Two families with autosomal dominant progressive external ophthalmoplegia

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PATIENTS AND METHODS

Clinical and electrophysiological findings, and muscle histology of the two index patients are summarised in table 1. The pedigrees are shown in fig 1.

Patient 1

This 67 year old man had experienced slowly progressive external ophthalmoplegia from the age of 15 years. At 49 years of age, dyspnoea during exercise, fatigue, peripheral oedema, no toria, and palpitations developed. Echocardiography showed an advanced dilated cardiomyopathy with marked reduction of ventricular wall movements and an ejection fraction of less than 25%. Mild improvement was achieved with diuretics, digitalis, and ACE inhibitor treatment. Because of atrial fibrillation with periods of paroxysmal ventricular tachyarrhythmia, anticoagulation was started and because of severe symptoms the patient was placed on the waiting list for heart transplantation. Neurological evaluation revealed ptosis, mild facial weakness, and limitation of eye movements in all directions. Electromyography of right biceps and facial muscles showed short duration, low amplitude voluntary motor unit potentials and an early recruitment of many motor units indicative of a myopathy. The family history was remarkable for progressive bilateral ptosis and ophthalmoplegia in the patient’s grandfather, mother (+ diabetes mellitus) and one of his two sons, but none had cardiac disease manifestation (fig 1).

Patient 2

This patient is a 68 year old woman. Ptosis and limited eye movements were noted at the age 50. Later on, she developed progressive atrophy and weakness of the shoulder and quadriceps muscles as well as exercise intolerance. More recently, she also showed axonal polyneuropathy, hearing loss, dysphagia, diabetes mellitus, and idiopathic osteoporosis. On neurological examination, she had almost complete bilateral ptosis and ophthalmoplegia. Her fundi were normal. There was a moderate weakness and atrophy of her quadriceps and shoulder muscles. She was able to walk, but had problems in climbing stairs and lifting her arms over the shoulder level. Achilles tendon reflexes were absent. Electromyography recording from shoulder muscles showed a prominent myopathic pattern. An MRI scan of the brain was unremarkable. The patient’s mother had had PEO as an isolated clinical feature. One brother had suffered from PEO.

Abbreviations: adPEO, autosomal dominant progressive external ophthalmoplegia; CS, citrate synthase; NCP, non-collagen protein; RC, respiratory chain; RFLP, restriction fragment length polymorphism.
diabetes, cardiomyopathy, and myopathy of the respiratory muscles, and died from respiratory insufficiency. The patient’s son and two children of her brother show incipient and isolated PEO.

Morphology and biochemistry of skeletal muscle
An open muscle biopsy was performed in both index patients (at age 55 and 65 years, respectively). Serial cross-sections (6 μm thick) were processed for histochemical stains according to standard procedures. A deep frozen part of the biopsy was used for biochemistry. Respiratory chain (RC) enzyme complex I‒IV activities were determined in skeletal muscle as described. In patient 1, muscle tissue was not sufficient for ultrastructural and biochemical analysis and a second biopsy was not considered because of long term anticoagulation.

DNA analysis
Total DNA was extracted from muscle and leucocyte samples using a commercial purification kit (Qiagen, Hilden, Germany). PCR, Southern blot and single strand conformational polymorphism analyses were performed as described previously. Cycle sequencing was performed on gel purified fragments using the ABI Prism Big Dye Termination kit (Perkin Elmer, Langen, Germany). Sequencing of all 22 mitochondrial tRNA genes, ANT1, C10orf2 (encoding for Twinkle), and POLG1 were performed by standard methods. The required primers were designed according to the following Genbank sequences: J04982 for ANT1, AL133215 for C10orf2, and AC005317 for POLG1. In patient 2, the novel F485L mutation was confirmed by restriction fragment length polymorphism (RFLP) analysis of a PCR product containing exon 2 of Twinkle. The mutation F485L introduced a new Msel restriction site. The patient’s affected son, her unaffected sister, and 150 control chromosomes were similarly tested for this mutation.

RESULTS
Morphology and biochemistry of skeletal muscle
In muscle biopsy specimens stained with Gomori trichrome, both patient 1 and 2 showed ragged red fibres (8 and 10%, respectively). These fibres were histochemically negative for cytochrome c oxidase. Histochemistry of a representative section of muscle from patient 1 is shown in fig 2A. Biochemical and ultrastructural examinations were performed for patient 2 only. The activities of all RC complexes were within normal ranges per gram of non-collagen protein (NCP) and citrate synthase (CS), but the activity of CS (a mitochondrial marker enzyme) itself was slightly increased (111 U/g NCP; normal range: 45–105) suggesting mitochondrial proliferation. On electron microscopy, ultrastructural abnormalities of mitochondria including paracrystalline inclusions were found (fig 2B).

DNA analysis
PCR, RFLP, and sequencing analysis of mtDNA tRNA genes in muscle of the two index patients revealed no abnormalities. Southern blot analysis could not be performed in patient 1 because of small sample size. In patient 2, multiple mtDNA deletions were observed on Southern blot. Sequencing of the ANT1, C10orf2, and POLG1 genes in leucocyte DNA did not show any mutations in patient 1. In patient 2 in the C10orf2 gene, encoding for Twinkle, a heterozygous missense mutation at nucleotide position C1640A was detected (according to the Genbank accession number AF292004). The mutation exchanged a leucine for a
conserved phenylalanine at the aminoacid 485 (F485L) (fig 3A). RFLP analysis of Twinkle exon 2 confirmed the mutation in the patient (lane 1) and in her affected son (lane 2), the unaffected sister and a normal control were negative (lane 3, 4). Marker, 1 kb; wild type, 342 bp; mutant, 269 bp.

DISCUSSION

We report here two families with dominant transmission of progressive external ophthalmoplegia. In one, a new mutation in Twinkle helicase was identified, whereas the other family had no mutations in the known PEO genes. Presence of multiple mtDNA deletions was verified in patient 2. Multisystem manifestations and morphological findings in our two families were typical for mitochondrial disease. The first symptom in both patients was PEO, but various other manifestations developed at a later stage of disease (10 to 34 years after onset of PEO) such as severe progressive dilated cardiomyopathy, generalised myopathy, axonal polyneuropathy, diabetes mellitus, and hearing loss. Involvement of extracranial tissues and organs showed high intra-familial variability in both cases. In previous adPEO families, similar systemic manifestations have been described including axonal polyneuropathy, ataxia, depression, dysarthria, tremor, hearing loss, cardiomyopathy, diabetes mellitus, hypogonadism and growth failure. The variety of clinical symptoms closely resembles that seen in mitochondrial encephalomyopathies caused by primary mtDNA mutations, which suggests that acquired mtDNA deletions caused by nuclear gene defects are actually responsible for the tissue dysfunction. Multiple deletions probably arise as somatic mutations and accumulate in non-dividing cells, but do not occur in cultured—that is, dividing, cells from adPEO patients. This may also explain the late onset and the variable outcome of the disease.

Recent breakthroughs in molecular genetics of PEO allow a more specific genetic classification. Sporadic or maternally inherited forms of PEO are often caused by single mtDNA deletions and several mutations in mitochondrial tRNA genes. Autosomal disorders of intergenomic communication cause multiple mtDNA deletions or depletion (for review see Moslemi et al). The estimated frequencies of mutations in adPEO have been reported to be 4–10% for ANT1 and 15–35% for C10orf2 (Twinkle), and 45% for POLG1. Mutations in ANT1, C10orf2 (Twinkle), and POLG1 were recently also described in sporadic patients with PEO. Cases of adPEO

Figure 2  (A) Modified Gomori trichrome staining of a representative section of muscle from patient 1 showing numerous ragged red fibres and mild myopathic changes with increased variability of fibre size and internalised myonuclei, original magnification x20. (B) Ultrastructure of a muscle fibre from patient 2 containing enlarged mitochondria with cristallloid inclusions (bar = 0.4 μm). The electron micrograph was kindly provided by Professor H Budka, Institute of Neurology, University of Vienna.

Figure 3  (A) Sequencing of Twinkle revealed a heterozygous missense mutation (arrow). (B) RFLP analysis of Twinkle exon 2 confirmed the mutation in the patient (lane 1) and in her affected son (lane 2), the unaffected sister and a normal control were negative (lane 3, 4). Marker, 1 kb; wild type, 342 bp; mutant, 269 bp.
still exist in which sequencing or linkage analysis excluded all the three genes as causative.13

In both patient 2 and her affected son, a new missense mutation in the gene C10orf2 encoding Twinkle, a putative mitochondrial ring helicase, was found to change a conserved amino acid at position 485. This mutation is located between Walker motifs A and B, next to two other previously described pathogenic mutations (W474C and A475P).14

Interestingly, in the Twinkle homologue of the T7 bacteriophage, a gene primase helicase, the amino acids corresponding to W474 and A475 in Twinkle are located in a helical loop that contacts the “linker region” of an adjacent subunit in the hexameric complex. Up to date, 8 of 13 published pathogenic mutations cluster in the linker region.11 13

According to previous functional studies and crystal structure data of the hexameric T7 gene4 protein, this linker region seems to be involved in the multimerisation process and/or to affect catalytic properties of the primase/helicase function. Furthermore, the adjacent subunit interfaces, joined together by the linker helix loop, form the nucleotide binding pocket. Therefore, mutations W474C, A475P, or the newly discovered F485L in the adjacent helical loop could likewise affect subunit interactions or nucleotide binding, or disturb catalytic activities of the complex. Previous functional studies suggest that the multimerisation of the protein is not drastically altered in linker mutants (352–364 duplication and W474C), which agrees with the late disease onset, most likely associated with moderate functional defect.10

In conclusion, our families illustrate the clinical and genetic variability of adPEO. In one family, sequencing of the gene encoding Twinkle unravelled a novel pathogenic mutation F485L, whereas in the other index patient with PEO and severe dilated cardiomyopathy, no genetic abnormalities in the ANT1, C10orf2 (Twinkle), or POLG1 genes could be detected, indicating the existence of a yet unknown nuclear gene defect. Genetic testing has become an important tool in the difficult diagnosis of inherited PEO.

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