Homozygosity mapping of autosomal recessive demyelinating Charcot-Marie-Tooth neuropathy (CMT4H) to a novel locus on chromosome 12p11.21-q13.11

A De Sandre-Giovannoli, V Delague, T Hamadouche, M Chaouch, M Krahn, I Boccaccio, T Maisonobe, E Chouery, R Jabbour, S Atweh, D Grid, A Mégarbané, N Lévy

**Key points**

- One Lebanese and one Algerian consanguineous family, comprising a total of 10 patients affected with autosomal recessive demyelinating Charcot-Marie-Tooth disease over three generations, were submitted to a genome-wide scan.
- The use of a homozygosity mapping approach showed linkage to a new locus (CMT4H) on chromosome 12p11.21-q13.11. Refinement of the linkage interval placed the CMT4H locus to a 11.5 cM region between markers D12S1648 and D12S1661, with a maximum LOD score of 6.97 (0.001) at marker D12S345. This interval spans about 15.8 Mb on the physical map and includes more than 90 genes.
- Mutation analysis of PRPH (a gene encoding a type III intermediate filament protein called peripherin) and CNTN1 (encoding contactin 1, a neuronal cell adhesion molecule) did not show any pathogenic mutation.
- The autosomal recessive demyelinating peripheral neuropathy segregating in the two families described here represents a novel entity which we designate CMT4H.

**LETTER TO JMG**

**Homozygosity mapping of autosomal recessive demyelinating Charcot-Marie-Tooth neuropathy (CMT4H) to a novel locus on chromosome 12p11.21-q13.11**

A De Sandre-Giovannoli, V Delague, T Hamadouche, M Chaouch, M Krahn, I Boccaccio, T Maisonobe, E Chouery, R Jabbour, S Atweh, D Grid, A Mégarbané, N Lévy

**METHODS**

Two families, one Lebanese (family 500) and one Algerian (family 295), including 10 individuals presenting with a severe form of autosomal recessive demyelinating Charcot-Marie-Tooth disease, were included in this study (figs 1 and 3).

**Abbreviations:**

CMT, Charcot-Marie-Tooth disease; LOD, log of odds ratio; STR, short tandem repeat
In the Lebanese family, patients 500.13, 500.14, 500.15, 500.17, and 500.21 had a clinical examination. The age at onset varied between 10 and 24 months. In all cases walking was delayed, to between 15 months to three years of age, gait was unsteady, deep tendon reflexes were absent, and mild symmetrical stocking-type hypoaesthesia was observed. All the patients examined except 500.21 presented with severe scoliosis and pes equinus with toe retraction. Patients 500.14 and 500.21 also had upper limb involvement consisting of thenar and hypothenar hypoplasia. Pupillary abnormalities, ataxia, nerve enlargement, tremor, deafness, and diaphragmatic or vocal cord paresis were absent in all patients. Progression of the disease was invariably slow.

Electrophysiological studies at the median nerve were carried out on Lebanese patients 500.14, 500.15, 500.17, and 500.21. Sensory action potentials could not be obtained, either in the median or in the sural or peroneal nerves. Severely reduced motor nerve conduction velocities at the median and cubital nerves, as well as low amplitude action potentials with prolonged distal latencies, indicated a peripheral nerve demyelinating process. A histological study of a sural nerve biopsy specimen was done in Lebanese patient 500.14 and showed a severe loss of myelinated fibres, probably secondary to a demyelination-remyelination process (fig 2). The remaining fibres had features of congenital hypomyelination as well as a small proportion of typical onion bulbs. Other signs of altered myelination were observed, such as circumscribed myelin swellings and proliferation, with or without myelin outfoldings (fig 2).

In the Algerian family, clinical and electrophysiological investigations were carried out in patient 295.6, but all patients had the same characteristics. The age of onset was two years. Neurological examination showed muscle weakness and atrophy in the distal extremities, marked feet abnormalities (pes cavus), absent tendon reflexes in the four limbs, ataxia, and a waddling gait. No cranial nerve abnormalities were noted. Dysmorphic features such as scoliosis and a short neck were present. Progression was slow until the age of 15. Electrophysiological results showed a severe demyelinating motor and sensory neuropathy, with similar results to family 500. Histological studies of a sural nerve biopsy were undertaken in Algerian patient 295.6, and the results were very similar to those obtained in the Lebanese patients (data not shown).

We investigated 29 individuals at the genetic level. After informed consent had been obtained from all affected individuals and parents of the children, EDTA blood samples were collected and genomic DNA was extracted from lymphocytes using standard methods. Exploration protocols were in accordance with the ethics guidelines of the institutions involved. After exclusion of linkage to loci CMT4A, CMT4B, CMT4F, CMT4G, a genome-wide screen was subsequently undertaken at the Centre National de Génétypage (CNG, Evry, France), using 400 polymorphic microsatellite markers with an average intermarker distance of 10 cM, as previously described.

In order to refine the size of the shared homozygous region, the following additional fluorescently labelled STR markers—chosen from the Généthon linkage map—were tested on all individuals collected in the two families: D12S1643 (AFMb013yb1), D12S1631 (AFMa288wd5), D12S1698 (AFM337tf5), D12S1648 (AFMb041xb9), D12S1653 (AFMb283xh5), D12S1661 (AFMb314yh5), D12S339 (AFM294w5c), D12S1635 (AFM196xa3), and D12S1677 (AFMb347vb9). Markers were amplified by polymerase chain reaction (PCR) under standard conditions and amplified fragments were separated by capillary electrophoresis on a Beckman CEQ 8800 genetic analyser (Beckman Coulter).

Parametric linkage analyses were carried out with an optimised version of the LINKAGE package, version 5.2, available free at Infobiogen (http://www.infobiogen.fr). Pairwise LOD scores were calculated using the MLINK program, assuming equal male–female recombination rates, autosomal recessive inheritance with complete penetrance, and a gene frequency of 0.002. Allele frequencies were chosen from the Genome Database (http://www.gdb.org), assuming that they were the same as those defined by Généthon in the white population.

The coding sequence and exon–intron junctions of two candidate genes (PRPH and CNTN1) were explored. Intronic primers were designed using the Primer3 software, available at the Massachusetts Institute of Technology (MIT, http://frodo.wi.mit.edu/) and DNA sequences obtained at the University of California Santa Cruz Human Genome Browser (UCSC, July 2003 freeze, http://genome.ucsc.edu/), by comparing genomic DNA with cDNA sequence (GenBank Accession Numbers: NM_001843 and NM_006262 for CNTN1 and PRPH respectively). Genomic DNA was amplified for one patient in each family under standard PCR conditions (primer sequences and amplification conditions are available on request). Amplified PCR fragments were fluorescently sequenced in both directions using sequencing facilities.
Chromatograms were compared with reference sequences using Sequencher v4.2 (Gene Codes Corporation, Michigan, USA).

**RESULTS**

We used a homozygosity mapping strategy, based on the assumption that in consanguineous families affected subjects of the same kindred are homozygous by descent, and for the disease causing mutation. Haplotypes were constructed manually from genotyping data and phases were assigned on the basis of the smallest number of recombinants. Analysis of the initial genome-wide screen data showed homozygosity in all affected individuals at markers D12S345 (AFM296yg5) and D12S85 (AFM122xf6) on chromosome 12q13.11. Significant linkage was obtained with a cumulative LOD score value of 6.97 and 5.09 at $\theta = 0.001$ respectively (table 1), although D12S85 was not fully informative in the Lebanese family (fig 3).

The minimum candidate interval at this point was restricted by D12S1617 (AFMa223yg1) on 12p12.1 and D12S368 (AFM128yd5) on 12q13.13, covering a 25.8 cM genetic region.

Additional genotyping of the nine STR markers allowed refinement of the candidate homozygous region in Lebanese patient 500.21 to a critical interval of approximately 11.5 cM between markers D12S1648 (AFMb041xb9) on the short arm of chromosome 12 (12p11.21) and D12S1661 (AFMb314yh5) on the long arm of chromosome 12 (12q13.11) (figs 3 and 4). The size of the interval is approximate because it overlaps the centromeric region of chromosome 12. In the candidate region defined above, all affected individuals were homozygous for the disease allele, and markers were informative in all matings, with the exception of marker D12S85, which was not fully informative in the Lebanese family (fig 3). All markers in the homozygous region show positive LOD score values with a maximum pairwise LOD score of 6.97 at $\theta = 0.001$ for marker D12S345 (table 1). More than 90 genes are described in the databases (GENATLAS, http://www.genatlas.org; UCSC, July 2003 freeze, http://genome.ucsc.edu/) within the candidate homozygous region.

No sequence variation was found in the coding sequence or in the exon–intron junctions of two genes, CNTN1 and PRPH. This probably excludes them as the genes responsible for CMT4H. However, further genotyping mapped PRPH outside the candidate interval (fig 4).

**DISCUSSION**

We describe the assignment of a new locus for autosomal recessive demyelinating Charcot-Marie-Tooth disease (CMT4H) to a genetic interval of approximately 11.5 cM at chromosome 12p11.1–q13.11 in an Algerian family and a large consanguineous Lebanese family. Disease haplotypes were not shared by the two families, excluding a founder origin of the disease. As this locus is the eighth one that has

---

### Table 1: Two point LOD scores between the CMT4H locus and informative STR markers on chromosome 12p11.1–q13.11

<table>
<thead>
<tr>
<th>Marker</th>
<th>$\theta = 0.001$</th>
<th>$\theta = 0.01$</th>
<th>$\theta = 0.05$</th>
<th>$\theta = 0.1$</th>
<th>$\theta = 0.2$</th>
<th>$\theta = 0.3$</th>
<th>$\theta = 0.4$</th>
</tr>
</thead>
<tbody>
<tr>
<td>D12S1643</td>
<td>0.71</td>
<td>2.01</td>
<td>2.80</td>
<td>2.77</td>
<td>2.11</td>
<td>1.24</td>
<td>0.45</td>
</tr>
<tr>
<td>D12S1631</td>
<td>5.48</td>
<td>0.93</td>
<td>1.86</td>
<td>1.99</td>
<td>1.60</td>
<td>0.94</td>
<td>0.30</td>
</tr>
<tr>
<td>D12S1698</td>
<td>0.51</td>
<td>0.89</td>
<td>1.76</td>
<td>1.79</td>
<td>1.24</td>
<td>0.56</td>
<td>0.09</td>
</tr>
<tr>
<td>D12S1648</td>
<td>5.64</td>
<td>6.28</td>
<td>6.27</td>
<td>5.71</td>
<td>4.20</td>
<td>2.52</td>
<td>0.96</td>
</tr>
<tr>
<td>D12S345</td>
<td>6.97</td>
<td>6.32</td>
<td>6.20</td>
<td>5.39</td>
<td>3.72</td>
<td>2.07</td>
<td>0.70</td>
</tr>
<tr>
<td>D12S1653</td>
<td>5.81</td>
<td>5.68</td>
<td>5.12</td>
<td>4.42</td>
<td>2.99</td>
<td>1.63</td>
<td>0.56</td>
</tr>
<tr>
<td>D12S85</td>
<td>5.09</td>
<td>4.97</td>
<td>4.51</td>
<td>3.92</td>
<td>2.70</td>
<td>1.50</td>
<td>0.54</td>
</tr>
<tr>
<td>D12S1661</td>
<td>3.35</td>
<td>3.92</td>
<td>4.02</td>
<td>3.63</td>
<td>2.51</td>
<td>1.31</td>
<td>0.36</td>
</tr>
<tr>
<td>D12S339</td>
<td>$\infty$</td>
<td>1.93</td>
<td>2.85</td>
<td>2.88</td>
<td>2.26</td>
<td>1.37</td>
<td>0.52</td>
</tr>
<tr>
<td>D12S1635</td>
<td>$\infty$</td>
<td>1.12</td>
<td>2.49</td>
<td>2.85</td>
<td>2.55</td>
<td>1.75</td>
<td>0.80</td>
</tr>
<tr>
<td>D12S1677</td>
<td>$\infty$</td>
<td>1.01</td>
<td>1.98</td>
<td>2.14</td>
<td>1.79</td>
<td>1.15</td>
<td>0.46</td>
</tr>
</tbody>
</table>
been mapped for autosomal recessive demyelinating CMT (CMT4), we named it CMT4H, considering that HMSN-Russe should be named CMT4G.

Recently, a locus for an autosomal dominant form of axonal CMT (CMT2G) has been mapped to the same chromosomal region,\textsuperscript{13} in an interval which partially overlaps the candidate region for CMT4H (fig 4). The overlapping region is 7.6 cM long (4.33 Mb) and contains about 35 genes.

Although the modes of transmission and the phenotypes are different between CMT2G and CMT4H, the two diseases could still be allelic. Indeed, mutations in several genes responsible for demyelinating CMT also result in axonal CMT—that is, \textit{GDAP1} mutations can result either in a demyelinating form of CMT (CMT4A)\textsuperscript{14} or in an axonal form (AR-CMT2C),\textsuperscript{11} but both of these have an autosomal recessive mode of inheritance. However, mutations in the same gene can be found in a heterozygous or a homozygous state; this is
the case for mutations in \( \text{PMP22} \), which usually cause autosomal dominant CMT1A,\(^{26}\) \(^{27}\) but are sometimes associated with a recessive pattern of inheritance.\(^{28}\) Nonetheless, fewer than half the CMT2G interval at the distal extremity overlap with the CMT4H critical region, suggesting that mutations in two distinct genes are likely to cause CMT2G and CMT4H. Further screening of candidate genes in families affected by CMT2G and in those presenting with CMT4H should definitely exclude the possibility that both diseases are allelic.

Of the 90 genes described in the databases (GENATLAS, http://www.genatlas.org) in the homozygous candidate, two candidate genes were tested for the presence of mutations in the coding sequence. The first, \( \text{PRPH} \), encodes a type III immunoglobulin superfamily, which mediates cell surface interactions during nervous system development. More precisely, in association with other proteins it plays a role in the formation of paranodal axoglial junctions in myelinated peripheral nerve.\(^{39}\) Although these functions are suggestive of implication in CMT, no disease causing mutations were identified in either gene, and \( \text{PRPH} \) has definitely been excluded as the causative gene for CMT4H, as it has been mapped outside the candidate interval by further genotyping (fig 4).

Further investigations are being undertaken to reduce the linkage interval and identify the molecular defect responsible for CMT4H. As the two families described here are from different ethnic backgrounds, it will be of value to test linkage to the CMT4H locus in more families presenting with severe demyelinating autosomal recessive CMT. A candidate gene screening strategy is also in process.

**ACKNOWLEDGEMENTS**

We express our gratitude to the families for their cooperation and their patience throughout the study. We are grateful to the team of the Medical Genetics Unit of Saint-Joseph University (Beirut-Lebanon) for their help in familial investigations and blood sampling. We also wish to thank the Centre National de Genotypage (CNG, Evry-France) for carrying out genome-wide screening, and Infobiogen (CRL, Evry-France) for allowing the access to linkage calculation software. This research project was supported by the network for rare diseases “GIS maladies rares”, the Association Française contre les Myopathies (AFM), and the Agence Universitaire de la Francophonie (AUF). Tarik Hamadouche is supported by a grant from INSERM/DRS for Franco-Algerian cooperation.

**REFERENCES**


CMT4H maps to chromosome 12p11.1-q13.11


