.Asn288*, p.Arg398* and p.Lys558*) that are predicted to cause nonsense-mediated messenger RNA decay. One of these,
p.Asn288*, is a novel mutation, whereas the others have been previously reported in hereditary spastic paraplegia type 7 patients (Schlipf et al., 2011; van Gassen et al., 2012). Our studies in fibroblasts derived from these patients demonstrate that emetine treatment increases the transcript levels. This was directly shown using reverse transcriptase quantitative PCR in Patients 1 and 2, who had increased SPG7 transcript levels (Fig. 5A), and indirectly in Patients 2 and 3 in whom the degraded transcript was detectable with Sanger sequencing upon treatment with emetine (Fig. 4). The consistency of our findings on western blot, reverse transcriptase quantitative PCR, and mitochondrial network imaging among Patients 1–4 (and as distinguished from control subjects) is indirectly suggestive that the two novel mutations in Patient 4 [p.(Glu741Lys) and p.(Asp742Asn)] are pathogenic.

**Functional consequences of the SPG7 mutations**

Several strands of evidence indicate that SPG7 mutations induce mitochondrial biogenesis. Histochemically we observed ragged-red fibres in skeletal muscle (Fig. 3), supported by a generalized upregulation of mitochondrial proteins on western blot analysis (SDHA, porin and HSP60); and mitochondrial network analysis revealed an increased cellular mitochondrial mass in fibroblasts. Reverse transcriptase quantitative PCR of transcript levels from muscle RNA did not demonstrate elevated SDHA although other mitochondrial proteins had increased transcript levels (SPG7, AFG3L2 and OPA1). Taken together, these findings all support upregulation of mitochondrial gene expression, protein synthesis and increased mitochondrial mass, which are typical for a mitochondrial disorder, where the organellar proliferation is thought to be a compensatory response to malfunctioning mitochondria. This increased mitochondrial biogenesis may attenuate end-organ dysfunction and explain the late onset of disease in most of our patients. The upregulation of mitochondrial proteins may also indicate an unfolded protein response caused by decreased paraplegin activity, which was demonstrated to occur in a SPG7 RNA knockdown study in a *Caenorhabditis elegans* model (Yoneda et al., 2004). It is intriguing that these findings are the mirror image of those seen in mice with mutations in Afg3l2, the binding partner of...
paraplegin, which exhibit decreased mitochondrial protein synthesis and fragmented mitochondrial networks, leading to neurodegeneration (Almajan et al., 2012). This is thought to be due to the impaired metabolism of OPA1, which mediates mitochondrial fusion (Maltecca et al., 2012). In contrast, in our patients with SPG7 mutations we observed increased mitochondrial biogenesis with hyper-fused mitochondria. This again is likely to be part of a compensatory response, known as stress-induced mitochondrial hyperfusion (Tondera et al., 2009). The generalized upregulation of OPA1 that we observed in skeletal muscle is likely to play a role in this response, as Opa1 isoforms are a key mediator of mitochondrial hyperfusion (Song et al., 2007). It is unclear whether the paraplegin defects in these patients would have directly caused the elevated OPA1 levels, as previous work in animal models indicated that abnormal paraplegin is not sufficient to alter OPA1 metabolism (Duvezin-Caubet et al., 2007; Ehses et al., 2009).

How are these abnormalities linked to the secondary mutations of mitochondrial DNA present in our patients? There was no significant increase in the point mutation burden on deep sequencing of muscle mitochondrial DNA from SPG7 patients, with similar levels to age-matched controls and OPA1 patients, but significantly lower than in POLG patients (who are known to have a proofread-deficient mitochondrial DNA polymerase). The major mechanism leading to the increase in detectable mutations is therefore likely to be the segregation and clonal expansion of pre-existing deletions and point mutations, rather than an increase in the mutation rate per se, given that low-level mitochondrial DNA heteroplasmy seems to be a common finding in healthy individuals (Payne et al., 2013). Initially this could be driven by mitochondrial biogenesis triggered by a disruption of mitochondrial quality control, in which paraplegin is intimately involved. The mitochondrial DNA replication which accompanied the biogenesis would lead to the accumulation of pre-existing mitochondrial DNA mutations. Once these mutations reach a critical level, they would lead to further biogenesis and the formation of ragged-red fibres. The combined effect would be a vicious cycle of events, leading to the accumulation of more mitochondrial DNA mutations, a COX-defect, and the subsequent PEO-phenotype.

The clonal expansion of somatic mitochondrial DNA mutations provides a common mechanism for the PEO, ptosis and myopathy seen in several mitochondrial DNA maintenance disorders, and our data suggest that the same is occurring in SPG7. However, it remains to be elucidated as to whether this same mechanism contributes to the motor system degeneration where a different mechanism may be operating. This also appears to be the case for OPA1, where the optic nerve degeneration does not appear to be mediated through clonally expanded mitochondrial DNA mutations (Yu-Wai-Man et al., 2009). When taken together, these findings highlight the multiple downstream mechanisms that contribute to the clinical phenotype of ostensibly simple single-gene (monogenic) disorders. Why this should only occur in some mutation carriers remains to be determined, and it may depend upon the region of SPG7 that is involved.

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