Frequency of mutations in the early growth response 2 gene associated with peripheral demyelinating neuropathies

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Materials and methods

Selection and phenotypical classification of the patients

One hundred and one unrelated probands presenting with peripheral neuropathy and without PMP22, MPZ, or GJB1 mutations were studied from the laboratory collections of Lyons (51 patients) and Cardiff (50 patients). They all presented with at least weakness and progressive wasting of the distal limb muscles, pes cavus, and absence of deep tendon reflexes.

The criteria for the classification of different conditions included:

- Congenital hypomyelination: hypotonia, delayed motor milestones, biopsy showing absence of myelination, NCV less than 10 m/s.
- Dejerine-Sottas syndrome: isolated CMT cases compatible with autosomal recessive transmission, NCV less than 10 m/s, onset in childhood. Biopsy, when available, must show demyelination.
- CMT1: NCV between 15 and 35 m/s associated with typical CMT phenotype.
- Unspecified phenotype: with the presence of only one bit of clinical information, either NCV or transmission mode.

Mutation analysis

The two exons of the EGR2 gene were analysed using nine overlapping primer sets based on the cDNA sequence. The coding region of EGR2 was amplified using 200 ng of genomic DNA, 0.5 U Taq polymerase (Eurobiotaq® DNA polymerase, Labo Eurobio, France), 2.5 µl 10 x PCR buffer, 0.75 µl 50 mmol/l MgCl₂ solution, 2 µl of each primer at a stock concentration of 20 mmol/l, 1 µl 10 mmol/l dNTPs, and H₂O to a total volume of 25 µl.

Amplification conditions were denaturation for one minute at 94°C, followed by 35 cycles of denaturation at 94°C for one
minute, annealing at the optimal temperature for each primer pair, and elongation at 72°C for one minute using the T Gradient Whatman Thermocycler 1999 (Biometra®, Goettingen, Germany). The PCR product was labelled with 1 μCi (0.1 μl) of [α-33P]dCTP or [α-33P]dCTP (Amersham Pharmacia Bio- tech, UK) in the reaction mixture.

For SSCP analysis, 5 μl of amplified DNA was mixed with 3 μl formamide sample buffer, denatured for five minutes at 100°C, and separated on a 25% Hydrolink MDE (BMA tech, UK) in the reaction mixture.

Patients T58 presented with an insertion of a triplet (A300-TAA). The mutation was absent in 70 normal control samples. A silent mutation in codon 300, a region which contains a repetition of alanine at position 300, a region which contains a repetition of alanine, upstream of the first zinc finger. T58 was a 23 year old male with distal and proximal muscle wasting and weakness. No affected subjects were present in preceding genera.

Table 1 Information on the 101 patients selected for EGR2 study

<table>
<thead>
<tr>
<th>Phenotypic classification</th>
<th>Origin</th>
<th>Sex</th>
</tr>
</thead>
<tbody>
<tr>
<td>LY</td>
<td>5</td>
<td>0</td>
</tr>
<tr>
<td>DSS</td>
<td>13</td>
<td>0</td>
</tr>
<tr>
<td>CMT1</td>
<td>33</td>
<td>25</td>
</tr>
<tr>
<td>Unspecified phenotype</td>
<td>0</td>
<td>25</td>
</tr>
</tbody>
</table>

DSS=Dejerine-Sottas syndrome, CMT1=Charcot-Marie-Tooth type 1, M=male, F=female.

Patient LY766.3 presented with a missense mutation in codon 381 (R381H: c.1142G>A), found in ampiclon 2.5b, which is located in the second zinc finger domain and leads to an amino acid substitution of His for Arg. This patient was a 9 year old girl with no family history of any neuromuscular disorder and her parents were not consanguineous. Her four brothers were healthy on clinical diagnosis. The patient's birth was normal but she presented with congenital hypotonia. Walking was acquired at 20 months. Very soon, left Duane syndrome (hypoplasia of the 8th cranial nerve, strabismus) was noted. Clumsiness was noted at the age of 3 at nursery school. The distal motor deficit was evident at the age of 5 in the lower limbs and at 7 in the upper ones. Right nystagmus was noted at the age of 8. Now, at the age of 9, the deficit is reaching the proximal part of the limbs, and sensory abnormalities are appearing in the distal part of the legs. The motor NCVs of the median nerve ranked between 7 and 14 m/s. This patient was classified in the CH group, despite the lack of a biopsy.

The R381H mutation was not present in the healthy parents of patient LY766.3, indicating that this is a de novo EGR2 mutation. This EGR2 mutation was absent in 70 normal control samples.

A silent mutation in codon 362 of the third base (R362R: c.1086A>C), found in ampiclon product 2.5c, was detected in six patients (6%), once in a DSS patient and five times in CMT1 patients. This mutation destroys a HinfI restriction site. The same mutation was present in two of 164 normal control samples (0.6%). Patient T14 with a CMT1 phenotype presents with a deletion of nucleotides 17, 18, and 19 downstream from the stop codon, found in PCR ampiclon 2.6 of the EGR2 gene (c.1442-1444delATA).

RESULTS

Classification of phenotype

The 101 patients (49 men, 52 women) with HMSN were classified in accordance with criteria described in the Materials and methods section. When clinical and paraclinical information was available, distinction was made between DSS, CH, and CMT1 (table 1). All patients had been screened and were negative for the CMT1A duplication and for mutations in GJB1, PMP22, and MPZ. The 33 CMT1 patients from the Lyon laboratory are familial cases with dominant transmission.

Mutations/polymorphisms

Nine patients had an altered SSCP pattern for EGR2 exon 2. Patient T58 presented with an insertion of a triplet (A300-301ins: c.900-902insGCA), found in ampiclon 2.4, coding for alanine at position 300, a region which contains a repetition of 10 alanines, upstream of the first zinc finger. T58 was a 23 year old male with distal and proximal muscle wasting and weakness. No affected subjects were present in preceding generations. However, this insertion in the coding sequence was not detected in the proband's 25 year old sister who presented with the same clinical features. This sequence variation was found only once in our collection of 101 patients and in 70 controls.

Patient LY766.3 presented with a missense mutation in codon 381 (R381H: c.1142G>A), found in ampiclon 2.5b, which is located in the second zinc finger domain and leads to an amino acid substitution of His for Arg. This patient was a 9 year old girl with no family history of any neuromuscular disorder and her parents were not consanguineous. Her four brothers were healthy on clinical diagnosis. The patient's birth was normal but she presented with congenital hypotonia. Walking was acquired at 20 months. Very soon, left Duane syndrome (hypoplasia of the 8th cranial nerve, strabismus) was noted. Clumsiness was noted at the age of 3 at nursery school. The distal motor deficit was evident at the age of 5 in the lower limbs and at 7 in the upper ones. Right nystagmus was noted at the age of 8. Now, at the age of 9, the deficit is reaching the proximal part of the limbs, and sensory abnormalities are appearing in the distal part of the legs. The motor NCVs of the median nerve ranked between 7 and 14 m/s. This patient was classified in the CH group, despite the lack of a biopsy.

DISCUSSION

Patient LY766.3 is part of a selected group of 18 patients with a severe phenotype and who presents with a heterozygous missense mutation in codon 381.

Cranial nerve involvement associated with R381H mutation may be related to the role of Krox20/EGR2 in brainstem development, because involvement of different cranial nerves has been rarely reported.10–11 Although oculomotor nerve palsy has not been reported before in DSS and CMT patients, a subclinical deficit cannot be excluded. The first two described cases of the R359W mutation with DSS were also associated with clinical cranial nerve involvement.10–11

It predicts an R381H substitution within the alpha helix of the second zinc finger. The DNA binding properties of the transcription factor are localised in the zinc finger domains and interact with DNA at the consensus EGR2 binding site (5′-GCCGGGGCG 3′).12 For DNA binding, the arginines are able to form hydrogen bonds on the G rich strand of the consensus binding site.12 These hydrogen bonds are most likely not established when the arginine residue is mutated to a histidine, suggesting that R381H is a loss of function mutation.12 The phenotype is probably the result of an altered interaction between EGR2 and the DNA binding sequence, since the protein sequence is highly conserved in that region.
To date, eight different mutations have been found in EGR2 (Table 2). The phenotypes in relation to mutations which fall within the region encoding a zinc finger domain are likely to be the result of the altered DNA binding properties of the transcription factor. The variation in clinical severity observed with the zinc finger mutations appears to correlate with the level of residual DNA binding. The most severe phenotype is associated with the mutant which confers the greatest level of DNA binding and transcriptional activation, while the least severe phenotype is observed in the mutant which shows no binding or transcriptional activity. This may explain the fact that DNA binding might be less affected by substitution of the cysteine residue than the histidine residue.

Six patients (6%) of our series had the R362R silent mutation (CGA→CGC) but the same polymorphism was found twice in 164 normal control samples. In another study, the same silent heterozygous mutation has been reported once in a patient with demyelinating neuropathy, but also once in 70 normal control samples. The frequency of this polymorphism in the general population should be about 2.5%.

The insertion of GCA, coding for alanine in position 300 of the EGR2 protein, is situated in a repeated sequence of 10 alanines, upstream of the first zinc finger. The insertion of the triplet does not disturb the open reading frame and there is no creation of a potential supplementary splice site as tested by a splice site prediction computer program. The repeated sequence forms an alpha helix, upstream of the first zinc finger domain. In mouse, the domain is partially conserved but is three alanines shorter. A modification of secondary structure shown any potential involvement in this group of peripheral neuropathies, have not observed for GJB1, PMP22, or indirectly. Sequence similarity searches for the EGR2 family in the other involved systems, and/or sensitivity of the PNS myelin to changes in myelin dosage (like in MPZ and PMP22). The specificity of the phenotype may reflect tissue specific interactions among the various constituents of the transcriptional machinery, complementation by the different members of the EGR2 family in the other involved systems, and/or sensitivity of the PNS myelin to changes in myelin dosage (like in MPZ and PMP22). Rather than acting as loss of function alleles, zinc finger mutations may instead be acting as dominant negative or gain of function alleles either by forming inappropriate interactions with cofactors, or by binding to inappropriate targets. Elucidation of the exact pathomechanism underlying these zinc finger mutants will require the identification of the relevant target genes in Schwann cells. Research showed no direct Krox20 binding to the MPZ promoter, although this study showed that Krox20 is capable of transactivating the MPZ promoter, but did not indicate whether it does so directly or indirectly. Sequence similarity searches for the EGR2 consensus binding site in the known promoters of PMP22 and GJB1, the other two myelin specific genes known to be involved in this group of peripheral neuropathies, have not shown any potential EGR2 binding sites.

Table 2 Previously reported EGR2 mutations

<table>
<thead>
<tr>
<th>No [Ref]</th>
<th>Mutation</th>
<th>Phenotype</th>
</tr>
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<tbody>
<tr>
<td>1 [1]</td>
<td>c.1225C&gt;T R409W substitution 3rd zinc finger</td>
<td>Familial CMT1 case with autosomal dominant transmission</td>
</tr>
<tr>
<td>2 [1]</td>
<td>c.803T&gt;a I268N substitution inhibitory domain R1</td>
<td>3 affected sibs (four boys) from consanguineous marriage with CH</td>
</tr>
<tr>
<td>3 and 4 [6,1]</td>
<td>c.1146T&gt;G + 1147G&gt;T S382R and D383Y substitution 2nd zinc finger</td>
<td>Patient with sporadic CH</td>
</tr>
<tr>
<td>5 [9]</td>
<td>c.1064A&gt;T D355V substitution 1st zinc finger</td>
<td>Severe CMT1 case (de novo mutation)</td>
</tr>
<tr>
<td>6 [10,11,14]</td>
<td>c.1075C&gt;T R359W substitution α-helix 1st zinc finger</td>
<td>3 cases with DSS (new mutations)</td>
</tr>
<tr>
<td>7 [13]</td>
<td>c.1141C&gt;T R381C substitution 2nd zinc finger</td>
<td>Familial moderate severe CMT1 case with autosomal dominant transmission</td>
</tr>
<tr>
<td>8 [12]</td>
<td>c.1142G&gt;A R381H substitution 2nd zinc finger</td>
<td>Familial CMT1 case with cranial nerve involvement (III, IV, V, VII, VIII, X, XI)</td>
</tr>
</tbody>
</table>
and CH (seven out of nine cases reported so far) but they are also, more rarely, associated with a CMT1 phenotype.

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