Presymptomatic diagnosis of myotonic dystrophy

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Abstract
The discovery of an expanded (CTG)ₙ repeat sequence in myotonic dystrophy (DM) has greatly improved our ability to detect DM gene carriers who have few or none of the classical signs of this disorder. We report here our experience with two such groups of gene carriers. We used a PCR based protocol that should be especially sensitive to small increases in CTG triplet number which might escape detection by conventional Southern blot analysis. Our analyses show that on 100 non-DM chromosomes the number of CTG triplets ranged from five to 37. We then studied 17 obligate gene carriers aged 55 years and over who showed no muscle weakness. All of the gene carriers in this group showed a relatively small increase in the number of CTG triplets (52 to 90 CTG triplets) with limited somatic mosaicism. We subsequently studied 11 subjects (aged 19 to 36 years) who had previously been identified as gene carriers by genetic linkage studies, but who lacked diagnostic signs. In this prospectively studied group, nine subjects showed an expanded allele, confirming the earlier prediction from linked genetic markers. The other two subjects had only two normal alleles and no expanded allele. Revision of the clinical data casts doubt on the original diagnosis of DM in their families. Preferential amplification of the normal non-expanded allele was noted in three asymptomatic gene carriers in this study (as well as in two of their clinically affected relatives). We caution that, at least in our hands, the DM mutation can be confidently excluded by this PCR based method only if both normal alleles have been identified. If an expanded allele is not seen, and only a single normal allele is visualised on 6% PAGE, confirmatory testing with linked genetic markers or conventional Southern blotting of the (CTG)ₙ repeat is advocated.

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Myotonic dystrophy (DM) shows a wide range of clinical expression in affected subjects.¹ Severity of the disease is at least partly correlated with the number of CTG trinucleotide repeat units found in the 3' untranslated region of a protein kinase gene located in band q13.3 of chromosome 19.²-⁴ There is a marked tendency for an increase in CTG triplet number from one generation to the next, which is paralleled by earlier onset of the disease in successive generations,¹¹² a phenomenon known as anticipation. Genealogical studies in DM families¹¹² suggest that in earlier generations additional asymptomatic gene carriers may have been present, presumably with only a minor expansion of the CTG motif. However, a premutation not involving expansion of the CTG trinucleotide repeat is another possibility. This situation is highly reminiscent of the CCG repeat expansion seen in the fragile X syndrome.¹⁶¹⁸ Our previous study using linked DNA markers has suggested that a considerable proportion of sibs and offspring of DM patients are asymptomatic in early adulthood.¹⁹ Therefore, asymptomatic subjects may not be confined to the early generations of a DM family.

We studied these issues in detail by assaying the CTG triplet number in 17 obligate carriers of the DM gene as defined by pedigree analysis and genealogical studies. We further studied a group of asymptomatic offspring of DM patients who had been identified previously as probable gene carriers by the application of closely linked DNA markers.

Methods
Families were ascertained through the DNA diagnostic service in our department. As from January 1992, this service has performed diagnosis with linked DNA markers in 164 DM families, of which 76% were referred by other genetic departments. Care was taken to ensure that all families met previously defined diagnostic criteria.²⁰ For the purposes of this study, we selected 13 families that contained one or more obligate gene carriers aged 55 and over who showed no muscular weakness. Obligate gene carriers were identified by pedigree analysis or through genealogical studies that linked independently ascertained pedigrees. There were 14 males and three females in this group, ranging in age from 55 to 92 years (mean 69-8 years). Among 17 obligate gene carriers, seven had undergone cataract surgery. The other 10 were considered asymptomatic. EMG and slit lamp examination had been performed in six out of 10. Typical lenticular opacities were noted in three out of six. EMG was normal in all six. In addition, 11 subjects from nine families were restudied, as our previous study²⁰ had indicated a high probability of carrying a DM mutation in spite of normal results on clinical examination. We used data from 50 normal Dutch subjects (100 chromosomes) who had married into DM
Figure 1 Distribution of allele sizes for 100 non-DM chromosomes. Allele sizes are given as the number of CTG triplets.

families to establish the normal range of CTG triplet number for controls.

Chromosomal DNA was isolated from peripheral blood. Genetic marker systems flanking the DM mutation have been described previously. Using a recently described PCR assay, we tested the expansion of the CTG repeat in genomic DNA. The CTG repeat was amplified with flanking primers 406 and 409 reported by Mahadevan et al. The resulting DNA fragments were resolved on 1% and 4% agarose gels. A Southern blot, made from the 1% gel on Gene Screen Plus, was screened with a 32P end labelled (CTG)10 oligonucleotide as a probe, and the hybridising fragments were subsequently visualised by autoradiography. Alleles containing up to approximately 140 CTG triplets could also be identified on a 6% polyacrylamide/7 mol/L urea sequencing gel after 32P end labelling of one of the amplification primers.

Results

NORMAL CONTROLS

Data from 100 normal chromosomes are summarised in fig 1. Allele lengths were found to range from five to 37 CTG triplets. The most common alleles in this sample were five, 13, and 14 CTG triplets (38, 22, and 15% respectively).

OBLIGATE CARRIERS

All of the 17 obligate gene carriers (14 males and three females) showed an expanded allele with multiple bands and weaker signals on 6% polyacrylamide gels, different from normal alleles at this locus (five to 37 CTG triplets). Allele size (estimated from the strongest signal among these multiple bands) ranged from 52 to 90 CTG triplets (fig 2). The apparent instability of the expanded allele could represent an in vitro artefact of the PCR reaction. However, in view of the strikingly different appearance of the 37 and 52 CTG triplet signals, it is more likely that the CTG repeat shows somatic mosaicism in vivo above a threshold of approximately 40 to 50 CTG triplets. With one exception (II.7, fig 3), CTG repeats were found to be larger in offspring than in these obligate carriers, confirming that the expanded repeat sequence was unstable.

A striking example of anticipation is shown in fig 3. In this family, two subjects (I.3 and II.7), aged 90 and 53 respectively, are asymptomatic on full examination, including EMG and slit lamp examination, except for a few typical lenticular opacities in I.3. A third subject (I.1) is also completely normal at the age of 85, but no EMG has been performed. These obligate heterozygotes showed CTG triplet numbers of 52, 60, and 52 respectively, based on results of 6% PAGE (lanes 16, 15, and 17, fig 2). The 1% agarose Southern blot of the PCR product shows the expected band of approximately 0.2 kb for these subjects. Above this band, a smear can be detected, which is frequently observed for alleles of this size, and which may be the result of heteroduplex formation of normal and expanded alleles, rather than somatic mosaicism. Symptomatic disease has been diagnosed in the descendants of these obligate carriers (III.1, 2, 3, fig 3). These
show extensive expansion subjects (I.1, asymptomatic 782 respectively. Clinically 1% (determined 2 0 m lid 200 affected a polyacrylamide gel analysis of PCR amplified C1TG 480 111.7), subjects repeat.}  

**Figure 3** Southern blot analysis of PCR amplified CTG repeat sequence run on a 1% agarose gel in a DM family. Transmission of DM through three clinically asymptomatic subjects (I.1, I.3, II.7), aged 90 years, 85 years, and 53 years, who show only mild expansion in this assay. CTG triplet numbers for these obligate carriers (determined from 8% polyacrylamide gel electrophoresis) were 52, 52, and 60 respectively. Clinically affected subjects (II.4, II.5, III.1, III.2, III.3) show more extensive expansion of the CTG repeat.

An expanded allele was not initially detected in three subjects with the primer pair (406 and 409 from Mahadevan et al) used in this study in spite of multiple (up to five) attempts. These subjects had previously been predicted to be gene carriers by linkage analysis. Since only a single normal allele was seen on 6% polyacrylamide gel electrophoresis, we assumed that an abnormal allele was present but undetectable. By choosing another primer combination (primer 406 from Mahadevan et al and a new primer GCC.ACA.GAA.GCC.CGG.CCC.ACC, nt position 11–32) the presence of an expanded allele was confirmed in two subjects. In the third subject an expanded allele could only be shown by direct restriction analysis and Southern blotting of the genomic fragment containing the CTG repeat sequence.

**Discussion**

We show here that asymptomatic carriers of the DM gene mutation can be diagnosed by PCR based analysis of the CTG trinucleotide repeat. This method is especially helpful in determining the origin of the mutation when both parents are clinically unaffected and the family history is negative.

Among 17 cases aged 55 years and over without muscle weakness, none showed an allele exceeding 90 CTG triplets. Larger alleles may not be compatible with absence of muscular symptoms in middle and old age. However, more data are needed before predictions are possible for individual cases.

Our results confirm the paucity of new mutations in DM suggested by genealogical studies, since subjects identified as obligate gene carriers always carried an expanded allele. This is consistent with the results of studies showing linkage disequilibrium in various populations. In fact, the finding of linkage disequilibrium in DM is difficult to explain, unless we assume that either the penetrance of the DM gene is virtually zero for many generations as suggested by the anticipation model, or that carriers of the DM mutation have increased fecundity, or both. The finding that all of the asymptomatic obligate carriers defined by pedigree analysis or genealogical studies showed only a small increase in CTG triplet number (52 to 90 CTG triplets) supports the anticipation model of DM. In
Results of CTG analysis in 11 asymptomatic subjects considered to be at high risk of carrying a DM mutation by linked DNA markers.

<table>
<thead>
<tr>
<th>Subject*</th>
<th>Age</th>
<th>Sex</th>
<th>Affected parent</th>
<th>Clinical examination</th>
<th>CTG analysis</th>
<th>Remarks</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>19</td>
<td>M</td>
<td>Father</td>
<td>Normal</td>
<td>Expanded smear (&gt;200 CTG triplets)</td>
<td>Mental retardation</td>
</tr>
<tr>
<td>2</td>
<td>19</td>
<td>M</td>
<td>Father</td>
<td>Atypical lens changes, equivocal clinical myotonia/normal EMG</td>
<td>Expanded smear (&gt;200 CTG triplets)</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>33</td>
<td>M</td>
<td>Father</td>
<td>Normal</td>
<td>Expanded smear (&gt;200 CTG triplets)</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>33</td>
<td>F</td>
<td>Father</td>
<td>Normal</td>
<td>Approximately 74 CTG triplets</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>24</td>
<td>F</td>
<td>Mother</td>
<td>Normal</td>
<td>Approximately 60 CTG triplets</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>29</td>
<td>M</td>
<td>Normal</td>
<td></td>
<td>Not at risk</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>36</td>
<td>F</td>
<td>Father</td>
<td>Slight ptosis, atypical lens changes</td>
<td>Expanded smear (&gt;200 CTG triplets)</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>28</td>
<td>F</td>
<td>Normal</td>
<td></td>
<td>Normal</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>33</td>
<td>M</td>
<td>Mother</td>
<td>Normal</td>
<td>Approximately 61 CTG triplets</td>
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</tr>
<tr>
<td>10</td>
<td>38</td>
<td>M</td>
<td>Mother</td>
<td>Normal</td>
<td>Approximately 88 CTG triplets</td>
<td></td>
</tr>
<tr>
<td>11</td>
<td>21</td>
<td>M</td>
<td>Father</td>
<td>Normal</td>
<td>Expanded smear (&gt;200 CTG triplets)</td>
<td></td>
</tr>
</tbody>
</table>

* Subjects at high risk were identified in a previous study of 139 asymptomatic offspring of DM patients.†
† Clinical examination included EMG, neurological examination, and slit lamp examination. Non-specific signs (such as colourless opacities or mental retardation) were found in three out of nine (33%), compared to 24 out of 128 (19%) at those at low risk.
‡ Based on results of 1% agarose gel electrophoresis and 6% polyacrylamide gel electrophoresis of PCR amplified products.
§ After DNA marker analysis, repeated EMG examination was performed, and myotonia was diagnosed.
¶ After DNA marker analysis, DM was diagnosed in a son.

spite of anticipation, the DM mutation may occasionally remain clinically silent, even among sibs and offspring of symptomatic cases. In five of our patients, (aged 19, 19, 21, 33, and 36 respectively) careful clinical examination including EMG and slit lamp examination failed to show any definite sign of DM. This may appear surprising since each showed an expanded allele which clearly exceeded 200 CTG triplets (subjects 1, 2, 3, 7, and 11 in the table). Follow up studies are required to establish whether these subjects will develop muscular symptoms in later life. So far, repeated EMG studies (performed after the results of the DNA analysis were known) have shown myotonic discharges in two of them (subjects 3 and 7, table). Neither clinical myotonia nor significant muscle weakness was detected on re-examination. In the other asymptomatic cases, CTG triplet numbers of 60, 61, 74, and 88 were within the range found for obligate gene carriers without muscular symptoms after the age of 55.

We currently estimate the chance that a clinically normal sib or offspring of a DM patient carries a mutated gene to be 78% for those aged between 20 and 39 years of age. This figure is very similar to our previous estimate in the same sample of DM families (83%).19 We have now excluded two subjects because of unreliable diagnosis, we had formerly anticipated the reclassification as low risk of two subjects because of genetic recombination with the marker loci.19 In addition, our study confirms that at the molecular level anticipation is the rule in DM, since in our sample of nine asymptomatic offspring we always found a CTG triplet number equal to or exceeding that of the affected parent. Finally, we do not know the explanation for the family in which expansion of the CTG repeat was not detected in either clinically affected member. Such families have been noted by others.1 It remains to be seen whether the results in these families are the result of diagnostic error or allelic mutation. The existence of allelic mutations, not causing expansion of the CCG repeat sequence, has been suggested for the fragile X syndrome.3

Finally, we want to stress that in subjects with only a single normal band by PCR, the DM mutation should not be considered excluded, because of the possibility of preferential amplification of the normal allele. In such instances, additional studies are required, using either alternative primer combinations, conventional Southern blotting of genomic fragments, or linked genetic markers. Only when such studies confirm the presence of normal alleles only, can the consultant be reassured that future offspring will not be at risk.

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