Atypical hereditary neuropathy with liability to pressure palsies (HNPP): the value of direct DNA diagnosis

Maria Sessa, Raffaello Nemni, Angelo Quattrini, Ubaldo Del Carro, Lawrence Wrabetz, Nicola Canal

Abstract
We report two patients with suspected hereditary liability to pressure palsies. Neurophysiological studies showed a mixed axonal-demyelinating sensory-motor polyneuropathy with focal slowing of conduction velocities at the common sites of entrapment. Morphological studies on sural nerve biopsy from the proband showed active axonal regeneration without typical tomacula. Molecular analysis confirmed the presence of a deletion of chromosome 17p11.2 in both patients. Our observation confirms the heterogeneity of hereditary liability to pressure palsies and the relevance of DNA testing for the diagnosis of this hereditary neuropathy.

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Hereditary neuropathy with liability to pressure palsies (HNPP) is an autosomal dominant disorder characterised by recurrent palsies or sensory disturbances after minor trauma to peripheral nerves. Pathological changes observed in peripheral nerves of patients with clinical and neurophysiological features of HNPP usually include sausage-like thickening of myelin sheaths, called tomacula.1 The majority of HNPP cases are characterised by a 1.5 Mb deletion in chromosome 17p11.2.2 After the introduction of DNA based tests for the diagnosis of HNPP, tomacula were described in the sural nerves from almost all biopsied patients with genetically defined HNPP.3,4

We report a family with clinical, neurophysiological, and genetic characteristics typical of HNPP in which morphological study performed in the proband did not show typical tomacula in the sural nerve biopsy.

Materials and methods
For morphological studies, a portion of sural nerve was fixed in 2% buffered gluteraldehyde and postfixed in 1% osmium tetroxide. After alcohol dehydration, nerve fragments were embedded in Epon 812. Transverse sections (0.5-1 μm thick) were stained with toluidine blue and examined by light microscopy. Morphometrical studies were performed as previously described.17

For molecular analysis, DNA was extracted from leucocytes from peripheral venous blood. Deletion of chromosome 17p11.2 was detected with quantitative or deletion breakpoint analysis by Southern blotting and by microsatellite polymorphisms by PCR. For Southern blotting, a single copy fragment of pVAW409R3a and pVAW412R3a, contained within the deletion, and a reference autosomal probe localised outside the deletion, detecting three EcoRI alleles of 4.2, 2.2, and 3.5 kb respectively, were used. The ratios pVAW409R3a/reference probe and pVAW412R3a/reference probe were expressed as a percentage of values obtained from control DNA.18 The breakpoints were detected on Southern blots of EcoRI/SacI digested DNA and hybridised with probe pJ7.8R.19 PCR was performed using the GT strand (CAGAACAAAATGTCTTGAGATC) and the CA strand (GGCAAGACGGCTCTG) oligonucleotide primers flanking the (GT)n repeat. The GT strand was labelled with γ-DATP using T4 polynucleotide kinase, according to the manufacturer's instructions. PCR was performed in a 100 μl final volume containing 300 ng genomic DNA, 50 mmol/l KCl, 200 mmol/l Tris HCl, pH 8.4, 1.5 mmol/l MgCl2, 100 μg/ml acetylated BSA, 50 pmol of cold primer, 4 pmol of labelled primer, 200 μmol/l each dNTPs, and 1.25 U Taq polymerase (Perkin Elmer, Norwalk, CT).

Results
CASE REPORTS
The father, a 45 year old man, reported the acute onset, three months earlier, of weakness and paraesthesia in the right hand after sustained pressure. On admission, the neurological examination showed normal cranial nerve function. Motor deficit was present in the distribution of the right ulnar and median as well as the right peroneal nerves where muscle strength was reduced to 4/5. Deep tendon reflexes were present with the exception of the right achilles tendon, which was elicitable with reinforcement manoeuvres. Plantar responses were flexor. Pes cavus and hammer toes were present. Vibration sensation was reduced distally in the legs; the other sensory modalities were preserved. Routine blood screening was negative; anti-GM1 antibodies were absent.

The son, an 18 year old parachutist, reported acute onset of weakness in his left shoulder after parachuting. Neurological examination
Figure 1  Transverse section of the sural nerve of the proband. There is a preferential loss of large myelinated fibres and numerous clusters of small myelinated fibres. No tomacula were detected. (Toluidine blue.)

Figure 2  Southern blot hybridisation pattern with probes pVAW412R3a, pVAW409R3a, and reference probe. The ratios pVAW409R3a/reference probe and pVAW412R3a/reference probe are approximately 50% of the ratios obtained from control patients. c: control patient. d: duplicated patient.

SOUTHERN BLOT ANALYSIS
Quantitative analysis by Southern blot showed that the ratios pVAW409R3a/reference probe and pVAW412R3a/reference probe were approximately 50% of the ratios obtained from healthy subjects (fig 2), suggesting that both patients have a single copy of pVAW409R3a and pVAW412R3a.

PCR ANALYSIS
Microsatellite analysis by PCR showed that both father and son have a single RM11-GT allele, each of different size (fig 3). The size of the son’s allele was the same as that of the mother. These data show that he inherited a deleted allele from his father and a normal allele from his mother.

BREAKPOINT ANALYSIS
In the mother four EcoRI/SacI restriction fragments of 6.0, 5.0, 2.8, and 1.8 kb respectively, corresponding to the CMT1A-REP restriction map, were detected. The additional 7.8 kb junction fragment generated by crossing over between the differential SacI and EcoRI sites in the CMT1A-REPs was detected both in the father and in the son, confirming the presence of the deletion in both patients (fig 4).

Discussion
HNPP is a distinct genetic entity whose clinical presentation may be extremely variable and should be differentiated from other hereditary or acquired neuropathies.
We report a patient with a clinical presentation suggestive of HNPP in whom pathological features were atypical and no tomacula were found in the sural nerve. The diagnosis, in the father and subsequently in his son, was confirmed by DNA testing.

Since the introduction of molecular studies, there has been only one report of three related HNPP patients in which tomacula were not found in the peripheral nerve. As pointed out by those authors, genetic analysis of that family was difficult because no probes from the deleted region were fully informative. They then performed quantitative analysis by Southern blotting using a reference probe located outside the deletion, which is a less sensitive technique. Moreover, one of the three patients with a normal biopsy was found not to be deleted.

Pathological studies are not sufficient for the diagnosis of HNPP. In fact, in our patient, sural nerve biopsy suggested axonal damage based on the presence of numerous clusters of small myelinated fibres that indicated axonal regeneration. Furthermore, many thinly myelinated fibres were present and no tomacula were detected. In the past, HNPP has been defined as tomacular neuropathy because of the presence, in the peripheral nerves, of characteristic sausage-like formations of the myelin sheath. Even if present, tomacula are not pathognomonic of HNPP, having been described also in other hereditary, acquired, and experimental neuropathies. Rather than on their presence, diagnosis of HNPP should rely on the number of tomacula. Generally, cases in which tomacula are not found have a more advanced neuropathy. This observation has been confirmed by studies in transgenic PMP deficient mice, suggesting that tomacula are unstable formations predisposing to subsequent myelin degeneration.

Recently, HNPP has been shown to be characterised by a 1.5 Mb interstitial deletion in chromosome 17p11.2. The introduction of DNA based tests for the diagnosis of HNPP has shown that the majority of clinically defined HNPP are deleted, although point mutations in the PMP-22 gene have been described and other genetic defects at other loci may be responsible for non-deleted patients. It has been reported that patients with PMP-22 point mutation showed a more severe phenotype, which is similar to the CMT1A phenotype.

It is now clear that HNPP is much more heterogeneous than previously thought from a clinical, morphological, and genetic point of view. Differential diagnosis is important for a correct prognostic evaluation and genetic counselling as well as for therapy.

Our observation, together with the previous report of Gonnau et al., supports the relevance of DNA analysis for the diagnosis of HNPP, especially when a family history is lacking. If the unequal crossing over hypothesis is correct, the prevalence of HNPP should be roughly similar to that of CMT1A. Up to now, the prevalence of HNPP seems to be underestimated both because of misdiagnosis and paucity of symptoms. Molecular analysis, which is less invasive than nerve biopsy, represents an important and specific tool for diagnosis of HNPP and should be used first. The routine use of molecular analysis would permit an estimate of the prevalence of the deletion and the selection of non-deleted patients to be analysed for new mutations.

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7 Mariman ECM, Gabreels-Festen AAWM, van Beersum SEC, et al. Evidence for genetic heterogeneity underlying...


