Diagnoses

Brief communication

A polymorphic AT-repeat causes frequent allele dropout for an MME mutational hotspot exon

Pathogenic variants in the MME gene cause dominant and recessive late-onset axonal hereditary neuropathy, that is, axonal Charcot-Marie-Tooth syndrome (LOCMT2). Here, we report next-generation sequencing (NGS) and Sanger sequencing (SS) results of 28 LOCMT2 patients carrying either the repeatedly reported c.467del p.(Pro156Leufs*14) or the c.440–2A>C variants. We demonstrate that an intronic AT-repeat in close proximity to these two mutations is frequently causing an allele dropout during SS that result in false genotyping in a considerable proportion of patients. This may result in an incorrect diagnosis, which has a considerable clinical impact for genetic counselling and prognosis.

Recent studies have demonstrated that both heterozygous and biallelic variants in MME (encoding the metalloprotease nerepi lyn) are a frequent cause of LOCMT2 (MIM: 617017).1–3 The heterozygotes variants cause a milder phenotype with reduced penetrance. Besides the large spectrum of rare or even single pathogenic MME variants, the frameshift deletion c.467del p.(Pro156Leufs*14) and the splice site mutation c.440–2A>C have been recurrently reported in patients with autosomal dominant and autosomal recessive LOCMT2.2,4 Although PCR is considered to be a robust technology and a reliable tool to be used for routine diagnosis, allele-specific sequence variations occasionally may provoke amplification failure of one of the two alleles at a given locus.4 Such an allele dropout has also been shown for the c.467del mutation in MME in one consanguineous family.4

In this study, registries at the Medical University of Vienna and Telemark Hospital Trust were searched for LOCMT2 individuals carrying the MME variants NM_007289.3:c.467del p.(Pro156Leufs*14) and NM_007289.3:c.440–2A>C. We ascertained 28 individuals from 16 families (MH1-MH16) afflicted with LOCMT2. For segregation analysis three healthy family members were also included. The families originated from Austria, Germany, Norway and Sweden.

Whole exome sequencing, NGS-based multigene panel sequencing or SS of the MME gene was performed and analysed as reported previously.5 SS was used to confirm MME variants detected by NGS and for segregation analysis in families. Due to conflicting results between NGS and SS at both laboratories, sequencing was repeatedly carried out using primers either including or excluding the adjacent AT-repeat of variable size, c.439+33_439+48AT[8-15], located 57 bp 5' of exon 6 (online supplemental material 1). Subsequently, six additional enzymes and two additional conditions for the original AccuPrime Taq DNA Polymerase System were tested to unravel the PCR enzymes' ability to amplify both the short and the long AT-repeat. A full list of the primers, enzymes and conditions used is described in the online supplemental material 1.

Moreover, the length of the intronic AT-repeats was assessed on 179 selected DNA samples by using NGS data, fragment length analysis (FLA) and/or multiplex ligation-dependent probe amplification (MLPA). FLA details are described in the online supplemental material 1, MLPA and NGS followed procedures as described.2,3

Tracking of the c.467del p.(Pro156Leufs*14) and the c.440–2A>C MME mutations previously detected by NGS or SS revealed conflicting results in 7/28 (25%) of the patients when using the original SS primers including the AT-repeat (table 1). In three families, MH-1, MH-2 and MH-6, the c.467del variant was first detected as heterozygous by NGS, but turned out to be homozygous by SS in several family members. On the other hand, in family MH-14, the index patient was tested heterozygous for the c.440–2A>C variant by NGS, whereas the same mutation was absent by SS. To unravel these discrepancies, an alternative primer-set

Table 1 Summary of results from SS, NGS and FLA in families MH-1 to MH-16

<table>
<thead>
<tr>
<th>Family</th>
<th>Patient ID</th>
<th>Result NGS</th>
<th>Result SS including AT-repeat</th>
<th>Result SS excluding AT-repeat</th>
<th>AT-repeat SS</th>
<th>AT-repeat NGS</th>
<th>AT-repeat FLA</th>
</tr>
</thead>
<tbody>
<tr>
<td>MH-1</td>
<td>3</td>
<td>c.467del/WT</td>
<td>c.467del/c.467del</td>
<td>c.467del/WT</td>
<td>8x/8x</td>
<td>8x/3x</td>
<td>8x/3x</td>
</tr>
<tr>
<td>MH-1</td>
<td>6</td>
<td>c.467del/WT</td>
<td>c.467del/c.467del</td>
<td>c.467del/WT</td>
<td>8x/8x</td>
<td>8x/3x</td>
<td>8x/3x</td>
</tr>
<tr>
<td>MH-1</td>
<td>7</td>
<td>c.467del/WT</td>
<td>c.467del/c.467del</td>
<td>c.467del/WT</td>
<td>8x/8x</td>
<td>8x/3x</td>
<td>8x/3x</td>
</tr>
<tr>
<td>MH-1</td>
<td>9</td>
<td>ND</td>
<td>c.467del/WT</td>
<td>c.467del/WT</td>
<td>8x/8x</td>
<td>ND</td>
<td>8x/8x</td>
</tr>
<tr>
<td>MH-1</td>
<td>10</td>
<td>c.467del/WT</td>
<td>c.467del/c.467del</td>
<td>c.467del/WT</td>
<td>8x/8x</td>
<td>ND</td>
<td>8x/8x</td>
</tr>
<tr>
<td>MH-1</td>
<td>11</td>
<td>c.467del/WT</td>
<td>c.467del/c.467del</td>
<td>c.467del/WT</td>
<td>8x/8x</td>
<td>ND</td>
<td>8x/8x</td>
</tr>
<tr>
<td>MH-1</td>
<td>12</td>
<td>c.467del/WT</td>
<td>c.467del/c.467del</td>
<td>c.467del/WT</td>
<td>8x/8x</td>
<td>ND</td>
<td>8x/8x</td>
</tr>
<tr>
<td>MH-1</td>
<td>13</td>
<td>c.467del/WT</td>
<td>c.467del/c.467del</td>
<td>c.467del/WT</td>
<td>8x/8x</td>
<td>ND</td>
<td>8x/8x</td>
</tr>
<tr>
<td>MH-1</td>
<td>14</td>
<td>c.467del/WT</td>
<td>c.467del/c.467del</td>
<td>c.467del/WT</td>
<td>8x/8x</td>
<td>ND</td>
<td>8x/8x</td>
</tr>
<tr>
<td>MH-1</td>
<td>15</td>
<td>c.467del/WT</td>
<td>c.467del/c.467del</td>
<td>c.467del/WT</td>
<td>8x/8x</td>
<td>ND</td>
<td>8x/8x</td>
</tr>
<tr>
<td>MH-1</td>
<td>16</td>
<td>c.467del/WT</td>
<td>c.467del/c.467del</td>
<td>c.467del/WT</td>
<td>8x/8x</td>
<td>ND</td>
<td>8x/8x</td>
</tr>
</tbody>
</table>

Results of NGS, FLA and SS using different primers with and without the AT-repeat. Contradicting results are highlighted in bold.

*Patient ID are listed according to the numbers on the pedigrees (figure 1A).

Due to lack of DNA, complete testing was not possible, but a homozygous long allele can be concluded from results obtained in the control group (data not shown).

Reference sequence according to NM_007289.3.

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Figure 1  (A) Pedigrees of the families (MH-1, MH-2, MH-16, MH-14) with conflicting results. The alleles for the mutations c.467del and c.440–2A>C are shown in red. The alleles for the AT-repeat are shown in blue. Brackets indicate estimated alleles. Empty: unaffected individuals; black: affected individuals; chessboard filling: unaffected/asymptomatic mutation carriers. Symbols with red frame: individuals with false result (homozygous) by Sanger sequencing (SS). Symbol with blue frame: individual with false result (wildtype) by SS. (B) Outline of exon 5–7 (NM_007289.3) of the MME gene. Exons (blue boxes), AT-repeat (orange), MME mutations (red arrows) and primers situated 5' and 3' of the AT-repeat (blue arrows) are marked. Top: SS traces from individual false homozygous for the c.467del mutation (top sequence trace) obtained with forward primer situated 5' of the AT-repeat and correct heterozygous c.467del result (lower sequence trace) obtained with forward primer situated 3' the AT-repeat. The false homozygous c.476del mutation is indicated by a yellow circle and a red arrow, the correct (heterozygous) c.476del mutation is indicated by a black arrow. Bottom: SS traces from an individual with a false wildtype at position c.440–2A>C (top sequence trace) obtained with a forward primer situated 5' of the AT-repeat and correct result (heterozygous, lower sequencing trace) obtained with a forward primer situated 3' of the AT-repeat. False wildtype at position c.440–2A>C is indicated by a yellow circle and a red arrow, correct heterozygous c.440–2A>C is indicated by a black arrow. (C) Fragment length analysis with AccuPrime Taq DNA (top) and Type-it Microsatellite PCR kit (bottom) analysed for three individuals. The fluorescence signal from each MME AT-repeat is shown as blue peak in the chart and the length of the AT-repeat is indicated by grey boxes below the peak. Acceptable error limits of repeat sizing are ±1. The fluorescence signal intensity (y-axis) is set at 7000. Reference sequence according to NM_007289.3.
to offspring, whereas a false negative diagnosis could influence further diagnostic and therapeutic procedures and has an impact for genetic counselling. Although to date, NGS is frequently applied for routine diagnostics, SS is still used for verification of a particular variant and segregation analysis in a family. The fact that a small increase in a repetitive sequence may lead to amplification failure is important to bear in mind when designing primers for SS as it may be relevant for other genes as well.

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REFERENCES


