plays a major part in the perception of introra-
oral sensation, whereas facial sensation pro-
jects to the medullary portion of this
nucleus.

As our case indicates, a small lesion at the
lateral pontine tegmentum can cause a pure
and crossed orocutaneous sensory deficit, by
involvement of the rostral spinal trigeminal
nucleus and the lateral side of the pons.

mic tract, where the respective sensory fibres
from the mouth and the lower part of the
body are immediately adjacent (figure, C).

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**Hereditary neuropathy with liability to
pressure palsies with a partial deletion of the
region often duplicated in Charcot-Marie-Tooth
disease, type 1A**

Hereditary neuropathy with liability to pres-
sure palsies (HNPP) is an autosomal domi-
nant disorder characterised by recurrent
peripheral nerve palsies, paraesthesiae, and
less often by a prominent symmetric
polyneuropathy. Nerve biopsies show thick-
enings of myelin of normal type. Chance et al.1
found such patients to have a large chromosomal deletion located in the
region as in Charcot-Marie-Tooth disease
(CMT) neuropathy, type 1A. This region
contains a gene for peripheral myelin protein
22 (PMP22). The role of this gene in the
pathogenesis of HNPP has been shown by
the discovery of a frame shift mutation cre-
atting a null mutation and resulting in the
HNPP phenotype.2 In the case of deletion/
duplication, a gene dosage effect has been
proposed.3

In a family affected with HNPP, we found a
deletion at locus D17S122 including the
PMP22 gene and sparing distal loci
(D17S61 and D17S125), hence confirming
the expectation that deletion of a smaller
region than that previously described, but
including PMP22, is capable of causing
HNPP, and therefore supporting the role of
PMP22 in HNPP.

Patient I.1 developed leg weakness at the
age of 30. Since the age of 26, he had
noticed episodes of paraesthesiae on multiple
erve trunks, at first transient, then lasting
and needing several surgical decompressions.
At the age of 58, he had bilateral pes cavus,
distal weakness, severe muscle atrophy, and
axillary hyperhidrosis in both arms with trans-
ient paraesthesiae and cramps; sensory examina-
tion showed hypoesthesia in the left per-
onal nerve territory. In the upper limbs,
only muscle atrophy and mild weakness of
interosseous muscles were noted. All tendon
reflexes were absent. Motor nerve conduc-
tion velocities (MNCVs) were severely
slowed in median nerves (42 m/s on the right
and 40 m/s on the left) and radically altered
in the ulnar nerves (32 m/s on the right and
24 m/s on the left at the elbow). A nerve
biopsy showed severe loss of myelinated
fibres, some having an overthin myelin sheet.
Rare onion bulbs were present. Tomaculae
were found in 7% of the 300 internodes
studied on teased fibres.

His daughter (patient II.1), had presented
since the age of 26 with paraesthesiae and
episodes of weakness of one or two weeks’
duration in the peroneal, ulnar, or median
erve territories. At the age of 27, she had
pes cavus, severe peroneal muscle atrophy,
weakness, and distal extramembranous and par-
tially lemniscal sensory impairment in the
lower limbs. Motor sensory impairment was
noted in the left ulnar and median nerve
distribution. Tendon reflexes were all absent.
In the upper limbs, MNCVs were normal
in 1990, but in 1995 a bilateral entrapment of
the ulnar nerve at the elbow and a left carpal
tunnel syndrome were present. In the median
cross sections of the sural nerve showed a
slightly reduced large myelinated fibre den-
sity, tomaculae, and lesions of remyelination.
All the teased fibres presented features of
tomaculae and of demyelination and remyelination. Tomaculae were found in
39% of the internodes.

Molecular genetic studies were carried out
for both patients by Southern blotting analy-
sis (figure, A) and pulsed field gel elec-
trophoresis (PFGE) (figure, B).

Probe pVAW409R3a (D17S122)
disclosed only one band for both patients
when probed pEW401HE (D17S61) and
pVAW412R3HEc (D17S125) were heter-
zygous for the second patient. Density
scanning showed the presence of a single
pVAW409R3a allele in both patients, and
the presence of two alleles for the other
probes in the first patient. The same tech-
nique showed only one copy of the
PMP22 gene in the patients (not shown).

In PFGE analysis, hybridisation of Eagle-
digested DNA with CMT1A-REP probes
usually detects deletion and duplication
junction fragments in HNPP and CMT1A
respectively. 4 No such junction
fragments were found for our patients with
HNPP.
Thus in our patients, molecular genetic analysis disclosed a smaller deletion than that previously reported by Chance et al,\textsuperscript{1} spanning about 1.5 Mb and including all markers mapping within the CMT1A duplication. In both our patients, the PMP22 gene, the dosage effect of which is thought to be responsible for the neuropathy, was deleted as well as locus D17S122, whereas both alleles D17S61 and D17S125 were present.

In addition to the deletion described by Chance et al,\textsuperscript{1} other molecular results underlying HNPP have been reported: a 2bp deletion was described by Nicholson et al,\textsuperscript{2} by sequencing exon 1 of the PMP22 gene, and resulting in a reading frame shift mutation. In these affected patients, analysis of DNA disclosed the presence of two alleles for D17S122 and PMP22 probes. Mariman et al,\textsuperscript{4} described an absence of deletion in a family with HNPP established by biopsy. Moreover, these authors were able to exclude linkage of the PMP22 gene and the surrounding region with the disorder present in this family. Finally, Thomas et al,\textsuperscript{5} described histological features of tomaculous neuropathy in two patients with clinical findings of CMT associated with a mutation of the Po gene.

We emphasise the unusual character of our patients, in which they present a clinical CMT phenotype associated with the pathological features of HNPP. Prominent motor and sensory neuropathies with or without nerve palsies and HNPP pathological features have already been mentioned, but genetic analysis has only been reported by Thomas et al.\textsuperscript{5} However, Nicholson et al,\textsuperscript{2} did not find any difference in the phenotype of patients either with or without the typical deletion of HNPP. In the study of Mariman et al,\textsuperscript{4} the clinical signs in the family with no “HNPP deletion” were those of HNPP. Further studies could help to find out whether atypical clinical features are associated with a certain genotype.

Both HNPP and CMT1A are thought to result from a reciprocal DNA deletion or duplication of a fragment of 1.5 Mb on chromosome 17. A partial deletion in our patients was not unexpected as partial duplications of the concerned region have also been described in CMT and the present case could be a reciprocal recombination product of such a duplication.

Probe pNEA102 detected a 7-8 kb proximal and a 6-0 kb distal fragment belonging to CMT1A-REP repeat sequences flanking the duplicated region in CMT1A. In unaffected persons, two copies of the 7.8 kb fragment and two copies of the 6.0 kb fragment are present, whereas patients with HNPP lack one distal CMT1A-REP sequence and thus show loss of one copy of the 6.0 kb fragment with a subsequent difference in band density.\textsuperscript{1} We did not find a density difference between the 7.8 and 6.0 kb fragments of our patients with a partial deletion. Similarly, pulse field gel electrophoresis did not show the deletion junction fragments specific for patients with HNPP with a 1.5 Mb deletion. This finding suggests that sequences other than those detected by the pNEA102 probe are involved in the mutation process of this partial deletion.

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