**ELECTRONIC LETTER**

*FBN2* mutation associated with manifestations of Marfan syndrome and congenital contractural arachnodactyly

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**Key points**

- Patients with *FBN2* mutations causing congenital contractural arachnodactyly (CCA) are expected to present with scoliosis, arachnodactyly, contractures, and abnormal ears, whereas patients with *FBN1* mutations causing Marfan syndrome (MFS) have skeletal and ocular complications, and develop aortic aneurysms over time. Cardiovascular anomalies have not been considered to be a part of the disease course of CCA.

- We describe a family in which the *FBN2* mutation that the children were followed led to progressive dilatation of the aorta at the sinuses of Valsalva in two children. This is the first report of a progressive dilatation over 5 years in a CCA patient.

- We identified a mother and her two children who presented with skeletal features of MFS, and contractures, scoliosis, and a crumpled appearance to the helices of the ear, suggesting a diagnosis of CCA. The children also had aortic root dilatation on echocardiograms, which progressed over the 5 years that the children were followed. Intron based, exon specific primers were used to sequence *FBN2* to identify a mutation.

- A heterozygous G→A transversion at the +5 bp position in intron 32 of *FBN2* was identified, resulting in the mis-splicing of exon 32. The mutation was present in DNA from all three affected family members.

- Current clinical practice differentiates CCA from MFS based on the absence of the cardiovascular and ocular complications that characterise MFS. The findings presented here further blur the distinction between MFS and CCA and suggest that CCA patients should also be evaluated for aortic disease and screened regularly for cardiovascular complications.

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**Materials and Methods**

Dermal fibroblasts were explanted from skin biopsies, and genomic DNA was isolated from white blood cells, fibroblasts, and buccal cells. PCR with intron based, exon specific primers for *FBN2* to amplify exons 22–36 from genomic DNA were used as reported previously. The fragments were sequenced in both the sense and antisense directions using an ABI Prism 3100 DNA sequencer (Applied Biosystems, Foster City, CA, USA). Total RNA was isolated from dermal fibroblasts using TRIZol reagents (Life Technologies, Grand Island, NY, USA). Two *FBN2* specific primers recognising the cDNA sequence between base pairs 4065 and 4372 were designed for reverse transcription PCR (RT-PCR). The amplified cDNA fragments were gel purified by the GFX PCR DNA and Gel Band Purification kit (Amersham Pharmacia Biotech Inc., Piscataway, NJ, USA) and sequenced. Dermal fibroblasts were explanted, and metabolic labelling and analysis of fibrillin was performed as previously described.

**Abbreviations:** CCA, congenital contractural arachnodactyly; ECM, extracellular matrix; MFS, Marfan syndrome; RT-PCR, reverse transcription PCR
Restriction digest analysis was performed using the Apol enzyme (New England Biolabs, Beverly, MA, USA). The samples were PCR amplified and then quantified using Pico Green reagents (Molecular Probes, Eugene, OR, USA) and imaged on a Storm Imager (Molecular Dynamics, San Francisco, CA, USA). A 1% agarose gel (Sigma) was prepared, and 200 ng of each sample loaded and run on it.

Patients
The proband (patient #2560) was a 12 year old girl from Mexico who presented with bilateral crumpled ears, severe scoliosis, kyphosis, pectus carinatum, a highly arched palate, contractures of all digits, bilateral pes planus, and arachnodactyly with a positive thumb sign and a negative wrist sign. She was born full term without any prenatal complications. Contractures were noted at birth, and she was initially diagnosed with MFS at the age of 1 year. At 7 years of age she had an echocardiogram, which revealed a dilated aorta (sinuses of Valsalva 2.8 cm, BSA 0.9 m²), and a small perimembranous ventricular septal defect (3.5–4.5 mm) with restrictive velocity. Repeat echocardiograms over the next 5 years indicated that her aorta at the sinuses remained markedly dilated (fig 1). Atenolol was prescribed but the patient did not take the medication. Ophthalmological evaluation was normal and she did not have any motor or language deficits.

The proband’s brother (#2561) had a highly arched palate, pectus carinatum, bilateral contractures of the elbows and all the digits, arachnodactyly, scoliosis, lower abdominal striae, and bilateral pes planus. At the age of 10.6 years, his aortal root was dilated, measuring 2.95 cm (Z score 3.11, BSA 1.23 m²), and remained enlarged as he grew over the next 4 years (fig 1). At the age of 14.5 years, his sinuses of Valsalva measured 3.48 cm with a BSA of 1.88 m². The shaded area shows the normal range for aortic root measurements at the sinuses of Valsalva based on the chart published by Nison et al. 

To determine if the mutated fibrillin-2 disrupted fibrillin incorporation into the matrix, pulse chase analysis of fibrillin synthesis, secretion, proteolytic processing, and matrix accumulation was performed using fibroblasts explanted from the mother. Analysis of cellular metabolism of fibrillin-1 indicated that the FBN2 mutation present in the mother’s fibroblast did not disrupt fibrillin-1 cellular metabolism, including fibrillin incorporation into the extracellular matrix (fig 3).

RESULTS
We screened exons 22–36 of FBN2 for mutations by sequencing the amino acid coding regions and splice junctions using DNA from the proband (#2560), and a heterozygous G→A transversion was found at the +5 bp position in intron 32 (fig 2A). The mutation was present in DNA from all three affected family members, and the mutation was not present in 70 unrelated Hispanic chromosomes. RNA isolated from control fibroblasts and from fibroblasts explanted from the mother’s cells (#2562) was used for RT-PCR of an FBN2 cDNA fragment from base pairs 4065–4372. RT-PCR of the control fibroblast RNA demonstrated one band of the correct size, whereas the mother’s cells demonstrated two bands, one 120 bps smaller than the normal (fig 2B). Sequencing of the smaller band confirmed the deletion of exon 32 (bp 4097–4220). Genomic DNA was obtained from the mother’s fibroblasts, blood, and buccal cells to determine if the mother was a somatic mosaic for the FBN2 mutation. The genomic FBN2 mutation introduced a new restriction site, Apol, which was used to confirm that the mutant and normal alleles were present in equal abundance in the mother’s genomic DNA in all the tissues studied (fig 2C).

A partial anti sense sequencing of the intron32–exon32 boundary using genomic DNA from patient 2562. The line indicates the intron–exon boundary. The mutation is a G→A transversion +5 bp into intron 32. (B) Reverse transcription and PCR amplification of an FBN2 cDNA fragment from bp 4097–4220 using control fibroblast RNA (C) and RNA from the cells of patient 2562. The patient’s RNA demonstrates two bands, the wild type fragment and a fragment that is 120 bp smaller. RT-PCR of the control fibroblast RNA demonstrated one band of the correct size, whereas the mother’s cells demonstrated two bands, one 120 bps smaller than the normal (fig 2B). Sequencing of the smaller band confirmed the deletion of exon 32 (bp 4097–4220). Genomic DNA was obtained from the mother’s fibroblasts, blood, and buccal cells to determine if the mother was a somatic mosaic for the FBN2 mutation. The genomic FBN2 mutation introduced a new restriction site, Apol, which was used to confirm that the mutant and normal alleles were present in equal abundance in the mother’s genomic DNA in all the tissues studied (fig 2C).

To determine if the mutated fibrillin-2 disrupted fibrillin incorporation into the matrix, pulse chase analysis of fibrillin synthesis, secretion, proteolytic processing, and matrix accumulation was performed using fibroblasts explanted from the mother. Analysis of cellular metabolism of fibrillin-1 indicated that the FBN2 mutation present in the mother’s fibroblast did not disrupt fibrillin-1 cellular metabolism, including fibrillin incorporation into the extracellular matrix (fig 3).

Figure 1 Aortic root measurements at the sinuses of Valsalva for 2560 and 2561. The shaded area shows the normal range for aortic measurements at the sinuses of Valsalva based on the chart published by Roman et al. A represents the proband (2560), O represents the proband’s brother (2561). The graph incorporates results from serial echocardiograms taken over 6 years; the aortic dilatation has persisted over that time.

Figure 2 Genomic FBN2 mutation in intron 32 results in mis-splicing of exon 32. A Partial anti sense sequencing of the intron32–exon32 boundary using genomic DNA from patient 2562. The line indicates the intron–exon boundary. The mutation is a G→A transversion +5 bp into intron 32. (B) Reverse transcription and PCR amplification of an FBN2 cDNA fragment from bp 4097–4220 using control fibroblast RNA (C) and RNA from the cells of patient 2562. The patient’s RNA demonstrates two bands, the wild type fragment and a fragment that is 120 bp smaller. (C) The mutation inserts an Apol site in the genomic DNA. Genomic DNA was isolated from blood, fibroblasts, and buccal cells and digested with Apol for patient 2562 (lanes 1, 2, and 3, respectively) to assess if this patient’s mild phenotype resulted from mosaicism.
DISCUSSION

We identified an FBN2 mutation in a family from Mexico with features of both CCA and MFS including crumpled appearance to the helix of the ear, contractures of multiple joints, dolichostenomelia, scoliosis, pectus carinatum, striae, and a highly arched palate. Both affected children had dilatation of their aortas at the level of the sinuses of Valsalva on initial echocardiographic evaluation, and the aortic root dilatation persisted over 5 years as the children grew. These echocardiographic findings support the conclusion that FBN2 mutations can lead to aortic root dilatation in a subset of patients, and that the dilatation can persist for years. The outcome of aortic involvement in CCA has not been determined but it is interesting to note that the affected mother did not have an aortic root dilatation when we examined her at the age of 34 years. We studied three tissues from the mother (blood, skin, and buccal cells) and did not find evidence that she was mosaic for the FBN2 mutation. It is possible that the mutation may lead to various levels of mutant and normal transcript from the mutant allele, which could affect the clinical phenotype, but this could not be tested because we were unable to obtain skin biopsies from the children. Finally, the lack of cardiovascular involvement in the mother raises the question on whether the aortic dilatation resolves rather than progresses and results in aortic dissection. Further studies are needed to verify the natural history of the aortic disease in patients with FBN2 mutations. Although we were not able to determine conclusively if the children acquired different FBN1 alleles from the parents by conducting studies using four FBN1 markers, we believe that the likelihood of an independent mutation in FBN1 is too low to merit sequencing FBN1. In addition, the normal fibrillin deposition in the matrix by the mother’s cells suggests the lack of an FBN1 mutation (fig 3). A reduction of fibrillin deposition in the matrix using dermal fibroblasts is a sensitive assay for the presence of a FBN1 mutation.14

The affected children met the diagnostic criteria of MFS including the major criteria in both the skeletal and cardiovascular systems, and involvement in another system (integument, striae).15 The children also had features that are found in MFS patients but are more common in CCA, including contractures of the fingers and a crumpled appearance to the helix of the ears. There have been two reports of CCA patients with aortic root dilatation and one report of a patient with mitral valve prolapse and a dilated aortic root.3 In all three cases, the patients were diagnosed with CCA before 6 months of age. The patients in this report are the first to establish that the aortic root dilatation in CCA can persist and progress over many years, indicating that these patients need to have their aortas imaged routinely, similar to MFS patients.

The major cardiovascular abnormalities associated with FBN1 mutations are aortic root dilatation progressing to aneurysm formation and aortic dissection, and mitral valve prolapse and regurgitation.14,15 This report establishes that FBN2 mutations can also lead to aortic root dilatation, but other cardiovascular abnormalities associated with FBN2 mutations are less clearly established. None of the three affected members of this family had mitral valve prolapse or regurgitation, and only 2 of the previous 21 individuals with previously reported FBN2 mutations had mitral valve prolapse, suggesting that this is not a common feature of CCA. It has been suggested in the literature that CCA is associated with congenital heart defects, but only 2/22 CCA patients with documented FBN2 mutations have had congenital heart disease, including one of the affected patients in this report. Therefore, congenital heart disease is also not a common finding in these patients.

The expression pattern of fibrillin-1 and -2 has been extensively studied in mouse cardiac development development.16 Fibrillin-1 and -2 expression is detected early in murine cardiovascular systems (10.5 days post-conception) when the heart is still a single tube undergoing active morphogenesis. Fibrillin-1 is expressed at a higher level than fibrillin-2, and both genes were expressed in the endocardial cushion tissue associated with the wall of the atrioventricular canal. Recent studies in human embryos suggest that both fibrillin-1 and -2 are expressed early in cardiac and aortic anlage, similar to findings in the mouse.14 The expression of both genes in the developing human cardiovascular system is consistent with the findings of aortic involvement in both MFS and CCA.

Establishing that the children meet the diagnostic criteria for MFS but have an FBN2 mutation raises some issues. Should the diagnosis be based on the mutation or clinical features? Should this be considered genetic heterogeneity for MFS? Does this case represent a failure of the diagnostic criteria for MFS? The conclusion drawn is that there is significant overlap in the clinical features in patients with mutations in FBN1 and FBN2, blurring lines of distinction between MFS and CCA.

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Conflicts of interest: none declared.

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Figure 3 Pulse chase analysis of the synthesis, secretion, proteolytic processing, and extracellular matrix (ECM) incorporation of fibrillin by 2562 and an age matched control cell strain. Fibroblasts were metabolically labelled using 35S-cysteine for 30 minutes (time 0), and then chased with cold cysteine for 4 and 20 hours. At 0, 4, and 20 hours, the cellular lysate (CL) was collected to follow the intracellular fate of fibrillin (profibrils). Both cell strains made similar amounts of profibrillin, and secreted the protein by 20 hours. The media (M) was collected at 4 and 20 hours, and shows that the secreted profibrillin was proteolytically processed into fibrillin, approximately 20 kDa smaller (fib-1). The ECM was scraped and pelleted, and showed that the amount of fibrillin in the ECM was similar for both the patient (2562) and the control. Samples were fractionated by 4% SDS-PAGE. Arrows indicate the migration of profibrillin/fibrillin.
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