Mutation in DHP receptor α1 subunit (CACLN1A3) gene in a Dutch family with hypokalaemic periodic paralysis

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Abstract
Hypokalaemic periodic paralysis (Hypo-PP) is characterised by transient attacks of muscle weakness of varying duration and severity accompanied by a drop in serum potassium concentration during the attacks. The largest known Hypo-PP family is of Dutch origin and consists of 277 members in the last five generations, 55 of whom have Hypo-PP inherited in an autosomal dominant pattern. Forty-eight persons including 28 patients with a proven diagnosis of Hypo-PP were used for linkage analysis. Microsatellite markers were used to exclude 45 to 50% of the genome and linkage to chromosome 1q31-32 was found. No recombinants were found between Hypo-PP and D1S412 and a microsatellite contained within the DHP receptor α1 subunit (CACLN1A3) gene. A previously reported G to A mutation causing an arginine to histidine substitution at residue 528 in the transmembrane segment IIS4 of the CACLN1A3 gene was shown in patients by restriction analysis of genomic PCR products.

Material and methods
PEDIGREE
The family has 277 members in the last five generations, 55 of whom have Hypo-PP. Forty-five affected persons were alive at the start of the investigations and 33 were personally investigated by one of the authors (TPL). Nineteen patients had typical attacks, myotonia, hypermyotonia congenita, and atypical myotonia congenita are all known from mutations at various sites in the gene coding for the α unit of the adult isoform of the skeletal muscle sodium channel (SCN4A) on chromosome 17q.
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Figure 1 The part of the Dutch HypoPP family used for linkage analysis. For a complete pedigree see Links et al.³⁰⁻¹¹

while 14 had muscle weakness without attacks.¹¹ The diagnosis of HypoPP was based on clinical history, neurological examination, and a reduced muscle fibre conduction velocity.²⁰ The diagnosis was based on the clinical history and notes from other hospitals in the remaining cases and in dead patients.¹⁰⁻¹¹ The mean age of onset of attacks was 15.6 (range 11–19) in men and 14.9 (range 9–18) in women. Forty-eight persons including 28 patients, all over the age of 20, were used for linkage analysis (fig 1). An autosomal dominant mode of inheritance was noted in the family. If the criteria mentioned above are used for diagnosis, the disease has complete penetrance.¹⁰⁻¹¹

DNA ANALYSIS
Blood samples were collected from 48 persons and genomic DNA was isolated by phenol-chloroform extraction.³¹ Typing of microsatellite markers was performed as previously described.²²⁻²³ Microsatellite markers from the Dutch Microsatellite Marker Collection²³ were used for the random gene search. For confirmation of linkage to chromosome 1q31–32, the following markers were used: D1S158, D1S53, D1S412, D1S413, D1S249, and CACNL1A3²⁴⁻²⁵; primer sequences are available through the Human Genome Data Base. PCR reactions were done on 50 ng of template DNA with \(\alpha^{32}\)P-CTP in a volume of 15 µl in 96 well microplates as previously described²³ except that end labelling of one of the primers was used for the CACNL1A3 marker. After electrophoresis, the gels were dried and exposed overnight to x-ray film (Kodak X-AR).

LINKAGE ANALYSIS
Two point and multipoint lod scores were computed with the LINKAGE program package version 5.¹⁰⁻²⁶²⁷ HypoPP was considered to be autosomal dominant with a penetrance of 100%. The frequency of the gene in the general population was estimated as 0.0001.¹⁷

MUTATION SCREENING
The G to A mutation in codon 528 of the CACNL1A3 gene causes the loss of a \(B_{bol}\) restriction site.¹⁹ Genomic DNA was amplified by PCR with the forward primer 5'-GGAGATCCTGCTGGTGGAGTCG-3' and the reverse primer 5'-TCCTCAGGAGGCGATGTCG-3' according to the protocol of Jurkat-Rott et al.¹⁰ After digestion with \(B_{bol}\), the PCR products were run on a 15% polyacrylamide gel. Normal controls show two bands of 44 bp and 33 bp; mutants show an additional band of 77 bp, representing the undigestable PCR product.

Results
At first, candidate regions containing ion channel or related genes were examined to exclude
Haplotype analysis showed several recombination between HypoPP and D1S158 and D1S53, but not with D1S412 and the microsatellite located within the CACNL1A3 gene. Recently Jurkat-Rott et al. found a G to A mutation in the transmembrane segment IS4 in several independent HypoPP patients. This mutation was also found in our Dutch HypoPP family.

This particular calcium channel is an oligomeric protein composed of two high molecular weight polypeptide subunits (α 1 and 2) and three smaller β, γ, and δ units. The α 1 units form the ion pore structure and also function as voltage sensors. The gene is mutated in the muscular dysgenesis mouse (mdg), a lethal autosomal recessive disorder in which there is a total lack of excitation-contraction coupling in homoyzgotes.

It is rather surprising to find a calcium channel gene defect implicated in the pathophysiology of HypoPP. As referred to above, most investigators have favoured other defects to explain the hypokalemic attacks. Nevertheless, early suggestions of disturbed Ca2⁺ release to the contractile elements and an enhanced deposition of Ca2⁺ in the sarcoplasmatic reticulum already suggested an inadequate release of calcium as the underlying defect in HypoPP. Furthermore, the skeletal muscle calcium channels do play a key role in the excitation-contraction coupling. These findings might contribute to the understanding of the occurrence of paralysis in HypoPP. Further studies need to be performed in order to elucidate the relationship between the calcium channel defect and the drop in serum K⁺ concentration and the pathogenesis of permanent progressive muscle weakness.

Discussion

Because this is the largest known family with HypoPP, our finding of linkage of HypoPP to chromosome 1q31-32 strongly supports the data of Fontaine et al. The penetrance of the gene defect appears to be complete, although the age of onset varies and the clinical manifestation may be permanent and progressive muscle weakness instead of paralytic attacks.

Figure 3 Multipoint analysis. Multipoint lod scores for the HypoPP locus with respect to chromosome 1q markers are shown.
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