Inheritance of CMT1A duplication from a mosaic father

E Sorour, P Thompson, J MacMillan, M Upadhyaya

Abstract
We describe a case with molecular duplication of chromosome 17 (p11.2-p12) whose duplicated chromosome was inherited from a mosaic father. The patient has clinical manifestations consistent with Charcot-Marie-Tooth disease type 1A (CMT1A), while the mosaic father has minimal findings of CMT1A. The father was found to be homozygous with DNA markers VAW409R3A (D17S122) and p132G8R1 (PMP-22) which are duplicated in CMT1A cases. Fluorescence in situ hybridisation (FISH) analysis with YAC clone 49H7 confirmed the duplication in the affected patient and diagnosed the mosaicism in his father. These findings based on clinical diagnosis and FISH analysis suggest that the mosaicism may have occurred early in embryogenesis leading to the disease in the father. This is the only reported case of CMT1A with transmission from a mildly affected mosaic father.

Materials and methods
SOUTHERN BLOT ANALYSIS
Genomic DNA was digested with the appropriate restriction enzymes and Southern blot was obtained as previously reported. DNA probes VAW409R3A(D17S122) and p132G8R1(PMP-22) were labelled with 32P-dCTP using primer extension and hybridised to the blot.

FISH ANALYSIS
Slides were prepared by standard cytogenetic protocols, and pretreated with RNase and pepsin to optimise the hybridisation. A YAC clone (49H7) which spans the smallest duplication region and includes the PMP22 gene and VAW409 was labelled with Biotin-16-dUTP (Boehringer) by a nick translation kit (Gibco BRL). After separation of the labelled probe using Sephadex G-50 spin column, 250 ng of the probe and 300 ng C0I DNA were added to a hybridisation mix consisting of 50% formamide, 20% dextran sulphate, and 2 × SSCP. The mixture was denatured at 80°C for 10 minutes and preincubated for 20 minutes at 37°C. The slides were denatured separately at 80°C for four minutes. Hybridisation was overnight at 37°C in a humidified chamber. Analysis of 125 interphase nuclei from the proband, his father, and a normal control was performed by counting the hybridisation signals per nucleus. Blood samples were not available from other members of the family.
Results
CLINICAL REPORT
The proband developed distal lower limb weakness at 10 years, and at the age of 19 required a right ankle arthrodesis. He noted some diminution in sensation in the feet but denied weakness or sensory loss in the upper limbs. He had a significant degree of bilateral sensorineural deafness. On examination his speech was slightly dysarthric and apart from his deafness his cranial nerves were normal. In the limbs there was no tremor, he had mild bilateral weakness of the intrinsic muscles of the hands, and marked weakness of ankle dorsiflexion. The ankle jerks were absent but knee jerks and all upper limb tendon reflexes were normal. Sensory loss was most marked in the feet and he had a painless ulcer over the head of the first left metatarsal. He had bilateral pes planus, clawing of the toes, and palpable enlargement of the common peroneal nerves. Electrophysiologically, the median motor nerve conduction velocity was 33 m/second, the median sensory action potential (MSAP) was 5 μV, and the ulnar sensory action potential (USAP) was 2 μV. His lateral popliteal motor conduction could not be measured as extensor digitorum brevis was denervated. His father had clawing of the toes from childhood and had been noted to be clumsy.

However, he was aware of increasing unsteadiness of gait from the age of 40 and some difficulty with coordination in the upper limbs from the age of 50. Neurological examination did not show any weakness in the lower limbs and all his tendon reflexes were intact. He had minimal sensory impairment in the feet, and had bilateral pes planus. Electrophysiological examination showed a normal median motor conduction velocity (54 m/second), a mild drop of the ulnar conduction velocity (46 m/second), and a significant slow sural sensory nerve conduction velocity (22 m/second). His ulnar sensory action potential was absent, and his median sensory action potential was 6 μV.

SOUTHERN BLOT ANALYSIS
The proband and his parents were homozygous for allele 1 with probe p132G8RL. However, with probe VAW409R3A the proband had two copies of allele 2 and one copy of allele 1, his father was homozygous for allele 2, while his mother was homozygous for allele 1.
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FISH ANALYSIS
Analysis of R banded metaphases of the normal control showed that the YAC clone 49H7 mapped to the CMT1A specific region (17p11.2-p12). Fig 1 shows hybridisation of Y49H7 in the mosaics. FISH analysis of interphases from a normal control showed the following distribution of signals: one signal in 3-5% of nuclei, two signals in 90%, and three signals in 6-5%. A comparative FISH analysis of a normal control, the mosaic father, and the duplicated patient is illustrated in fig 2.

Discussion
The use of FISH with the YAC clone 49H7 that lies within the duplicated region in CMT1A has resulted in the detection of a mosaic case for this disorder. A mildly affected father of an affected son with CMT1A was shown to have a duplication of 17p in 47-6% of interphase nuclei examined from peripheral blood. The mutation event most likely arose de novo during early embryonic development owing to misalignment of the sister chromatids of one chromosome 17, which can result in unequal crossing over, leading to duplicated progeny in the father. The Southern blot analysis with probe VAW409R3A in this family has clearly suggested that the proband had inherited two copies from the father and one copy from the mother. These results indicate that the proband is unlikely to have a de novo duplication. The new mutations for CMT1A duplication appear to be predominantly of paternal origin. The mechanism that underlies this mutation, in contrast to the present case, might be unequal non-sister chromatid exchange during spermatogenesis.

Examination of the proband's father showed minimal clinical findings. His electrophysiological findings are clearly abnormal in sural sensory and ulnar motor conduction but within normal limits of median motor conduction. This clinical picture will fit in with his being a mosaic.

Somatic mosaicism is an important cause of phenotype modification resulting in variation in the clinical expression of an inherited trait or disorder, with the proportion of affected cells in the expressing tissue(s) of the person concerned clearly being an important factor in determining phenotypic severity. Mosaicism for a specific gene mutation may be confined to somatic cells or the germline, or be present in both, depending on the developmental stage at which the lesion occurred. Germline mosaicism provides an explanation for the inheritance pattern in cases where multiple affected offspring are born to clinically and phenotypically normal parents. Moreover, if the germline of an affected subject is also involved, subsequent progeny may be at risk of developing a much more severe phenotype, for example, as in cases of osteogenesis imperfecta and Smith-Magenis syndrome.

The possibility of undetected mosaicism has been suggested in a CMT1A family. Mosaicism for deletion within this region of chromosome 17 has been previously reported. In this family, the mildly affected mother of a proband with Smith-Magenis syndrome associated with a visible deletion of 17p11.2-p12 was also found to have the deletion in 55% of cells examined. Our findings show the potential importance of using FISH as a first line diagnostic test for CMT1A, and at present the technique would appear to be the only way of detecting mosaicism in the disease. The result also raises the issue of whether parents of sporadic CMT1A cases should be tested by FISH to exclude the possibility of mosaicism.

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References
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