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.

Key points

- A panel of 101 patients with different clinical features of Charcot-Marie-Tooth disease was screened for mutations in the EGR2 gene.
- The presence of the CMT1A duplication and mutations in the GJB1, PMP22, and MPZ genes were preliminarily excluded.
- Only one mutation in a zinc finger domain of EGR2 was found in a patient with congenital hypomyelination.
- Three other sequence variants were found not directly associated with the disease.
- The frequency of mutations in the EGR2 gene is estimated to be less than 1% among CMT patients.

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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 (Eurolabataq® 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-32P]dCTP or [α-32P]dCTP (Amersham Pharmacia Biotech, 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 Biowhitaker Molecular Applications, Rockland, ME) gel at 12 W for 17 hours at room temperature. Some mutations were only detected by electrophoresis in the additional presence of 4% glycerol. Gels were vacuum dried and autoradiographed only detected by electrophoresis in the additional presence of 100°C, and separated on a 25% Hydrolink MDE (BMA Biowhitaker Molecular Applications, Rockland, ME) in the reaction mixture.

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Sequencing
The PCR products were purified (QIAquick PCR Purification Kit, Qiagen SA, Courtaboeuf, France) and sequenced using dideoxy terminator technology (PRISM™ Ready Reactions Rhodamine Terminator reagent set; Applied Biosystems, Foster City, CA) and an automated sequencer (ABI Prism 310, Applied Biosystems, Perkin Elmer).

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, DMP22, 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 amplicon 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 amplicon 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 11th 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 R362 of the third base (R362R: c.1086A>C), found in amplicon product 2.5c, was detected in six patients (6%), once in a DSS patient and five times in CMT1 patients. This mutation destroys a Hinfl 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 amplicon 2.6 of the EGR2 gene (c.1442-1444delATA).

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 have been rarely reported.1011 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 R335W mutation with DSS were also associated with clinical cranial nerve involvement.1011

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’ GCCGTCGGC G 3’).12 For DNA binding, the arginines are able to form hydrogen bonds on the G rich strand of the consensus binding site.13 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.13 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.

Table 1 Information on the 101 patients selected for EGR2 study

<table>
<thead>
<tr>
<th>Phenotypic classification</th>
<th>Lyon</th>
<th>Cardiff</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hypomyelination</td>
<td>5</td>
<td>0</td>
<td>5</td>
</tr>
<tr>
<td>DSS</td>
<td>13</td>
<td>0</td>
<td>13</td>
</tr>
<tr>
<td>CMT1</td>
<td>33</td>
<td>25</td>
<td>58</td>
</tr>
<tr>
<td>Unspecified phenotype</td>
<td>0</td>
<td>25</td>
<td>25</td>
</tr>
</tbody>
</table>

DSS=Dejerine-Sottas syndrome, CMT1=Charcot-Marie-Tooth type 1, M= male, F= female
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.\(^7\)

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.\(^7\) This may explain the fact that DNA binding might be less affected by substitution of the cysteine residue than the histidine residue.\(^6\)

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,\(^1\) 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.\(^3\) 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 in this region could be responsible for loss of function of the EGR2 protein.

Codon 300 falls within a probable R1 inhibitory domain. Does the insertion of an alanine abolish or perturb the interaction with coexpressors NAB1 and NAB2 which are known to increase the transcriptional activity of EGR2 as has been shown for the I268N mutation?\(^3\) The proband’s sister, however, shows the same phenotype and does not show the heterozygous insertion. We can thus deduce that the insertion probably has no pathological effect. We tested 70 normal control samples, none of which showed the polymorphism. We can conclude that the insertion is a very rare variant, with or without a minor effect on secondary structure of the R1 inhibitory domain of EGR2.

The patient who has deletion of three nucleotides with positions 17, 18, and 19 immediately following the stop codon has a CMT1 phenotype. Downstream of the termination codon, the primary transcript is cleaved some 15-30 nucleotides after a polyadenylation signal. In EGR2, the polyadenylation signal is located 1180 nucleotides beyond the termination codon.\(^1\) It is unlikely that the present deletion in some way affects the correct cleaving and addition of the poly(A) tail. Although not found in the 100 other patients of our series or in 70 normal controls, this is probably a very rare sequence variant. No relatives of this patient were available for analysis.

The fact that the CMT, CH, and DSS phenotypes are associated with mutations of the same gene has previously been observed for MPZ and PMP22. Altered expression of a dosage sensitive gene in the peripheral nervous system can modify myelin structure and could potentially cause CH, in much the same way that increased PMP22 expression owing to the CMT1A duplication results in CMT1.\(^3\) Discordance between PMP22 point mutations in humans and mice with both a severe phenotype and a mild phenotype produced by PMP22 +/- (heterozygous deletion of the gene) underlines the important fact that the partial deletion of PMP22 seems less deleterious than a point mutation. This finding suggests that point mutations in PMP22 are not responsible for simple loss of gene function but represent a toxic gain of function.\(^3\)

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,\(^3\) 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 GB1, the other two myelin specific genes known to be involved in this group of peripheral neuropathies, have not shown any potential EGR2 binding sites.\(^3\)

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 PMP22).\(^3\)

In conclusion, we confirm that EGR2 mutations are not frequent in HMSN and represent <1\% of the cases. Their occurrence seems restricted to the more severe phenotypes of DSS.

### Table 2 Previously reported EGR2 mutations

<table>
<thead>
<tr>
<th>No [Ref]</th>
<th>Mutation</th>
<th>Phenotype</th>
</tr>
</thead>
<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, XII)</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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