A TaqI map of the dystrophin gene useful for deletion and carrier status analysis

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Abstract
We describe a partial TaqI map of the dystrophin gene, obtained mainly by analysis of 87 overlapping DMD/BMD deletions with small fragments of the dystrophin cDNA probes; exon 6 of the dystrophin gene was identified on the TaqI map using the polymerase chain reaction. The cDNA probes detect five polymorphisms with TaqI, more than with HindIII (one), BglII (four), or PstI (three). The five polymorphisms are analysed concomitant with screening for deletions on the TaqI map, and in the one-third of DMD/BMD cases with no detected deletion the polymorphism information may be used for counselling. Correlation of the TaqI map with the HindIII map in the region of probes 5b–7 and 8 allowed the establishment of reading frame in this region of the dystrophin gene, all of 41 DMD deletions resulting in a shift of reading frame and all of 10 BMD patients maintained reading frame, in agreement with the 'reading frame hypothesis'.

Duchenne and Becker muscular dystrophies (DMD/BMD) both arise from mutation of the dystrophin gene on the short arm of the X chromosome. In most cases, deletions of the dystrophin gene are detected, allowing direct DNA based prenatal and carrier diagnosis.1,2 However, in approximately one-third of cases, no mutation is detected and counselling is offered by linkage analysis of polymorphic markers. The entire dystrophin cDNA has been cloned and the HindIII exon containing fragments have been ordered into a partial map.3 The normal exon containing restriction fragments and polymorphisms detected by hybridisation with the cDNA probes have been described for HindIII and BglII, and polymorphisms were reported for two additional restriction enzymes, PstI and TaqI.4 In order to facilitate concomitant screening for deletions, duplications, and polymorphisms, we characterised the normal cDNA hybridisation pattern for TaqI and arranged the exon containing fragments into a partial TaqI map.

Materials and methods
CLINICAL EVALUATION
A total of 128 families (98 DMD and 30 BMD) was examined by neurologists of the MDA clinics at Duke University Medical Center, Durham, NC, USA, and the Australian Neuromuscular Research Institute, Queen Elizabeth II Medical Centre, Perth, WA, Australia. One additional sample of patient DNA was provided by Dr M J Denton, the Prince of Wales Hospital, Sydney, NSW, Australia. The probands were diagnosed using standard clinical diagnostic criteria for DMD/BMD in conjunction with raised creatine kinase activity and typical dystrophic changes on muscle biopsy. Diagnosis was also confirmed in 14 families by dystrophin analysis (Genica, Inc, Worchester, MA) or immunohistochemistry using antidystrophin antibodies.5

RESTRICTION DIGESTION, SOUTHERN TRANSFER, AND HYBRIDISATION
DNA isolated from whole blood or from lymphoblast cell lines was digested with restriction enzymes TaqI, HindIII, BglII, or PstI (BRL, Gaithersburg, MD, USA; NEB, Beverly, MA, USA; Toyobo, Kitaku, Osaka, Japan). The resulting DNA fragments were separated by agarose gel electrophoresis, Southern transferred onto GeneScreen Plus membrane (NEN DuPont, Boston, MA), hybridised to an olioglabelled probe, and autoradiographed. These methods have been described in detail previously.1,6

DNA PROBES
The six probes comprising the 14 kb dystrophin cDNA were kindly provided by Dr L M Kunkel1 or were obtained from ATCC. To order the TaqI exon containing fragments, probes 1–2a, 5b–7, and 9–14 were each divided into smaller probe fragments (fig 1) for

Figure 1  Dystrophin cDNA probe fragments. Restriction enzymes: B = BamHII, C = HindIII, E = EcoR1, G = BglII, H = HindIII, P = PstI, X = XbaI.
Figure 2  Normal hybridisation pattern of the cDNA probes for TaqI. (A) cDNA probes 1–2a to 5b–7, (B) cDNA probes 8 to 11–14. Constant bands are indicated by horizontal bars; the five polymorphisms are indicated by arrows (sizes in kb). DNA in the left hand lane for probe 2b–3 and the right hand lane for probe 8 is from a female; all other lanes contain DNA from males.

hybridisation in some experiments. Probe 5b–7 was used to prepare two different sets of probe fragments, so that the order of TaqI exon containing fragments at the 5' end of this
region could be resolved. Digestion of the EcoRI insert of probe 5b–7 with XbaI and HindIII yielded probe fragments 5b–7–a, 5b–7–b, and 5b–7–c, which were used for routine deletion screening; digestion of the 5b–7 insert with PstI and BglII yielded alternative probe fragments 5b–7–P and 5b–7–G (fig 1), plus two small fragments (0.2 and 0.5 kb) not used for hybridisation.

PCR AMPLIFICATION

Oligonucleotide primers for exon 6 were designed from the published sequence of the gene\(^6\): forward 5’-GTC AAA ATG GTA ATG AAA ATAT ATG-3’; reverse 5’-TAT GAC TAT GGA TGA GAG CAT TCA AAG-3’. Amplification was performed using Taq DNA polymerase (Biotech International, Bentley, Western Australia) with 5 ng target DNA in a final volume of 25 μl under the supplier’s reaction conditions. The cycle profile was: 94°C for three minutes, 55°C for one minute, 75°C for two minutes (one cycle); 94°C for 30 seconds, 55°C for one minute, 75°C for two minutes (39 cycles).

Results

The normal hybridisation pattern of the cDNA probes on TaqI digested DNA shows a total of 68 exon containing TaqI fragments, representing approximately 250 kb of genomic DNA (fig 2). The cDNA probe 1–2a detected 10 TaqI fragments, with four of these detected by 1–2a–a and seven by 1–2a–b. Both parts of 1–2a detected the 1.8 kb fragment containing the cDNA HindII site of exon 4.\(^4\) Probe 2b–3 detects a two allele RFLP and eight constant fragments. One of the constant fragments (2.4 kb) is also detected by probe 1–2a owing to overlap of the two probes in exon 11.\(^5\) Probe 4–5a detects eight fragments. Probe 5b–7–a detects six constant fragments and a two allele RFLP. Probes 5b–7–b and 5b–7–c detect three and four fragments, respectively. Probe 8 detects two allele RFLP and four constant fragments, one of which (3.9 kb) is also detected by 5b–7–c. A common fragment is also detected by these two probes on HindIII digests.\(^3\) Probe 9 detects five constant fragments; probes 10 and 11–14–a both detect a two allele RFLP, as well as five and eight constant fragments, respectively. Probe 11–14–b detects four constant fragments; one of these (4.4 kb) is also the only fragment detected by 11–14–c.

The cDNA probes 2b–3, 5b–7–a, 8, 10, and 11–14–a each identified a TaqI RFLP, making a total of five cDNA RFLPs which are detected with this enzyme, spanning the length of the dystrophin gene\(^1\) (table 1). When intact cDNA 5b–7 is hybridised to TaqI blots, the lower 1.7 kb allele comigrates with a constant band, so that densitometric scanning of the autoradiograph is necessary for RFLP analysis.\(^6\) However, the smaller cDNA fragment 5b–7–a detects the RFLP but not the comigrating constant fragment, so that RFLP analysis can be performed directly (fig 2). The 1.7 kb constant band is detected by probe segment 5b–7–c.

A total of 128 patients (98 DMD, 30 BMD) was screened with the cDNA probes, and deletions were observed in 72% (71/98) of DMD cases and 53% (16/30) of BMD cases, for an overall deletion frequency of 68%. In two of the DMD cases, all exon containing bands were detected, plus an additional junction fragment, seen both on TaqI and BglII digests; these cases were presumed to arise from duplication events. TaqI and HindIII digests of individual DNA samples were screened sequentially with the entire cDNA in most cases, allowing the extent of any deletion to be determined. Deletions in different families were compared, and regions of overlap were used to determine the order of TaqI exon containing fragments (fig 3). The TaqI fragment corresponding to exon 6 was identified by hybridising radiolabelled reaction product from a PCR reaction to a TaqI digest previously hybridised with cDNA 1–2a. This was done since no patients were deleted solely for either the 7.7 or 1.4 kb bands, now identified as corresponding to exons 6 and 7, respectively. In the region detected by probe fragments 5b–7–a and 5b–7–b (fig 1), only one deletion was informative for fragment order. Hybridisation of alternative probe fragment 5b–7–P (fig 1) to TaqI digests detected the 4.6, 2.5, 0.9, 0.8, and 3.6 kb bands also seen by probe fragment 5b–7–a. The alternative probe fragment 5b–7–G detected the 3.6, 7.0, and 3.3/3.7 kb bands of probe fragment 5b–7–a, plus the 9.4 and 2.2 kb bands of probe fragment 5b–7–b. Combining information derived from the informative deletion and from hybridisation with the two sets of probe fragments, the order of TaqI fragments at the 5′ end of 5b–7 could be determined (fig 3). In the region detected by probes 5b–7–c and 8, which is the region of most frequent deletion, each exon containing TaqI restriction fragment was correlated with the

### Table 1 TaqI polymorphisms detected with dystrophin cDNA probes.

<table>
<thead>
<tr>
<th>Probe</th>
<th>Allele size (kb)</th>
<th>Frequency</th>
<th>No</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Frequent allele</td>
<td>Rare allele</td>
<td></td>
</tr>
<tr>
<td>2b–3</td>
<td>3–4</td>
<td>3.6</td>
<td>0.94/0.46</td>
</tr>
<tr>
<td>5b–7–a</td>
<td>3–7</td>
<td>3.7</td>
<td>0.52/0.48</td>
</tr>
<tr>
<td>8</td>
<td>6–7</td>
<td>5.9</td>
<td>0.94/0.06</td>
</tr>
<tr>
<td>9–14–b</td>
<td>1–7</td>
<td>2.2</td>
<td>0.93/0.07</td>
</tr>
<tr>
<td>9–14–c</td>
<td>1–12</td>
<td>1.4</td>
<td>0.73/0.27</td>
</tr>
</tbody>
</table>

*One probable duplication also detected (see Results).*

### Table 2 Deletion frequencies detected with cDNA probes on TaqI digested DNA.

<table>
<thead>
<tr>
<th>Probe</th>
<th>Deletions/families tested</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>1–2a</td>
<td>18/133</td>
<td>14</td>
</tr>
<tr>
<td>2b–3</td>
<td>19/136</td>
<td>14</td>
</tr>
<tr>
<td>4–5a</td>
<td>10/127</td>
<td>8</td>
</tr>
<tr>
<td>5b–7–a</td>
<td>5/15*</td>
<td>4</td>
</tr>
<tr>
<td>5b–7–b</td>
<td>4/135</td>
<td>3</td>
</tr>
<tr>
<td>5b–7–c</td>
<td>42/133</td>
<td>32</td>
</tr>
<tr>
<td>8</td>
<td>57/140*</td>
<td>41</td>
</tr>
<tr>
<td>9</td>
<td>7/117</td>
<td>6</td>
</tr>
<tr>
<td>10</td>
<td>1/107</td>
<td>1</td>
</tr>
<tr>
<td>11–14–a</td>
<td>0/63</td>
<td>0</td>
</tr>
<tr>
<td>11–14–b</td>
<td>0/52</td>
<td>0</td>
</tr>
<tr>
<td>11–14–c</td>
<td>0/56</td>
<td>0</td>
</tr>
</tbody>
</table>
corresponding fragment of the HindIII map. The fragment order for TaqI was consistent with that for HindIII in all cases tested. This allowed the exon border type of deletions in this region to be established. In all 41 DMD and 10 BMD cases tested, DMD patients had deletions which are predicted to cause a frameshift in the translational reading frame, while BMD patients had deletions which are predicted to maintain the reading frame (fig 4). Additional screening with intragenic genomic probes was performed, and XJ1.1, pERT87-15, pERT87-JBir, and P20 were located on the TaqI map. The TaqI RFLP detected by genomic probe pERT87-15 was found to be identical to that detected by cDNA 2b-3 (fig 5).

**Discussion**

Deletion screening on TaqI digested DNA allows for concurrent analysis of five RFLPs, so in those families with no detected deletion or duplication counselling by conventional linkage analysis may be facilitated. The TaqI and HindIII maps were correlated over nine exons detected by cDNA probes 5b-7 and 8. Although absolute confirmation of order would require sequencing of the TaqI exon containing fragments to ensure that no small fragments had been omitted, in all 51 cases tested in this region the deduced order of exon containing fragments for TaqI and the HindIII order were consistent.

Similar deletions were observed in DMD and BMD patients, although in no case were the same exon containing fragments deleted in a DMD and a BMD family (fig 3 and 4). The reading frame hypothesis predicted that frameshift deletions result in production of a truncated, unstable dystrophin protein, leading to severe phenotypes, while deletions that maintain the reading frame result in production of an internally deleted dystrophin protein that is partially functional, leading to mild phenotypes. Testing in a number of different
patient populations has shown that in the majority of cases the predictions of disease severity based on the expected effects of deletion on dystrophin translation are correct; however, a few exceptions have been observed, particularly at the 5' end of the gene.13b-20 In the frequent deletion region of probes 5b-7 and 8 that we tested, all BMD patients had deletions that preserved the translational reading frame downstream to the deletion; all DMD patients had deletions that resulted in frameshift (fig 4). In the present study, deletion of the 4.1 kb HindIII exon containing fragment in family 91 produced a DMD phenotype. Baumbach et al19 reported that this same exon deletion could result in either a DMD or an 'intermediate' DMD/BMD phenotype, so that the predicted effects of exon deletions on transcriptional reading frame do not always allow accurate prognosis of disease severity.

Four genomic probes have been localised on the TaqI map, and permit more precise delineation of deletions. Genomic probe pEERT87-15 was found to detect the same polymorphic exon containing TaqI fragment that is detected by the cDNA probe 2b-3. Fig 5 shows the use of cDNA 2b-3 in a DMD family for screening of deletions and polymorphisms concurrently.

Division of the cDNA to yield 15 probe segments ordered the TaqI exon containing fragments into 15 groups. For routine deletion screening, however, it was not necessary to divide probe 1-2a, as all the bands were well separated; the alternative probe fragments 5b-7-P and 5b-7-G were also not needed for routine screening. Fig 3 shows the distribution of deletions detected, with 5b-7-P and 5b-7-G also detected in the region of the 4.1 kb HindIII exon containing fragment.

In conclusion, a partial TaqI map of exon containing fragments of the dystrophin gene is described, allowing concurrent detection of deletions/duplications and analysis of five polymorphisms. Genomic probes have been localised on the TaqI map, improving resolution of deletion detection. Oligonucleotide primers are described for the amplification of exon 6, allowing its identification on the TaqI map, so that fragments 6 and 7 could be ordered. The TaqI map has been correlated with the HindIII map in the high deletion frequency region of probes 5b-7-c and 8; all 51 deletion families screened in this region confirmed with the 'reading frame hypothesis'. Although multiplex polymerase chain reaction (PCR) will probably be increasingly used for initial deletion screening, owing to the rapidity
of the process,\(^7\) primers for all exons have not yet been identified and characterised. Southern hybridisation allows conventional linkage analysis to be used in those families with no detected deletion, and will remain an important analytical tool until better techniques are developed for identification of putative microdeletions and point mutations in the more than 2 Mb of the dystrophin gene.

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