Identify a Location at Chromosome 19p in a Big Chinese Family with Charcot-Marie-Tooth Disease

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Abstract

Background: Autosomal dominant Charcot Marie Tooth disease (CMT) diseases is an inherited peripheral neuropathies disease, the prevalence is 17-40 per 100,000 individuals 17-40 per 100,000 individuals. The complex genetic mode and large number of CMT causing genes and loci made it is very hard for clinicians and researchers when trying to determine the underlying genetic diagnosis. In this work, we want to identify the cause for a Chinese family with Charcot-Marie-Tooth disease.

Methods: Family history data were recorded. Clinical and Electromyography examinations were performed on the ten affected and ten unaffected family members. All the members were genotyped with microsatellite markers at loci considered to be associated with CMT. Two-point LOD scores were calculated using the Linkage software after genotyping. Some highly suspect genes were excluded by direct sequencing.

Results and Conclusions: The clinical and pathological features were relatively gently, but which became gradually worse, with the increased genetic generation, and the onset age of the affected members. Linkage analysis was obtained at markers D19S433 (LOD score |Z|=2.03, recombination fraction (θ)=0.0) and D19S916 (Z=1.6, θ=0.0). Sequencing the dynamin 2 gene (DNM2) didn’t found any variation in the translated region. There may be some other gene or loci associated with this disease.

Keywords: CMT; Linkage analysis; Gene mutation; DNM2; MNCV

Introduction

Charcot-Marie-Tooth (CMT) disease is a genetically and clinically heterogeneous inherited disease, affecting peripheral neuropathies [1,2]. The prevalence of the disease is 17-40 per 100,000 people [3]. So far, more than 40 genes and 900 loci have been identified for their association with the disease (http://www.molgen.ua.ac.be/CMTMutations/Mutations/MutByGene.cfm). The hereditary modes of CMT include Autosomal Dominant (AD) demyelinating (CMT1), AD axonal (CMT2), autosomal recessive and X-linked (CMTX) forms. The highly complex genetic modes and extraordinary large number of loci to cause CMT make it difficult for clinicians and researchers to determine the actual underlying genetic etiology. CMT is also known as hereditary motor and sensory neuropathy (HMSN), because it also affects the motor and sensory nerves. Variable ages of onset and progressive distal muscle weakness and atrophy are the main clinical characteristics, usually starting from the lower limbs and subsequently affecting the upper extremities [4]. The most typical features of the disease are gradual atrophy of distal muscles of the feet and legs, and the thin legs have been likened to an “inverted champagne bottle”.

Point mutations and sequence deletions in the dynamin 2 (DNM2) genes have been associated with the CMT disease. In 2005, the DNM2 gene was first reported to be associated with CMT [5]. Since then, three point mutations and two sequence deletions in the DNM2 gene have been described in DNM2 related CMT disease [5,6]. But the full spectrum of genetic changes leading to this disease is yet unknown. Here, we report a 4-generation Han Chinese family with CMT; we located the responsible locus at chromosome 19p13.2-19q12, which is flanked by markers D19S433 and D19S916.

Materials and Methods

Affected and unaffected individuals in the family

We ascertained a 4-generational Chinese Han family with non-syndromic CMT (Figure 1) at the First Affiliated Hospital of Harbin Medical University, Harbin, China. Informed consent was obtained from each participant, consistent with the Declaration of Helsinki. We recorded their medical history in detail. Physical and electromyography examination was carried out on each of the family members. Genomic DNA was extracted from peripheral blood leukocytes using standard protocols.

Genotyping

Polymerase Chain Reactions (PCRs) were carried out with microsatellite markers close to candidate loci associated with autosomal
dominant CMT. PCR products from each DNA sample were separated on a 6% polyacrylamide gel and analyzed. Pedigree and haplotype data were managed using Cyrillic (version 2.1) software. Exclusion analysis was performed by allele sharing in affected individuals.

**Linkage analysis**

A two-point linkage was calculated with the LINKAGE (version 5.1) package. Autosomal dominant CMT was analyzed with full penetrance and a gene frequency of 0.001. Allele frequencies for the markers were assumed to be equal in both genders. The marker order and distances between the markers were taken from the NCBI (http://www.ncbi.nlm.nih.gov) databases.

**DNA sequencing:** Individual introns and exons of DNM2 were amplified by PCR using primer pairs shown in Table 1. The PCR products were sequenced on an ABI3130 Automated Sequencer.

**Results**

**Clinical data**

The proband was a 38-year-old male (III: 24; Figure 1), who had difficulties in walking and frequently tripped starting at the age of 4. Gradually, the other clinical manifestations were also observed, including loss of muscle bulk in the lower limbs, inability to lift feet, hollow feet and sensory loss in the feet (Figure 2). At the age of 30, he started experiencing mild weakness and muscle atrophy in the hands, resulting in problems with fine motor skills. Neurological examination showed reduced biceps and triceps reflexes, and patellar and plantar reflexes were absent. The touch and vibration sensations of distal lower extremities were lost. Finger-to-nose and heel-to-shin tests were normal. There was no disturbance of autonomic function. Nerve conduction studies showed that motor nerve conduction velocities were reduced, amplitudes were decreased, and distal latencies were prolonged. Median motor nerve conduction was 12.7 m/s. The Compound Motor Action Potential (CMAP) of the bilateral tibial nerves could not be elicited. Sensory nerve conduction velocities were reduced, amplitudes were decreased, and distal latencies were lost.

**Linkage and haplotype analysis**

All the candidate genes were examined by allele sharing and linkage analysis or direct sequencing. Linkage was found with markers D19S433 and D19S916, and the maximum LOD score was 2.03 (at θ=0). Haplotype analysis showed that the responsible locus was localized at chromosome 19p13.2-19q12, flanked by markers D19S433 and D19S916 (Figure 1 and Table 2).

**Mutation analysis for DNM2**

Direct cycle sequencing of the amplified fragments of DNM2 in all affected individuals did not reveal any variation in the translated region. We also analyzed additional genes with direct gene sequencing, including PMP22 (CMT1A and CMT1E), MPZ (CMT1B), LITAF (CMT1C), EGR2 (CMT1D) and YARS (DI-CMTC), but we did not find any variation in the translated regions of those genes either.

**Discussion**

The phenotypes of CMT disease vary greatly according to the families and pathogenic genes. The clinical features can range from severe muscle atrophy, sensory loss to no symptoms in affected members [7-9]. Notably, in the patients, the clinical symptoms became gradually worse and the onset age of the affected members were advanced with the increased genetic generation (Table 3). The clinical features of the second generation affected members were mainly the loss of deep tendon reflexes and sensation of distal extremities (II: 5,7,13,15); the third generation affected members were more serious, one affected (III: 21) showed absence of patellar reflexes and loss of the pain sensation of distal extremities; the clinical features of the proband (III:24) were more serious (Table 3).

The clinical and pathological features of CMT include approximately 88% CMT1A patients have slow Motor Nerve Conduction Velocities...
Table 2: Two Point LOD scores for linkage between disease locus and markers on chromosome 19.

<table>
<thead>
<tr>
<th>Marker</th>
<th>LOD scores by recombination fraction (θ)</th>
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<tbody>
<tr>
<td></td>
<td>0</td>
</tr>
<tr>
<td>D19S433</td>
<td>2.03</td>
</tr>
<tr>
<td>D19S916</td>
<td>1.60</td>
</tr>
</tbody>
</table>

Note: The highest observed LOD score was 2.03 (θ=0) for marker D19S433.

Because nerve conduction studies of the family showed that Motor Nerve Conduction Velocities (MNCV) were reduced, amplitudes were decreased, and distal latencies were prolonged. Median motor nerve conduction was 12.7 m/s. Sensory nerve conduction velocities were slightly reduced. Median sensory nerve conduction was 32.2 m/s. Therefore, we also focus on the seven genes by direct gene sequencing, since the genetic changes of these genes may lead to the same clinical phenotype.

Although significant linkage was found with markers D19S433 and D19S916, and haplotype analysis showed that the responsible locus was localized at chromosome 19p13.2-19q12. The DN2M gene was loci in this region. By direct gene sequencing, we didn’t found any variation in the translated region of the DN2M gene. But we found a “C” insertion in the DN2M gene intron between the exon3 and 4, in four affected family members (III:22, III:24, IV:3 and IV:4), the other affected or normal family members did not have the insertion (Figure 3). DN2M mutations can also be identified in DN2M-CN patients [9,18-20]. The clinical and pathological features of DN2M-CN were plantar muscle, calf and posterior atrophy [20], cardiac or respiratory failure, ptosis or ophthalmoplegia [18]. None of the patients in this family showed any abnormality in muscle, cardiac, respiratory or ocular. We also excluded the other genes, which had been identified linked with the CMT diseases, by allele sharing.

**Linkage analysis**

In conclusion, we described a four generation Chinese family with CMT disease. The clinical and pathological features were relatively gently, but which became gradually worse, with the increased genetic characteristics. Neuroepidemiology 35: 171-177.

**References**


