Improved molecular diagnosis of facioscapulohumeral muscular dystrophy (FSHD): validation of the differential double digestion for FSHD

M Upadhyaya, J Maynard, M T Rogers, P W Lunt, P Jardine, D Ravine, P S Harper

Abstract
A major advance in the molecular diagnosis of facioscapulohumeral muscular dystrophy is the recently reported elimination of confounding DNA fragments arising from homologous sequences located at 10q26. In order to evaluate the specificity and sensitivity of this important diagnostic test, we have compared a group of 130 patients fulfilling the diagnostic criteria for FSHD with 200 control subjects not known to have an increased risk of having an FSHD mutation. Among the FSHD cases the smallest Bln1/EcoRI fragment sizes ranged from 10 to >48 kb with 94.6% (95% CI 89.2-97.8%) of cases having fragment sizes of 34 kb or less. Among the 400 chromosomes from controls the smallest Bln1/EcoRI fragment observed with the EcoRI/Bln1 double restriction enzyme digest was 38 kb ± 2 kb, suggesting a test specificity at a fragment size <34 kb of or very near to 100% (lower 95% CI 98.2%). Test sensitivity at <34 kb is estimated at 94.6% (95% CI 89.2-97.8%), all outliers having fragments >38 kb. The Southern blot analysis with DNA probe p13E-11 has created a valuable molecular diagnostic test for FSHD. (J Med Genet 1997;34:476-479)

Keywords: molecular diagnosis; FSHD; sensitivity

Facioscapulohumeral muscular dystrophy (FSHD) is an autosomal dominant neuromuscular disorder characterised by progressive weakness and atrophy of the muscles of the face, upper arm, and shoulder girdle. The clinical features of the disease are variable, both within and between families. Disease onset is usually between the first and second decade, and gradually progresses with about 20% of patients eventually becoming wheelchair bound and with up to two-thirds of patients having disease related problems in their daily activities. The gene for FSHD has been mapped to 4q35 and is closely linked to the locus D4F104S1 defined by the probe p13E-11. In a small minority of FSHD families (estimated to be 5-10% at most), the disease locus may be unlinked to 4q35, but no other specific chromosomal locations have yet been identified. To date, the molecular prediction of FSHD with D4F104S1 has been most secure in those families which are linked to other 4q35 markers but has not permitted a molecular diagnostic test for general application. Even in some 4q35 linked families with small D4F104S1 EcoRI fragments, testing has been complicated by recombinations occurring between the locus D4F104S1 and FSHD, with a maximum reported recombination fraction of 0.05.

Using the restriction enzyme EcoRI, the probe p13E-11 identifies two highly polymorphic loci located at 4q35 and 10q26. The polymorphic EcoRI fragment at 4q is composed almost entirely of 3.3 kb KpnI tandem repeat units identified as DAZ4. Among chromosomes from control subjects, the size of the 4q derived fragments usually ranges from 40 kb to approximately 200 kb, whereas in two-thirds of FSHD patients, a deletion of an integral number of the DAZ4 repeats generates a shortened EcoRI fragment which is usually smaller than 28 kb. Unfortunately, the size distribution of approximately 10% of EcoRI fragments from the homologous polymorphic locus at 10q overlaps with the range seen in FSHD cases, and consequently many non-FSHD cases have EcoRI fragment sizes of less than 28 kb, thus giving a test specificity from EcoRI digest alone of 76% at this level. It is evident that these smaller polymorphic EcoRI fragments arising from the 10q locus, coupled with the lesser risks of recombination and locus heterogeneity, create considerable difficulties when assessing the diagnostic significance of a shortened fragment in a person with clinical features suggestive of FSHD or in an at risk relative from a family with FSHD.

Recent detection of sequence divergence between the KpnI tandem repeat units located at 4q and 10q has shown a different distribution of restriction enzyme sites, and has shown that the enzyme Bln1 specifically cleaves the 3.3 kb repeats derived from 10q, leaving intact the tandem repeat units at 4q. Thus, a double restriction enzyme digest (DD) with the enzymes EcoRI and Bln1 allows the specific detection of 4q fragments and should greatly facilitate the molecular diagnosis of FSHD. In order to define the sensitivity and specificity of this improved molecular test, we have rescreened samples from a group of previously diagnosed FSHD patients, as well as from a group of unaffected controls.
Subjects and methods
Affected cases were selected at random from familial and sporadic cases of FSHD studied over the past 10 years. The clinical record of each patient was reviewed and only those with an unequivocal diagnosis of FSHD or scapulohumeral dystrophy were included.1 2 12 One hundred and thirty unrelated FSHD patients were studied, of whom 27 represented new mutation cases with apparently normal parents. The control group comprised 200 subjects with no known background family history of FSHD. Blood was collected from all patients and controls and high molecular weight DNA isolated by use of standard methods. Using the same method previously used for the restriction enzyme EcoRI, 10 μg genomic DNA was simultaneously digested with EcoRI and BlnI (Amersham) for eight hours and then fractionated on a 0.5% agarose gel for 48 hours at 0.5 volts/cm. High molecular weight DNA markers (Gibco BRL) were used for accurate sizing of the double digested fragments (fig 1). The DNA on the gel was irradiated with 260 nm UV light for 60 seconds to induce random “nicks” throughout the DNA which was then transferred onto a Zetaprobe membrane (Bio-Rad) by Southern blotting. The 800 bp insert from p13E-11 was labelled with [32P]dCTP using primer extension.13 The posthybridisation wash was 2 x SSC, 0.1% SDS at 65°C as required, followed by autoradiography for one to seven days at ~70°C using Fuji x ray film with an intensifying screen. To determine the accuracy of our assessment of fragment sizes, repeated measurements of the fragments of 30 affected subjects with shortened fragments and 105 controls with fragment sizes between 38 and 48 kb showed a variation of reported fragment size that was ±1 kb for fragments up to 30 kb, ±2 for those from 30 to 40 kb, and ±3 for those greater than 40 kb. The autoradiographs were assessed blindly by two separate observers. A 95% CI (confidence interval) was calculated using the Clopper-Pearson exact method.14

Results
Among those with previously diagnosed sporadic or familial FSHD, the size of the smaller fragment varied from 10 kb to >48 kb (fig 2). One hundred and twenty-three out of the 130 FSHD patients (94.6%) (95% CI 89.2-97.8%) had fragment sizes that were 34 kb or less. Among the seven cases with larger fragments, the fragment sizes varied from 38 kb (±2 kb) to >48 kb. The clinical details of each of these cases with larger fragments are summarised in table 1. Among 27 sporadic FSHD cases, the size distribution ranged from 10 to 48 kb (mean 17.8, SD 8.83), while the size distribution among 103 familial cases ranged from 10 to >48 (mean 22.0, SD 7.1) (p=0.01). Three fragment bands were evident in three unrelated subjects with FSHD. Among the control population, the smallest fragment size detected was 38 kb (±2 kb), while the majority had fragment sizes that were within the limiting mobility of the DNA on the agarose gel (>48 kb). Nineteen subjects had smaller fragment sizes that ranged between 38 and 48 kb (fig 2). In each FSHD patient with a double digest (EcoRI/BlnI) fragment of <28 kb, there was an approximately 3 kb reduction in the size of the double digest fragment compared to the EcoRI single digest fragment and without the appearance of other new fragments <48 kb.

Discussion
Among the 400 control chromosomes, the smallest fragment observed with the EcoRI/ BlnI double restriction enzyme digest was 38 kb (±2 kb), indicating that test specificity below this level is at or very near to 100% (lower 95% CI 98.2%). This is in contrast to the 76% test specificity associated with the presence of frag-

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Table 1  Details of subjects and families clinically affected with FSHD with an EcoRI/BlnI smallest fragment greater than 35 kb

<table>
<thead>
<tr>
<th>FSHD</th>
<th>Smallest fragment size (kb)</th>
<th>Clinical details</th>
</tr>
</thead>
<tbody>
<tr>
<td>No</td>
<td></td>
<td></td>
</tr>
<tr>
<td>221</td>
<td>38</td>
<td>Typical small FSHD family assumed sporadic case, onset in infancy</td>
</tr>
<tr>
<td>260</td>
<td>38</td>
<td>Typical FSHD, 2 affected members in 2 generations. Linkage of disease to 4q35 unclear although 38 kb fragment appears 4q35 linked</td>
</tr>
<tr>
<td>224</td>
<td>38</td>
<td>Brother and sister with typical but mild FSHD “FSHD plus”. Classic FSHD plus hypothyroidism or early cardiac death, separately, in daughters of historically affected mother</td>
</tr>
<tr>
<td>003</td>
<td>42</td>
<td>Sporadic FSHD with de novo 48 kb fragment</td>
</tr>
<tr>
<td>016</td>
<td>42</td>
<td>Four affected sibs with typical FSHD, father very mild. Distant consanguinity (parents second cousins once removed)</td>
</tr>
</tbody>
</table>

Figure 1  The distribution of the smallest EcoRI/BlnI fragment sizes. Lane 4 contains DNA sample from a control subject. Lanes 1-3 contain samples from FSHD patients with smallest EcoRI/BlnI fragment sizes of 10, 20, and 30 kb respectively. The 9.4 kb band specific to the Y chromosome is observed in lanes 1, and 4. The presence of the 2.8 kb fragment is generated as a result of complete digestion of the 10q fragment with the enzyme BlnI.
The occurrence of a deletion of an integral number of D4Z4 repeats which do not appear to contain any expressed sequences and are in close proximity to 4q telomeric sequences has led to the suggestion that the mechanism underlying the disease could be position effect variegation (PEV). Experiments in Drosophila and yeast have shown that physical proximity to telomeric heterochromatin may actively suppress gene expression. The occurrence of normal range fragment sizes in seven FSHD cases confirms that there is more than one mechanism responsible for FSHD. Disease phenocopies may occur with the presence of an indistinguishable muscular dystrophy possibly overlapping with another clinical phenotype. Diseases which may produce a very similar phenotype, although usually distinguishable by EMG and biopsy features, include spinal muscular atrophy and the scapuloperoneal neuropathies. Some cases, however, are not distinguishable even when the strictest of diagnostic criteria used in linkage studies are applied. Indeed, most linkage studies suggest that up to 5% of families are not linked to the 4q35 locus. It is possible that some of these people may either have a mutation elsewhere in the genome (genetic heterogeneity) or have point mutations or other rearrangements in a separate 4q35 gene, located proximal to D4Z4.

This study has identified a potential subgroup of FSHD patients in whom there is no apparent correlation between smaller EcoRI/BlnI fragments and the expression of the disease. Reassessment of the seven unrelated FSHD patients with fragment sizes of 38 kb or more showed a range of unusual aspects, although all had typical features of FSHD that fell within the diagnostic criteria for FSHD. In one sporadic case with a fragment of 38 kb, onset was in early infancy and another subject had a de novo fragment of 48 kb compared to clearly distinguishable fragments >48 kb in the parents. In another family the mother was reported to have had typical but mild FSHD, one of two daughters with FSHD died at 17 years of age from cardiac failure, and in the other the FSHD was associated with treated hypothyroidism. Among the four familial cases, linkage data from at least one family suggest that it may not be linked to the 4q35 locus. Interestingly, the 38 kb fragment observed in this family is at the extreme low end of the range seen in the control population. In addition, six of the seven cases have fragment sizes that fall within the lowest 10% of the size range seen in the control population. Consen-
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