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Evidence for subtelomeric exchange of 3.3 kb tandemly repeated units between chromosomes 4q35 and 10q26: implications for genetic counselling and etiology of FSHD1

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Facioscapulohumeral muscular dystrophy (FSHD) is an autosomal dominant myopathy, clinically characterized by asymmetric weakness of muscles in the face, shoulder girdle and upper arm. Deletion of an integral number of 3.3 kb repeated units within a highly polymorphic EcoRI fragment at chromosome 4q35, generating a relatively short EcoRI fragment (<35 kb), has been shown to cause FSHD1. Probe p13E-11 detects these short fragments in FSHD1 patients, and has therefore been used for diagnostic DNA analysis. However, the reliability of this analysis has been hampered by cross-hybridization of p13E-11 to chromosome 10q26-linked EcoRI fragments of comparable size, which also contain a variable number of 3.3 kb repeated units. Recently, a BstEII restriction site was identified within each of the repeated units derived from chromosome 10q26, which enables differentiation of the two polymorphic p13E-11 loci in most cases without haplotype analysis. Remarkably, applying the differential analysis to screen DNA of 160 Dutch cases referred to us for FSHD1 diagnosis, we obtained evidence for subtelomeric exchange of 3.3 kb repeated units between chromosomes 4q35 and 10q26 in affected and unaffected individuals. Subsequently, analysis of 50 unrelated control samples indicated such exchange between chromosomes 4q35 and 10q26 in at least 20% of the population. These subtelomeric rearrangements have generated a novel interchromosomal polymorphism, which has implications for the specificity and sensitivity of the differential restriction analysis for diagnostic purposes. Moreover, the high frequency of the interchromosomal exchanges of 3.3 kb repeated units suggests that they probably do not contain (part of) the FSHD1 gene, and supports position effect variegation as the most likely mechanism for FSHD1.

INTRODUCTION

Facioscapulohumeral muscular dystrophy (FSHD) is clinically characterized by progressive weakness of the facial, shoulder-girdle and upper arm muscles, and in some cases, also the abdominal, foot extensor and pelvic girdle muscles (1,2). The autosomal dominant inherited myopathy shows a variable phenotypic expression with a high penetrance of 95% at the age of 20, and an estimated prevalence of 1 in 20 000 (1,3). Linkage analysis assigned the major FSHD locus (FSHD1) to chromosome 4q35 (4,5) distal to D4S139 (6–8). However, genetic heterogeneity was demonstrated for a small number of FSHD families, not linked to 4q35 (9–12). In patients, the FSHD1 locus on chromosome 4q35 is characterized by a DNA rearrangement within a highly polymorphic EcoRI fragment detectable using probe p13E-11 (D4F104S1) (13). In patients, these FSHD1-associated rearrangements generate EcoRI fragments which are shorter than 35 kb (13–17), while the size of the 4q35-linked EcoRI fragments in unaffected individuals varies from 35 to 300 kb (13). Analysis of the p13E-11 EcoRI fragments of four unrelated FSHD1 patients and controls revealed that the polymorphic fragment contains a variable number of 3.3 kb repeated units (D4Z4), a critical number of which is deleted in patients (18).

As short EcoRI fragments (<35 kb) linked to 4q35 are associated with FSHD1, probe p13E-11 has been used for diagnostic DNA analysis (17). However, a straightforward analysis is hampered by cross-hybridization of p13E-11 to another polymorphic locus which has recently been assigned to

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chromosome 10q26 (12,19). This locus is similarly characterized by EcoRI fragments containing a variable number of 3.3 kb repeated units. The size of these chromosome 10 fragments can be up to 300 kb, but also less than 35 kb in 10% of the population (12,17). Hence, short EcoRI fragments derived from 10q26 may incorrectly be interpreted as chromosome 4q35 deletion fragments. Haplotype analysis in FSHD families using chromosome 4q35 and 10q26 markers had to be performed to determine the chromosomal origin of a short (<35 kb) p13E-11 fragment (17). However, due to the presence of small families and isolated cases, only about 50% of short p13E-11 fragments could unambiguously be assigned to chromosome 4q35, and subsequently used for diagnostic purposes (17).

Recently, comparative sequence analysis of 3.3 kb repeated units derived from chromosomes 4q35 and 10q26 revealed the specific presence of a BlnI site within each repeated unit from chromosome 10q26. As this restriction site is not present in the repeated units from chromosome 4q35, differential restriction analysis using BlnI enabled direct differentiation of the chromosomal EcoRI fragments without haplotype analysis (19). By double digestion of genomic DNA with EcoRI and BlnI (or AvrII), the p13E-11 EcoRI fragments from 4q35 are reduced in size by 3 kb, while the EcoRI fragments derived from chromosome 10q26 are fragmented completely. This differential restriction analysis enabled presymptomatic and prenatal diagnosis to be performed with an improved efficiency and reliability.

Here, we report the screening of 160 independent Dutch familial or isolated cases referred to us for FSHD1 diagnosis, using the differential restriction analysis. In most cases an unequivocal diagnosis was achieved. Remarkably, a few individuals appeared to be ‘monosomic’ or ‘trisomic’ for the 4q35-linked p13E-11 fragment. Further analysis of these cases suggested the occurrence of subtelomeric exchanges of 3.3 kb tandemly repeated units between chromosomes 4q35 and 10q26, generating hybrid EcoRI fragments. As interchromosomal exchanges would have implications for the specificity and sensitivity of the diagnostic DNA testing, the frequency of such events in the population was determined by screening 50 unrelated control DNA samples.

RESULTS
 Diagnostic application of differential restriction analysis

EcoRI and EcoRI/BlnI digested DNA of FSHD patients and family members was analyzed by conventional agarose gel electrophoresis and subsequent Southern blot hybridization using probe p13E-11. To illustrate the potency of the differential restriction analysis for diagnostic purposes, the results of family 87 (17) are shown in Figure 1. After EcoRI digestion only, probe p13E-11 detected a fragment of approximately 30 kb in affected as well as in some unaffected individuals. Haplotype analysis using chromosome 4q35 and 10q26 markers revealed that the 30 kb p13E-11 EcoRI fragment does not cosegregate with either the chromosome 4q35 or 10q26 haplotype (17) (Fig. 1). However, recently, differential restriction analysis using EcoRI and BlnI indicated heterogeneity of the 30 kb EcoRI fragments. In the affected individuals, the 30 kb EcoRI fragment was reduced in size by 3 kb indicating a chromosome 4 origin (Fig. 1, haplotype ‘A’), whereas in the unaffected individuals the 30 kb EcoRI fragment was completely fragmented, revealing a chromosome 10 origin. The chromosomal origin of the 30 kb EcoRI fragments as suggested by the differential restriction analysis, was confirmed by haplotype analysis performed previously (17). Accordingly, an unequivocal diagnosis was achieved in this family.

In total, 160 independent Dutch familial or isolated FSHD index cases were screened using the differential restriction analysis. In 46 of 160 cases long (>35 kb) EcoRI fragments were observed only. Almost all of these 46 cases were clinically unambiguous, and referred for exclusion of FSHD1. So far, no unambiguously diagnosed FSHD patient without short EcoRI fragment was observed, which might carry a mutation in the FSHD1 gene itself, or be linked to a second FSHD locus. In 114 of 160 cases, EcoRI digestion revealed a short (<35 kb) p13E-11 fragment. By double digestion with EcoRI and BlnI, this short fragment was found to originate from chromosome 4 in 102 of 114 cases, indicating a high probability of FSHD1. Short EcoRI fragments completely fragmented by BlnI digestion, were detected in 12 of 114 individuals. Accordingly, these fragments were assumed to originate from chromosome 10q26, suggesting a lowered probability of FSHD1. However, at least three 4q35-linked familial and three isolated cases carrying such short, apparently chromosome 10q26 derived, EcoRI fragments, were clinically unambiguously diagnosed with FSHD (GWP). Although differential restriction analysis and clinical diagnosis implied that these cases either contain a mutation in the FSHD1 gene itself or are linked to a second FSHD locus, further analysis suggested another explanation (see below).

Subtelomeric exchange of repeated units

In applying the differential restriction analysis we observed several FSHD index cases and unaffected spouses which appeared to be either ‘monosomic’ or ‘trisomic’ for the p13E-11 fragment on chromosome 4q35. To demonstrate such aberrant BlnI restriction patterns, a very interesting family (family 28, Fig. 2a) was selected. In this family, a 25 kb EcoRI fragment was detected which cosegregates with FSHD1 and which was reduced in size by 3 kb after BlnI digestion (Fig. 2b). Therefore, a clear diagnosis was achieved. Remarkably, the father (individual 28.1) who is asymptomatic, also carries a short second BlnI-resistant EcoRI fragment (22 kb). As the father is transmitting both his chromosomes 4 and both his chromosomes 10 whereas the 22 kb fragment is not inherited by any of his children (Fig. 2a), he is considered somatic mosaic for this 22 kb fragment. In addition, the father strikingly showed two other BlnI-resistant, 4q35-like fragments. In his offspring, three BlnI-resistant EcoRI fragments were also detected in sons 28.4 and 28.5, while one BlnI-resistant EcoRI fragment only was observed in the youngest son 28.6. Moreover, the unaffected mother (individual 28.2) also shows one BlnI-resistant EcoRI fragment only. Pulsed-field gel electrophoresis was performed (Fig. 2b), which confirmed the apparent ‘monosomic-trisomic’ observed by conventional gel electrophoresis. We hypothesized that an exchange of 3.3 kb repeated units between chromosomes 4q35 and 10q26 might have occurred, generating hybrid p13E-11 fragments (Fig. 3). In cases 28.1, 28.4 and 28.5, one of the chromosome 10q26 fragments contain repeated units without BlnI sites, probably derived from chromosome 4q35. In cases 28.2 and 28.6 one of the chromosome 4q35 fragments contains 10q26-like repeated units including BlnI sites.
Haplotyping analysis using chromosome 4q35 and 10q26 markers (D4S163–D4S139 and D10S555–D10S590, respectively) was performed to differentiate the chromosomes 4 and 10 segregating in this family (Fig. 2a). One of the 4q35-like EcoRI/BlnI fragments observed in individuals 28.1, 28.4 and 28.5 indeed segregated with a chromosome 10q26 haplotype indicating it to be a hybrid p13E-11 fragment. In addition, one of the 10q26-like fragments observed in individuals 28.2 and 28.6 segregates with a chromosome 4q35 haplotype, also supporting the interchromosomal exchange hypothesis.

Subtelomeric exchange of 3.3 kb repeated units between chromosome 4q35 and 10q26 has implications for the specificity and sensitivity of the differential restriction analysis as a method for diagnostic DNA analysis. As illustrated in Figure 3, short EcoRI fragments linked to chromosome 4q35 may be either BlnI-sensitive or BlnI-resistant. Healthy individuals may carry short hybrid EcoRI fragments linked to chromosome 10q26, while a chromosome 4q35 origin and therefore a high probability of FSHD1 would be suggested by the differential restriction analysis. In parallel, cases carrying short, 4q35-linked EcoRI fragments exhibiting BlnI-sensitive repeated units, might incorrectly be diagnosed with a low probability of FSHD1. Examples of such cases are mentioned in the previous paragraph: in six of 114 cases which were unambiguously diagnosed with FSHD, a short chromosome 10q26-like EcoRI fragment was observed. One of these cases is member of a well-studied 4q35-linked FSHD1 family (family 25) (18,20) in which a short 15 kb EcoRI fragment is cosegregating with the disease. This 15 kb fragment was cloned from the index case (patient 250301) in a previous study (18). Detailed Southern blot analysis using probes p13E-11 (D4F104S1), 9B6A (D4Z4) and pLAM1 (D4Z3) (Fig. 4), indicated this fragment to contain repeated units each carrying a BlnI site, incorrectly suggesting a chromosome 10q26 origin.

To determine the frequency of subtelomeric exchanges of repeated units between chromosomes 4q35 and 10q26 in the population, 50 male control individuals were screened using pulsed-field gel electrophoresis of EcoRI/BlnI double-digested DNA. In five cases (10%) apparent ‘monosomy’ was observed, while in five other cases (10%) ‘trisomy’ was detected. One ‘monosomic’ case and one ‘trisomic’ case are shown in Figure 5. Accordingly, the frequency of interchromosomal exchanges was estimated to be 20% (10 of 50). However, the frequency is probably higher given the higher frequency of recombination events in females, not included in this control study. Moreover, ~1% of cases may contain two types of hybrid fragments. These cases appear to be ‘disomic’ and will remain unnoticed (see Fig. 5, control 2).

**DISCUSSION**

The differential restriction analysis of FSHD cases is based on the presence of a BlnI restriction site in each of the 3.3 kb repeated units derived from chromosome 10q26 (19). As this BlnI site is not present in the repeated units of chromosome 4q35, differentiation between the two polymorphic p13E-11 loci can easily be achieved in most cases. Therefore, especially in isolated cases suspected of having FSHD, the differential restriction analysis accounts for an important improvement of the diagnostic DNA analysis. In addition, in some familial cases haplotype analysis may not reveal clear differentiation between chromosome 4q35
Figure 2. a) High resolution analysis of family 28, using chromosome 4p13-11 and 4p16.4 markers. The sizes of the 4p13-11 and 4p16.4 marker loci were determined from Southern blot analysis of DNA isolated from family 28. The 4p13-11 and 4p16.4 marker loci were all present in affected relatives of family 28. The chromosomes were separated using a high resolution ligation method and analyzed using a fluorescent in situ hybridization (FISH) method. b) Southern blot analysis of DNA from family 28. The chromosomes were separated using a high resolution ligation method and analyzed using a fluorescent in situ hybridization (FISH) method.

The specificity of the differential restriction analysis was determined by the percentages of unaffected individuals carrying the 4p13-11 and 4p16.4 marker loci. The percentages of unaffected individuals carrying the 4p13-11 and 4p16.4 marker loci were not significantly different from the percentages of affected individuals carrying the same marker loci. The percentages of unaffected individuals carrying the 4p13-11 and 4p16.4 marker loci were not significantly different from the percentages of unaffected individuals carrying the 4p13-11 and 4p16.4 marker loci.

In conclusion, the differential restriction analysis facilitates an efficient and specific diagnosis of the 4p13-11 and 4p16.4 marker loci, and can be used to diagnose individuals carrying the 4p13-11 and 4p16.4 marker loci.
Figure 3. Model to explain the aberrant Bln1 restriction patterns observed after differential restriction analysis, which suggest some cases to be 'monosomic' or 'trisomic' for the chromosome 4q35 EcoRI fragment. On top, the subtelomeric regions of chromosomes 4q35 (filled bars) and 10q26 (open bars) and potential subtelomeric exchanges are depicted. Below, normal and hybrid and long or short EcoRI fragments derived from chromosome 4q35 or 10q26, are shown. As the origin of the telomeric regions of the hybrid fragments might be either chromosome 4q35 or 10q26, they are indicated by grey bars. Note that short, 4q35-linked, hybrid EcoRI fragments containing Bln1-sensitive repeated units are also diagnostic for FSHD1, but might lead to misdiagnosis when based on differential restriction analysis only.

Bln1 suggesting a chromosome 10q26 origin, should be further analyzed by pulsed-field gel electrophoresis and haplotype analysis to confirm the chromosomal origin of the short fragment, and to prevent misdiagnosis.

The molecular mechanism behind the subtelomeric exchanges between chromosomes 4q35 and 10q26 remains to be elucidated. Chromosomal rearrangements occur more often in (sub)telomeric regions than in other parts of the genome. Translocations of chromosome ends have recently been reported as the cause for idiopathic mental retardation syndrome (21), α-thalassemia mental retardation syndrome (22), Wolf–Hirschhorn syndrome (23), Miller–Dieker syndrome (24) and cri-du-chat syndrome (25). However, in this paper we report an interchromosomal polymorphism without phenotype, which is to our knowledge a remarkable novelty in human genetics. Owing to high homology between the chromosome 4q35 and 10q26 subtelomeric regions, it is plausible that there is an interchromosomal ‘cross-talk’ during meiosis. Two types of chromosomal rearrangements might have generated the exchange of 3.3 kb repeated units: either translocations including the particular telomeres, or gene conversions limited to the repeated units only. As the respective telomeric regions of chromosomes 4q and 10q contain non-unique sequences only, it will be difficult to determine whether the telomeres are involved in the interchromosomal exchanges. In addition, in most cases analyzed the p13E-11 EcoRI fragments revealed Bln1 restriction patterns as expected; either completely fragmented, or reduced in size by 3 kb. Therefore, probably complete arrays of repeated units have been exchanged, suggesting that in case of telomeric translocations the proximal breakpoint might even be proximal to the repeated units. However, in rare cases the EcoRI fragment was found to be reduced in size by more than 3 kb after Bln1 digestion, indicating that hybrid p13E-11 EcoRI fragments may also contain a mixture of Bln1-resistant and Bln1-sensitive repeated units. Finally, whether the hybrid EcoRI fragments are due to a recurrent event of interchromosomal exchange in the population, or part of a polymorphism which is due to one unique interchromosomal exchange event in evolution, remains to be elucidated.

Independent of the molecular mechanism, the interchromosomal exchanges of repeated units have implications for the etiology of FSHD1: a short 4q35-linked EcoRI fragment will give FSHD1, irrespective of origin of the repeated units. A de novo exchange generating a short 4q35-linked fragment containing Bln1-sensitive repeated units from chromosome 10q26, will cause FSHD1 in the same way as a chromosome 4q35 intra-repeat fragment deletion. However, the frequency of such an event is bound to be low given the low percentage (<10%) of short chromosome 10q26-linked EcoRI fragments (12,17). Interchromosomal exchanges of the 3.3 kb repeated units between chromosomes 4q35 and 10q26 with a rather high frequency (20%) suggest that it is unlikely that the FSHD1 gene (partially) resides within the repeated units at chromosome 4q35. Moreover, an Italian family was reported recently, in which an abnormal chromosome 4, a derivative of an unbalanced translocation of 4q35 with an acrocentric chromosome, segregates through three generations in phenotypically normal individuals (26). The resulting monosomy of the 4q35 region in unaffected individuals supports the
Southern blot analysis

Individually was used in the control study.

Material and Methods

Molecular mechanism of FSHD.
REFERENCES

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Pulsed-field gel electrophoresis

7°C using Konica AX film with an intensifying screen.

SSC/0.1% SDS, followed by autoradiography for 16-36 h at


