A novel PHF6 mutation results in enhanced exon skipping and mild Börjeson-Forssman-Lehmann syndrome

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Börjeson-Forssman-Lehmann syndrome (BFLS) is a rare X linked recessive disorder characterised by moderate to severe mental retardation, obesity with gynaecomastia, hypogonadism, and large prominent ears. However, a clear diagnosis is often difficult. BFLS may be confused with other obesity related mental retardation syndromes as there can be intrafamilial and interfamilial phenotypic variability and women may also be affected, possibly because of skewed X inactivation. Following the identification of the PHF6 gene (Xq26–27) as the cause of BFLS, Turner et al showed that the phenotype may be milder and broader than originally appreciated.

Mutations in the PHF6 gene have been identified in 11 families and they are localised throughout the gene, suggesting a loss of function mechanism. Primary sequence analysis has suggested that PHF6 encodes a transcriptional regulator based on the presence of two PHD zinc finger domains, a motif common to chromatin remodelling proteins including the ATRX protein. Nonetheless, little is known of the function of the PHF6 protein or how different mutations give rise to the phenotypic variability observed in patients. Clearly, the identification of additional mutations will enhance our understanding of PHF6 function and provide insight into the clinical spectrum of this disorder. Here we describe mutational analysis in two Canadian families, one with classic features of BFLS and another with milder phenotypic features.

METHODS

Case reports

The affected individual from family 1 (fig 1A) was diagnosed at age 19 because of a classical phenotype that was consistent with that described in the most comprehensive clinical review of BFLS patients. He is severely intellectually handicapped with psychiatric challenges that include self-injurious behaviour. He has characteristic facial features, a stooped kyphoscoliotic posture, central obesity, marked gynaecomastia, hypogonadism, incomplete virilisation, and anomalies of the hands and feet. In contrast, the two affected half brothers in family 2 (fig 1C) have a less severe phenotype, both physically and intellectually. Patient III-1 had several of the diagnostic features of BFLS including large prominent ears, truncal obesity, and gynaecomastia. However, he had only mild to moderate intellectual handicap and his digital findings were less striking than those of the proband in family 1. His half brother (III-2) had global developmental delay and some characteristic facial findings, yet otherwise displayed few of the typical physical features of BFLS, the exception being very large and prominent ears. Similarly, their mother and maternal grandmother displayed mild physical features of BFLS, most notably the large ears (in both) and tapered fingers (in the mother). Intellectually, both were able to function independently but had significant academic difficulties. A more detailed clinical description will be presented elsewhere (Graham GE, et al, in preparation).

Written consent was obtained from all individuals in the study and mutation testing was in accordance with the Ottawa Hospital research ethics board approved protocol 1998577-01H.

Mutational analysis

DNA isolated from peripheral blood was used to amplify each exon and the corresponding flanking intron sequence for analysis of splice junctions of the PHF6 gene according to the previously published protocol. Polymerase chain reaction (PCR) products were run on a 1% agarose gel and purified with a Qiaquick gel extraction kit (Qiagen, Valencia, California, USA). Purified PCR products were directly sequenced by the Ottawa Genomics Innovation Centre. DNA sequence was assembled and analysed for mutations using the Sequencher program (Gene Code Corporation). Subsequent to the identification of the mutation in intron 3, primers were designed to amplify exons 2–4 as follows: BFLSrRf (5’-CTACAAGACAGCGCAAATG-3’) and BFLSrR (5’-GCAATGCACAGTGGTAGTG-3’). RNA (10 μg) isolated from EBV transformed lymphoblasts was reverse transcribed using random primers and Superscript II as previously used and the cDNA was amplified using the previously published protocol. Primers were designed to amplify exons 2–4 as follows: BFLSrRf (5’-CTACAAGACAGCGCAAATG-3’) and BFLSrR (5’-GCAATGCACAGTGGTAGTG-3’). RNA (10 μg) isolated from EBV transformed lymphoblasts was reverse transcribed using random primers and Superscript II as previously used and the cDNA was amplified using the previously published protocol.
described. PCR amplification was undertaken for 35 cycles using the following conditions: 30 seconds at 94 °C, 40 seconds at 56 °C, and 30 seconds at 72 °C. Samples amplified in the absence of reverse transcriptase served as controls. Southern blot analysis was undertaken using standard conditions for oligonucleotide hybridisation with the oligonucleotide BFLSexon2–4 (5'-GCATGATGTG-3').

Isolation of polysomes
EBV transformed lymphoblast cell lines established from patients and normal individuals were expanded (1 × 10^7) before treatment with 0.1 mg/ml cyclohexamide for three minutes at 37°C. Cells were harvested, washed twice with ice cold phosphate buffered saline containing cyclohexamide, and resuspended in 1 ml of lysis buffer (1% Triton-X, 0.3 M NaCl, 15 mM MgCl_2, 15 mM Tris-HCl (pH 7.4), 0.1 mg/ml cyclohexamide, and 100 units of RNase inhibitors (Amersham)) at 4°C. The nuclei were removed by centrifugation at 10000 × g for five minutes at 4°C. The supernatants were subjected to an additional spin at 10 000 × g for five minutes at 4°C to remove any residual cellular debris and generate the cytoplasmic fraction. The cytoplasmic lysate was then layered onto a 10 ml continuous sucrose gradient (10–50% sucrose; 15 mM MgCl_2, 15 mM Tris-HCl (pH 7.4), 0.3 M NaCl). After a 90 minute centrifugation at 39 000 rpm at 4°C in an SW41-Ti rotor (Beckman), the absorbance across the gradient was read at 254 nm.

Immunofluorescence and transient transfection
The following primers were designed to amplify and directionally clone the coding sequence of the PHF6 gene: PHF6Fwd-2 (5'-GCTAAGCTTGATATGTGCAG-3'), and PHF6Rev (5'-GCTGAAATTCCTAGTTTCCATTA-3'). Purified PCR products were digested with EcoRI and HindIII, cloned into the pEGFP-C3 expression plasmid (BD BioSciences Clontech, Mississauga, Ontario, Canada), and sequenced for confirmation. HeLa cells were grown in Dulbecco’s modified Eagle’s medium (DMEM) supplemented with 10% fetal bovine serum in 5% CO_2 at 37°C. Cells were transiently transfected with the GFP-PHF6 constructs using Lipofectamine 2000 (Life Technologies Inc) as previously described. Cells were processed after 24 hours by fixing in cold ethanol/methanol (3:1) and counterstaining with 4',6-diamidino-2-phenylindole (DAPI). Co-localisation to nucleoli was examined using a mouse anti-human nucleoli monoclonal antibody (Chemicon, Temecula, California, USA; MAB1277). Anti-mouse Alexa Fluor 594 conjugated secondary antibodies were used.

Figure 1  Mutational analysis in two Canadian families with Börjeson-Forssman-Lehmann syndrome (BFLS). (A) The affected individual from family 1 is a 27 year old man with classical findings of BFLS. (B) Sequence chromatograms of a normal (wt) or affected family member (a), demonstrating an A to G transition (marked with a dot) at position 769 which results in an Arg257Gly missense mutation in this patient. (C) The pedigree of family 2 complete with the corresponding haplotype analysis. The markers in the Xq26-27 region are shown in blue. (D) Sequence chromatograms of a normal (wt) or affected family member (a) demonstrating an A to G transition (position indicated by dot) in intron 2 which creates a novel cryptic acceptor splice site.
were obtained from Molecular Probes (Eugene, Oregon, USA). Fluorescent images were captured using a Zeiss Axioplan 2 microscope outfitted with an AxioCam camera and AxioVision software.

RESULTS

Mutation analysis

Two Canadian families with a diagnosis of BFLS were examined for mutations in the PHF6 gene. The proband of family 1 (fig 1A) presented with the classical hallmarks of BFLS and he was found to have an A to G change at nucleotide 769 within exon 8 (fig 1B) which results in the substitution of glycine for an arginine residue (Arg257Gly). This mutation has previously been described in another BFLS family and lies within an uncharacterised domain of the PHF6 protein.

The second family (fig 1C) was diagnosed with BFLS despite a milder phenotype than is typically described and apparent in the proband of family 1. As family 2 was suspected to have a mild form of BFLS we first examined 16 markers spanning the X chromosome. Both affected boys, their mother (II-3), and their maternal grandmother (I-2) shared a common haplotype for markers in the Xq26–27 region (DXS1047, gata31e08, DXS1114, DXS8074, and DXS9908; fig 1B). We proceeded to screen the PHF6 gene, identifying an A to G change within intron 2 that was located eight nucleotides upstream of the acceptor splice site (fig 1D). The nucleotide change creates a cryptic 3' splice site (AG) which was also present in the proband's affected brother, his mother, and his maternal grandmother (data not shown). It was not present in unaffected members of the family or in DNA isolated from over 100 control individuals, suggesting

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**Figure 2** A novel PHF6 spliceform lacking exon 3. (A) Schematic diagram showing the exon structure surrounding the cryptic acceptor splice site identified in family 2 and the corresponding splicing possibilities amplified by RT-PCR using primers in exons 2 and 4 (depicted by arrows). (B) The excision of exon 3 maintains the reading frame generating a protein 34 amino acids shorter in length. Use of the cryptic splice site results in a frameshift and early truncation of the PHF6 protein. (C, left) Reverse transcriptase polymerase chain reaction (RT-PCR) analysis using primers located in exons 2 and 4 shows a high level of PHF6 exon 3 transcript in the affected brothers from family 2 (F2) compared with normal individuals (N), or the affected individual from family 1 (F1). (C, right) Southern hybridisation using an oligonucleotide comprising the last five nucleotides of exon 2 and the first five of exon 4 confirmed the absence of exon 3 in the lower band.
that this alteration does not represent a rare polymorphism but is probably a disease causing mutation (data not shown). Use of the cryptic acceptor splice site would predict the inclusion of seven nucleotides, thereby creating a frame shift and truncation of the protein soon afterwards (fig 2B). We hypothesised that the mild phenotype associated with this mutation resulted from the use of both acceptor splice sites within intron 2 such that a significant amount of normally spliced product would be produced (fig 2A).

**Altered splicing of the PHF6 gene**

To assess the functional significance of the splicing defect, lymphocyte RNA was isolated from affected individuals from both families and from a normal individual for RT-PCR analysis across exons 2–4 (fig 2A). In the patient sample with the cryptic splice site alteration, we expected to observe bands of 297 base pairs (bp) and 304 bp that corresponded to the normally spliced product and the mutant protein containing the additional seven nucleotides, respectively. However, we observed only a small amount of the mutant product and a prominent fragment of 195 nucleotides (fig 2C). Sequencing of the larger band confirmed that it was the mutant band containing the additional 7 bp of intronic sequence.

The size of the smaller band was consistent with a fragment lacking exon 3 and it was also present, albeit at very low amounts, in normal control samples and in the patient with a PHF6 mutation in the coding region (fig 2C). We confirmed that exon 3 was skipped in the patient sample by sequencing the smaller fragment. The low abundance of the Δexon3 transcript in normal samples made sequencing somewhat difficult, so for confirmation we designed an oligonucleotide that contained the last five nucleotides of exon 2 and the first five nucleotides of exon 4 for hybridisation to the PCR products. As shown in fig 2C, we confirmed that normal individuals consistently produce a small amount of the shorter product; it thus represents a novel spliceform of the PHF6 gene (referred to herein as PHF6Δexon3). Alternate splicing of the PHF6 gene was previously documented but the spliceform reported retained intron 10 sequence. Exclusion of exon 3 maintains the ORF, but is probably a disease causing mutation (data not shown). Use of the cryptic acceptor splice site would predict the inclusion of seven nucleotides, thereby creating a frame shift and truncation of the protein soon afterwards (fig 2B). We observed strict nuclear expression of the fusion protein that was concentrated in the nucleolus, as confirmed by co-localisation with an anti-nucleoli antibody for both the wild type and PHF6Δexon3 proteins (fig 4). Similarly, the Arg257Gly mutation in family 1 did not affect subnuclear localisation. The truncated protein of 59 amino acids created by the use of the cryptic splice site and the inclusion of seven additional nucleotides gave a weak, non-nuclear signal when fused to GFP (data not shown). Taken together, these studies imply that the PHF6Δexon3 protein is translated and probably functionally compensates for loss of the PHF6 protein.

**DISCUSSION**

Here we present two Canadian families with features of Börjeson-Forssman-Lehmann syndrome and mutations in the PHF6 gene. One patient presented with classical features...
of BFLS (family 1) and we identified an A→G nucleotide change that resulted in an Arg257Gly missense mutation within PHF6. This mutation was identical to that previously described in an Australian patient. The other mutation we identified was a novel splicing mutation in intron 2 that resulted from an A→G nucleotide transition creating a cryptic 3’ splice site eight nucleotides from the canonical site. To date, the two mutations in our Canadian families increase the number of unique mutations in the PHF6 gene to 10, identified from 13 families. The mutations are mainly missense; additionally, two truncations, a single amino acid deletion, and a splicing defect (this report) have also been identified. The PHF6 protein contains two conserved PHD domains suggesting a role in transcription but is otherwise a protein of unknown function. However, unlike the ATRX syndrome, in which 60% of the mutations fall within the PHD domain, only one mutation has been identified within these conserved motifs of the PHF6 gene. The broad range of mutations are localised throughout the gene and thus a “loss of function” model is suggested as the disease mechanism.

Regardless, the presence of the PHF6Δexon3 transcript suggests that it may account for the milder phenotype observed in these patients, and the exciting possibility that exon 3 contains a domain critical to some aspects of PHF6 function. In support of this idea we showed that the PHF6Δexon3 transcript is most probably translated through its association with polysomes. Furthermore, PHF6Δexon3-GFP fusion proteins were localised to nucleoli, suggesting that the shorter PHF6 polypeptide is correctly targeted within the cell. Taken together, this suggests that the PHF6Δexon3 translated protein probably maintains many of the properties of the full length PHF6 protein and as such would functionally compensate for the loss of PHF6 in the affected individuals of family 2.

Figure 4 The GFP-PHF6Δexon3 fusion protein localises to the nucleolus. Previous studies showed that PHF6 encodes a nucleolar protein. GFP fusion proteins comprising either PHF6 wild type, PHF6Δexon3, or the R257G mutations were transfected into HeLa cells and co-localisation to the nucleolus was demonstrated using an antibody against nucleoli, suggesting that the shorter PHF6Δexon3 protein is correctly localised.
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Conflict of interest: none declared

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