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***Filamin C* Truncation Mutations Are Associated With Arrhythmogenic Dilated Cardiomyopathy and Changes in the Cell–Cell Adhesion Structures**

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Abstract

OBJECTIVES—The purpose of this study was to assess the phenotype of *Filamin C* (*FLNC*) truncating variants in dilated cardiomyopathy (DCM) and understand the mechanism leading to an arrhythmogenic phenotype.

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APPENDIX For expanded Methods and Results sections, as well as supplemental figures and tables, please see the online version of this paper.

BACKGROUND—Mutations in *FLNC* are known to lead to skeletal myopathies, which may have an associated cardiac component. Recently, the clinical spectrum of *FLNC* mutations has been recognized to include a cardiac-restricted presentation in the absence of skeletal muscle involvement.

METHODS—A population of 319 U.S. and European DCM cardiomyopathy families was evaluated using whole-exome and targeted next-generation sequencing. *FLNC* truncation probands were identified and evaluated by clinical examination, histology, transmission electron microscopy, and immunohistochemistry.

RESULTS—A total of 13 individuals in 7 families (2.2%) were found to harbor 6 different *FLNC* truncation variants (2 stopgain, 1 frameshift, and 3 splicing). Of the 13 *FLNC* truncation carriers, 11 (85%) had either ventricular arrhythmias or sudden cardiac death, and 5 (38%) presented with evidence of right ventricular dilation. Pathology analysis of 2 explanted hearts from affected *FLNC* truncation carriers showed interstitial fibrosis in the right ventricle and epicardial fibrofatty infiltration in the left ventricle. Ultrastructural findings included occasional disarray of Z-discs within the sarcomere. Immunohistochemistry showed normal plakoglobin signal at cell–cell junctions, but decreased signals for desmoplakin and synapse-associated protein 97 in the myocardium and buccal mucosa.

CONCLUSIONS—We found *FLNC* truncating variants, present in 2.2% of DCM families, to be associated with a cardiac-restricted arrhythmogenic DCM phenotype characterized by a high risk of life-threatening ventricular arrhythmias and a pathological cellular phenotype partially overlapping with arrhythmogenic right ventricular cardiomyopathy.

Keywords

arrhythmias; arrhythmogenic dilated cardiomyopathy; cardiovascular genetics; Filamin C; familial dilated cardiomyopathy; heart failure

Dilated cardiomyopathy (DCM) is a major cause of heart failure and disproportionately leads to cardiac transplantation (1–3). The condition is familial in ~50% of cases, and genetic variants residing in over 40 genes have been found to cause DCM through a variety of pathological mechanisms associated with perturbations of the cytoskeleton, intercalated disc region, nuclear envelope, and muscle sarcomere (1,3). Filamin C (FLNC) is an actin cross-linking protein (4) that provides structure for the sarcomere and is one of the largest Z-disc proteins (2,725 amino acids) in cardiac and skeletal muscle. FLNC also localizes to the sarcolemma, where it connects the muscle cell to the extra-cellular matrix and is involved in related signaling pathways (5).

Originally, *FLNC* gene mutations were associated with distal and myofibrillar skeletal myopathies (MFM) (6), characterized by loss of myofibrils and filamentous intracellular aggregates of myocyte proteins, including desmin, dystrophin, and sarcoglycans. Further investigations have revealed that *FLNC* missense mutations may lead to hypertrophic cardiomyopathy (HCM) (7) and restrictive cardiomyopathy (RCM) (8). Recently, using whole exome sequencing, we identified an *FLNC* splicing variant as causing DCM in the absence of skeletal muscle involvement in 2 families (9), a finding further supported by the

report of *FLNC* truncation variants in 4% of DCM and 3% of arrhythmogenic DCM patients (10–12).

In the current study, we report the characterization of the clinical features of *FLNC* truncating variant carriers, which include a prominent arrhythmogenic DCM phenotype (13), sarcomere structural changes by transmission electron microscopy (TEM), and changes in the distribution of cell–cell junction proteins in the myocardium and buccal mucosa. These structural and cellular changes overlap with arrhythmogenic right ventricular cardiomyopathy (ARVC), and represent a critical link between DCM and ARVC, leading to a more comprehensive understanding of complex familial arrhythmia syndromes as well as an appreciation of the need for mutation-directed clinical monitoring and treatment of this population.

METHODS

STUDY POPULATION AND CARDIOMYOPATHY EVALUATION

We analyzed 319 U.S. and European DCM families from the Familial Cardiomyopathy Registry. Study subjects underwent extensive clinical evaluations (details in the Online Appendix) (14). Medical records from deceased subjects were reviewed when available (9). Informed consent was obtained from living subjects, and local institutional review boards approved the study protocols.

NEXT-GENERATION SEQUENCING AND BIOINFORMATIC ANALYSIS

Twenty larger families were evaluated by whole-exome sequencing (9). In 299 smaller families, probands were evaluated using the Illumina TruSight One-Sequence panel (Illumina, Redwood City, California), which queries 4,813 genes associated with known clinical phenotypes (15). Briefly, subject deoxyribonucleic acid (DNA) was captured with the panel, sequenced on an HISEQ 2500 (Illumina) with v4 chemistry, and mapped with Genomic Short-read Nucleotide Alignment Program (version 2012-07-20) (16). Variants were called with the Genome Analysis Toolkit (version 2.1-8-g5efb575, Broad Institute, Cambridge, Massachusetts) and classified with Annovar (version 2012-07-28) (17). Functional predictions were made with the database for Nonsynonymous SNPs and Their Functional Predictions (version 2.0) (18). All variants were confirmed by Sanger sequencing (19). Variants predicted to be damaging in at least 1 of the prediction algorithms were retained, whereas missense and truncation variants present in >1% in the 1000 Genomes Project were discarded (9,20).

Variant frequency information was obtained from the 6,500 National Human, Lung, and Blood Institute Exome Sequencing Project (21) and the Exome Aggregation Consortium (ExAC, Cambridge, Massachusetts) (22) on February 27, 2017, and was cross-referenced to the ClinVar database (23). Gene variant locations are provided in reference to *FLNC* transcript NM_001458. Cosegregation analysis was performed when DNA from biological relatives was available. Variants in other cardiomyopathy-related genes were also identified using the Illumina TruSight One Sequencing Panel, as described in the previous text, and confirmed using Sanger sequencing.

HISTOLOGY AND TRANSMISSION ELECTRON MICROSCOPY

Cardiac muscle tissue was obtained from 2 affected siblings of family DNFDC057 (Figure 1), including left ventricular (LV) tissue at the time of LV assist device placement in subject II:1 and LV and right ventricular (RV) tissue from the explanted heart of subject II:2. Fresh heart tissue samples were processed according to standard histology protocols for hematoxylin and eosin, Masson's trichrome, and immunohistochemistry staining and fixed for TEM. Details can be found in the Online Appendix.

IMMUNOSTAINING

Cotton-tipped swabs (Medi-Choice, Mechanicsville, Virginia) were used to collect buccal mucosa cells from 2 siblings with truncating variants in *FLNC* and from normal control subjects. Each cheek was rubbed with a slight rolling and scraping motion, and the resulting material was smeared on standard microscope slides. Immunostaining of buccal mucosa and myocardial tissue was performed as previously described (24), and is detailed in the Online Appendix. For immunofluorescence microscopy, antibodies included: mouse monoclonal antiplakoglobin (P8087, Sigma-Aldrich, St. Louis, Missouri), mouse monoclonal anti–connexin 43 (Cx43) (Millipore, Burlington, Massachusetts), mouse monoclonal anti–N-cadherin (Sigma-Aldrich), mouse monoclonal antidesmoplakin (Fitzgerald, Acton, Massachusetts), mouse monoclonal anti–synapse-associated protein 97SAP97 (Santa Cruz, Dallas, Texas), and rabbit polyclonal antiglycogen synthase kinase 3 β (GSK3 β) (Cell Signaling Technology, Danvers, Massachusetts). Immunostained preparations were analyzed by confocal microscopy (LSM-510, Zeiss, Oberkochen, Germany).

RIBONUCLEIC ACID SEQUENCING OF EXPLANTED HEART TISSUE

Ribonucleic acid (RNA) was extracted from frozen LV tissue using the mirVana miRNA isolation kit (Thermo Fisher Scientific, Waltham, Massachusetts) enriched for total RNA according to manufacturer's instructions with the exception of replacing the lysis/binding buffer with mechanical homogenization in TRIzol (Thermo Fisher Scientific). The library was sequenced 1 \times 50 (Illumina HiSeq 2500). Reads were filtered for quality and aligned to the GRCh37hg19 reference human genome using the Genomic Short-read Nucleotide Alignment Program. Transcripts aligning to *FLNC* were visualized using the Integrative Genomics Viewer (Broad Institute).

RESULTS

IDENTIFICATION OF *FLNC* TRUNCATIONS

Pathogenic/likely pathogenic variants have been identified in approximately 40% of dilated cardiomyopathy samples from the Familial Cardiomyopathy Registry (data not shown), and include *TTN* (11%), sarcomeric genes (10%), structural cytoskeleton genes (5%), *LMNA* (4%), ion channel genes (2%), and other rare genes (5%). A total of 6 *FLNC* truncation variants (Figure 1), including 2 *FLNC* stopgain (families DNFDC079 and TSSDC130), 1 frameshift (DNFDC057), and 3 splicing variants (families DNFDC195, TSFDC029, TSFDC031, and TSFDC043), were identified in 7 of the 319 DCM families, for an overall frequency of 2.2% (7 of 319) (Figure 2, Table 1), 100-fold more frequent than the 0.02%

FLNC loss of function variants reported in ExAC (22). Five of the *FLNC* truncation variants were absent from the 1000 Genomes Project, 6,500 Exome Sequencing Project, ExAC, and ClinVar databases; c.805C>T had a minor allele frequency of 8.3×10^{-6} in ExAC (Online Table 1). *FLNC* variants p.Y2381Gfs21X and p.G1891Vfs61X have been previously reported (9). The 6 *FLNC* truncation variants reported here (Figures 1 and 2) occur in the immunoglobulin domains of the *FLNC* protein with no apparent geographical clustering or relationships to HCM, RCM, and MFM *FLNC* variants described to date. The presence of a secondary “likely pathogenic” unique variant was found in a known cardiomyopathy-related gene in the TSFDC043 proband (*SCN5A* c.5270delT; p.F1757fs, not reported in ExAC and ClinVar databases) who did not show signs of Brugada or long QT syndromes. Finally, *FLNC* missense variants detected in the overall population of 319 families are charted to the *FLNC* protein in Online Figure 1 and details are reported in Online Table 2.

RNA-Seq was performed on the explanted heart of DNFDC057 patient II:2. The majority of *FLNC* transcripts (141 of 162 total reads; 87.0%) were wildtype, and the remaining reads predominantly contained the c.5669-1delG, resulting in a frameshift and subsequent premature stop codon (as nucleotide 5670 is also a G, splicing occurs normally but introduces a frameshift into exon 34). These data support a mechanism of nonsense-mediated decay leading to haploinsufficiency, consistent with our zebrafish studies in which morpholino knockdown of the *flncb* transcript led to a cardiac phenotype.

CLINICAL PHENOTYPES OF *FLNC* TRUNCATION AFFECTED INDIVIDUALS

Clinical features of *FLNC* truncation carriers are reported in Table 1, and a detailed clinical description is reported in the Online Appendix. None of the patients fulfilled Task Force criteria of ARVC (25). Comprehensive physical examination of the skeletal muscle of all probands revealed no skeletal muscle abnormalities; serum creatine kinase levels were normal in all tested probands.

Supraventricular and ventricular arrhythmias as well as conduction disease were prominent clinical features (Figure 1, Table 1). Ventricular arrhythmias appear to originate from the LV or appeared polymorphic. Sudden cardiac death (SCD) occurred before the age of 55 years in 5 of 22 (23%) confirmed (n = 13) or suspected by family history (n = 9) truncation carriers. RV involvement with dilatation and/or dysfunction was present in 5 of 13 (38%) cases. The overall penetrance of *FLNC* truncation variants in our 7 families was 92% (1 unaffected of 13 total confirmed truncation carriers).

HISTOLOGICAL AND ULTRASTRUCTURAL CARDIAC ANALYSIS OF *FLNC* G1891Vfs61X VARIANT

Cardiac muscle tissue was studied from 2 affected siblings of family DNFDC057. In the proband II:2, light microscopic analysis of the LV from the explanted heart showed myocyte hypertrophy, diffuse interstitial fibrosis, and focal replacement fibrosis (Figure 3A). Epicardial fat tissue infiltrated focally into the LV myocardium, especially in areas of replacement fibrosis containing clusters of degenerating myocytes with myofibrillar loss (Figure 3A). The RV showed increased interstitial fibrosis and mild fatty infiltration (Figure

3B). In the affected sibling II:1, cardiac tissue taken upon LV assist device placement showed similar cardiac tissue pathology in the LV (Online Figure 2).

Ultrastructural analysis of LV tissue of affected patient II:1 (DNFDC057) using TEM (Figures 4A and 4B) revealed largely normal sarcomere structures, although abnormal Z-discs were noted. In LV tissue from individual II:2 and II:1 (DNFDC057), the Z-discs appeared less compact and diffuse along the Z-disc axis (Figures 4C and 4D). In contrast to MFM cases, no intracellular aggregates were seen.

IMMUNOHISTOCHEMICAL ANALYSIS OF FLNC AND ARRHYTHMOGENIC-ASSOCIATED PROTEINS

Abnormalities in the distribution and expression of desmosomal and gap junction proteins have been reported in cardiac tissue of patients with arrhythmogenic cardiomyopathy (26). Because some of the clinical (SCD, ventricular arrhythmia) and structural (RV involvement, fibrofatty infiltration) features in our *FLNC* patients mirrored features of arrhythmogenic cardiomyopathy, we used immunohistochemistry to characterize selected protein distribution in the LV myocardial tissue in affected individual II:2 of family DNFDC057 (Figure 5).

Immunohistochemistry staining for the desmosomal protein desmoplakin and SAP97, a membrane-associated guanylate kinase involved in trafficking sodium and potassium channel subunits to the cell surface, revealed overall decreased signal intensity for both of these proteins compared with healthy control tissues (Figure 5), agreeing with previous studies that showed decreased expression of these proteins in ARVC (27). Additionally, staining for GSK3 β revealed that this protein retained its cytoplasmic distribution and did not translocate to the intercalated discs, which has been shown previously to occur in classical ARVC (28). Last, staining for the desmosomal protein plakoglobin and the major cardiac gap junction protein Cx43 (normally located in the intercalated discs) revealed these proteins to have immunoreactive signals similar in intensity and distribution to the healthy control tissues, although the expression of these proteins is usually reduced at cardiac cell-cell junctions in classical ARVC (26,27). Immunohistochemical staining of *FLNC* revealed no significant intracellular protein aggregates in cardiac myocytes (Figure 6).

Desmosomal and gap junction protein abnormalities have similarly been previously reported in the buccal mucosa of patients with ARVC (26), which led us to also perform immunostaining of buccal mucosa smears obtained from affected patients DNFDC057 II:1 and II:2 (Figure 7). Our buccal mucosa cell staining results were generally concordant with the LV myocardial immunostaining of patient II:2, including diminished signal intensity for desmoplakin and SAP97, and signal intensity near normal levels for plakoglobin. However, unlike the normal levels of Cx43 observed in the LV myocardial immunostaining, staining for Cx43 was found to be reduced in the buccal mucosa cells.

DISCUSSION

In a cohort of 319 DCM families, prospectively enrolled in the Familial Cardiomyopathy Research Registry at the University of Colorado Hospital and Azienda Sanitaria Universitaria Integrata of Trieste Hospital, we identified 7 families (2.2%) harboring 6

different *FLNC* truncation variants distributed across the *FLNC* gene. These truncation carriers had a prominent arrhythmogenic phenotype characteristic of arrhythmogenic DCM, family history of SCD, frequent RV involvement, and displayed no clinical signs of skeletal muscle involvement. As we previously reported, arrhythmogenic DCM patients have a higher risk for life-threatening ventricular arrhythmias and SCD, in particular when a family history of SCD is present, highlighting the importance of early identification of patients carrying *FLNC* truncation variants (13).

Filamins are large cytoskeletal actin cross-linking proteins that stabilize the actin filament networks and link them to the cell membrane by binding transmembrane proteins and ion channels (29). *FLNC* encodes a large protein (2,725 amino acids) primarily expressed in the cardiac and skeletal muscle that interacts with sarcomeric proteins in the Z-disc and the sarcolemma (6). Mutations in *FLNC* were initially reported to cause MFM (6), while cardiac involvement may have been noted, but not studied extensively. A study of German families with the p.Trp2710* founder mutation reported that 8 of 31 patients had LV hypertrophy, atrial flutter, and right bundle branch block (30). More recent reports support *FLNC* involvement in a spectrum of cardiomyopathies, including HCM, RCM, and DCM, where arrhythmias, cardiac conduction disease, and SCD were also described (7,8) in the absence of skeletal muscle pathology (7–12). Similarly, our *FLNC* truncation carriers also exhibited no clinical evidence of skeletal muscle abnormalities. Our current report provides additional evidence of an arrhythmogenic DCM phenotype likely caused by *FLNC* truncation variants, including LV dysfunction, RV involvement, severe arrhythmias, and conduction disease.

All variants identified in our study are expected to lead to a truncated or absent *FLNC* protein. Our analysis of *FLNC* transcripts revealed that most (87.0%) were wildtype, suggestive of a haploinsufficiency model. This agrees with our previous investigation reporting that explanted heart tissue from a *FLNC* truncation carrier had reduced levels of *FLNC* protein compared with healthy control samples by Western blot, lending support for a haploinsufficiency mechanism of *FLNC* pathology (9). We also previously found that a reduction in *flncb* (ortholog of human *FLNC*) RNA expression in zebrafish results in structural and functional cardiac abnormalities (9), further supporting the theory that reduced *FLNC* expression may result in the observed cardiac dysfunctions.

We additionally found irregular and thickened Z-discs in the tissue of *FLNC* truncation carriers (Figures 4A to 4D). Similarly, in our *flncb* MO knockdown zebrafish model, the cardiac muscle ultrastructure displayed prominent Z-disc disarray and malformations, and in some instances the Z-disc was absent (9). Surprisingly, our current study did not find cytoplasmic protein aggregates in the heart, which have been described previously in *FLNC*-associated patients with MFM (in muscle biopsies) as well as HCM and RCM patients (7,8). In these cases, accumulations of protein aggregates are believed to result from the inability of *FLNC* to dimerize and cross-link with actin at the C-terminal end of *FLNC*. The absence of *FLNC* protein aggregates in our study and in the series of Ortiz-Genga et al. (12), is again more in line with a haploinsufficiency model.

The highly arrhythmogenic phenotype and the pattern of biventricular subepicardial fibrosis and fatty infiltration seen in 2 siblings from family DNFDC057 is more reminiscent of

features previously described specifically in left-dominant arrhythmogenic cardiomyopathy and *PLNR14del* cardiomyopathy (31) rather than classical ARVC. For example, reduced junctional signal for desmoplakin, seen in both the heart and buccal mucosa in siblings from family DNFDC057, is more closely linked with biventricular involvement. Similarly, changes in the distribution of cell–cell junction proteins in the heart and buccal mucosa of these patients are more typical of left-dominant arrhythmogenic cardiomyopathy than classical ARVC. Interestingly, we also observed reduced signal for the membrane-associated guanylate kinase protein SAP97 in both the heart and buccal mucosa in 2 siblings from kindred DNFDC057. Such reduced SAP97 signal has been implicated in abnormal trafficking of ion channel proteins involved in channeling sodium and potassium ions, specifically related to regulating the I_{Na} , and I_{K1} currents, which help maintain normal cardiac ventricular resting membrane action potential (27). This may be relevant to the highly arrhythmogenic phenotype seen in our patients: reduced junctional signals for plakoglobin and Cx43 and translocation of GSK3 β to cell–cell junctions are all features consistently seen in classical ARVC, but were not seen in our patients. Finally, although we have previously shown that buccal mucosa cells exhibit changes similar to those seen in the hearts of ARVC patients (24), studies here are the first to directly compare buccal cells and myocardium from the same patients. These results add further credence to the idea that changes in the heart of complex familial arrhythmia syndromes may also be seen in the buccal mucosa.

STUDY LIMITATIONS

Our study may be limited by the low frequency of *FLNC* truncations, the inability to perform extensive segregation analysis due to small family sizes, and an incomplete availability of DNA samples from biological members of *FLNC* truncation families. Efforts to recruit additional family members, especially reportedly affected individuals, have not been fruitful to date. In addition, cardiac tissue was only available from 1 family (2 siblings), which hinders our ability to systematically evaluate the effects of different variants on cardiac cellular structure and function. The presence of a variant in another DCM-related gene (*SCN5A*) in combination with the *FLNC* truncation variant in patient TSFDC043 I:1 presents an additional confounding variable. Although all patients are routinely examined for muscle wasting, rigidity, muscle strength, and coordination, invasive skeletal muscle studies that may reveal more subtle pathology, such as electromyography and muscle biopsy, were not performed. Additional phenotypic characterization, such as with contrast-enhanced cardiac magnetic resonance, was also not done in our population. Finally, future studies are needed to elucidate how *FLNC* truncation variants lead to cardiomyocyte dysfunction and cardiac muscle disease.

CONCLUSIONS

Our report provides new evidence that *FLNC* truncation variants are associated with a severe arrhythmogenic DCM phenotype in the absence of overt skeletal muscle disease. *FLNC* should be included in DCM genetic testing panels, particularly when arrhythmias complicate the presenting phenotype. Additionally, patients with *FLNC* truncation variants should be clinically monitored for arrhythmias and considered for implantable cardioverter-

defibrillators. Histological and ultrastructural analysis of heart muscle showed no protein aggregates as described in MFM, but instead showed biventricular subepicardial fibrofatty infiltration, Z-disc abnormalities, and redistribution of cell–cell junction proteins. We theorize that haploinsufficiency of FLNC (9) may disrupt its normal functions of cross-linking actin filaments, connecting subsarcolemmal sarcomere Z-discs to the cell membrane and integrins, and connecting actin to cell–cell adhesion junctions in intercalated discs, to result in interference with the desmosomal/cell–cell junction pathway and manifest as a phenotypically arrhythmogenic cardiomyopathy.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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ABBREVIATIONS AND ACRONYMS

Cx43	connexin 43
DCM	dilated cardiomyopathy
DNA	deoxyribonucleic acid
ExAC	Exome Aggregation Consortium
FLNC	Filamin C
SK3β	glycogen synthase kinase 3 beta
HCM	hypertrophic cardiomyopathy
LV	left ventricle/ventricular
MFM	myofibrillar skeletal myopathy
RNA	ribonucleic acid
RV	right ventricle/ventricular
SAP97	synapse-associated protein 97
SCD	sudden cardiac death
TEM	transmission electron microscopy

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PERSPECTIVES

COMPETENCY IN MEDICAL KNOWLEDGE

As the number of genes associated with DCM continues to increase, differences in clinical presentations are becoming recognized. Patients with *FLNC* truncation variants should be clinically monitored for arrhythmias and considered for implantable cardioverter-defibrillator devices.

TRANSLATIONAL OUTLOOK

DCM is a common cause of heart failure and life-threatening arrhythmias, and it is frequently caused by gene mutations. The whole spectrum of genetic determinants of DCM is still unknown: however, recently, a novel disease gene known to cause muscular dystrophy, filamin C, has been reported in human dilated cardiomyopathy and zebrafish models. Here, we report that *FLNC* truncating variants are not rare, are associated with a cardiac-restricted phenotype, are characterized by a high risk of life-threatening ventricular arrhythmias, and are a pathological cellular phenotype affecting the cell–cell adhesion structures, which partially overlaps with ARVC.

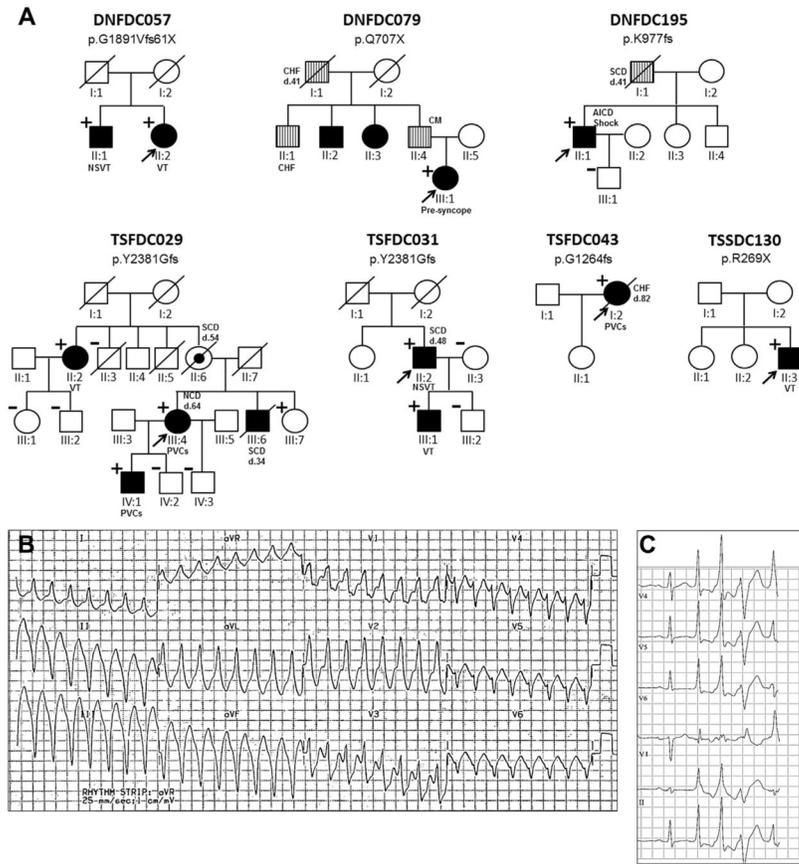


FIGURE 1. Pedigrees of DCM Families With *FLNC* Truncating Variants Displaying an Arrhythmogenic Phenotype
(A) Squares indicate males, circles indicate females, slashes indicate deceased individuals, black shading indicates a dilated cardiomyopathy (DCM) phenotype, and vertical lines indicate history of heart disease. The arrows indicate the proband. Carriers (+) and noncarriers (–) of a *FLNC* truncation variant are shown. **(B)** Electrocardiogram of subject TSSDC130 (II:3) shows sustained ventricular tachycardia. **(C)** Electrocardiogram depicts nonsustained ventricular tachycardia from individual II:1 (family DNFD057) (9).

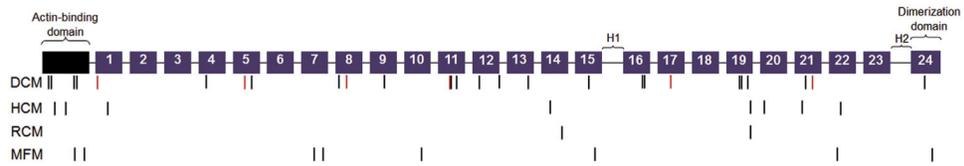


FIGURE 2. Structural Distribution of Truncating Variants in the Human FLNC Protein
 Schematic of the FLNC immunoglobulin-like repeats labeled 1 to 24 using transcript NP_001449.3. Hinge 1 and 2 domains are labeled as H1 and H2, respectively. **Red vertical lines** indicate protein positions of the 6 *FLNC* truncation variants detected in our dilated cardiomyopathy (DCM) families. **Black vertical lines** represent previously reported hypertrophic cardiomyopathy (HCM) (7), restrictive cardiomyopathy (RCM) (8), DCM variants (12), and myofibrillar skeletal myopathies (MFM) (6) variants.

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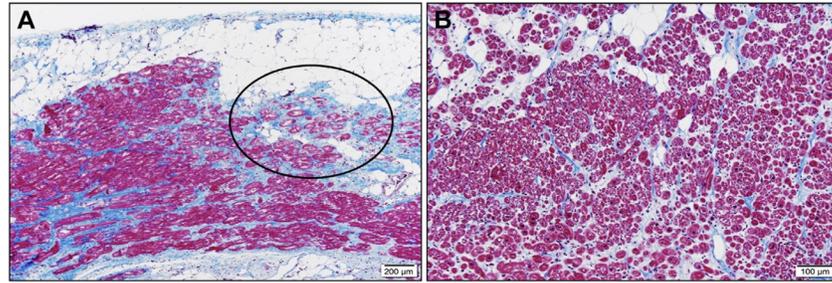


FIGURE 3. Cardiac Tissue Analysis of *FLNC* Truncation Variant Carrier From Family DNFDC057 (II:2)

(A) Trichrome staining of the left ventricle shows subepicardial interstitial and focal replacement fibrosis and fatty infiltration (**circle**) in areas containing degenerating cardiac myocytes. Scale bar = 200 µm. (B) Fatty infiltration and mild fibrosis are seen in the right ventricle. Scale bar = 100 µm.

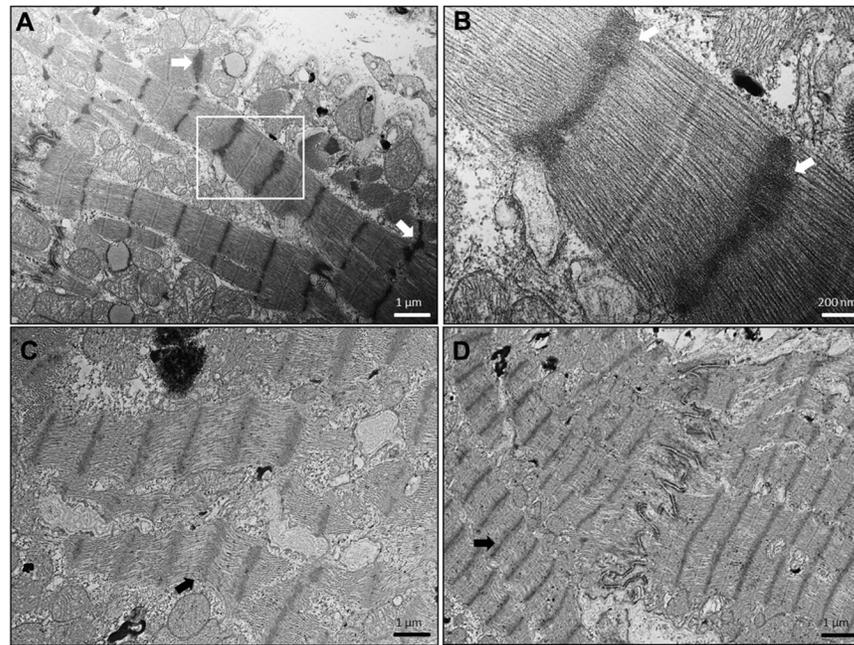


FIGURE 4. Electron Microscopy Images of Left Ventricular Cardiac Muscle From Family DNFDC057

(A) Representative images from individual II:2 show disarrayed Z-discs (**white arrows**). (B) Magnified image of the **white box in A**, showing a thickened Z-disc pattern. (C and D) Representative TEM images from individual II:1 exhibiting disarray of Z-discs (**black arrows**). No aggregates are seen in cardiac myocytes. Scale bars: (A) 1 μm , (B) 200 nm, (C and D) 1 μm .

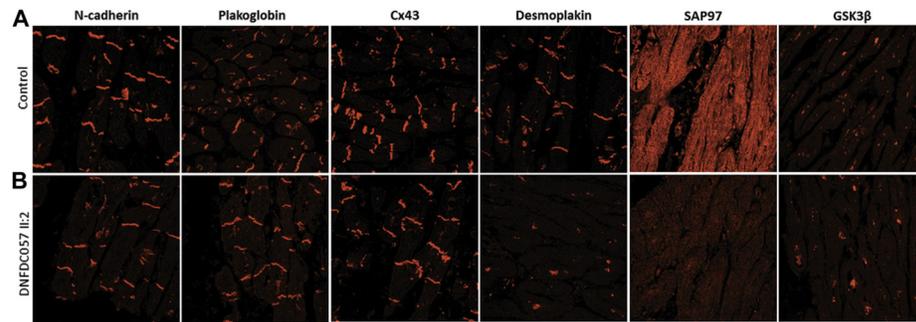


FIGURE 5. Immunohistochemistry of Left Ventricular Myocardial Tissue

Immunostaining of the explanted heart of patient DNFDC057-II:2 carrying the G1891Vfs61X *FLNC* truncation. **(A)** Immunoreactive signals for plakoglobin and connexin 43 (Cx43) at intercalated discs are normal compared with control samples, whereas junctional signal for desmoplakin is reduced. N-cadherin is used as a tissue quality control and is normal in all samples. **(B)** SAP97 signal is depressed compared with control samples. GSK3 β maintained its normal cytoplasmic distribution.

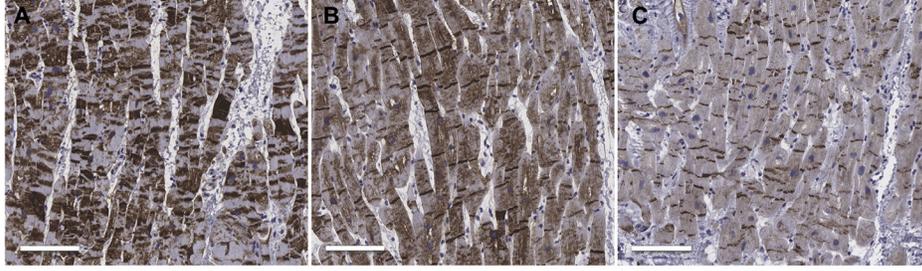


FIGURE 6. FLNC in Cardiac Tissue

Immunohistochemical staining of FLNC does not show significant presence of aggregates in cardiomyocytes, and the weaker staining in the patient (C) suggests a reduced amount of FLNC protein compared with control subjects (A and B), as previously shown by western blot (9).

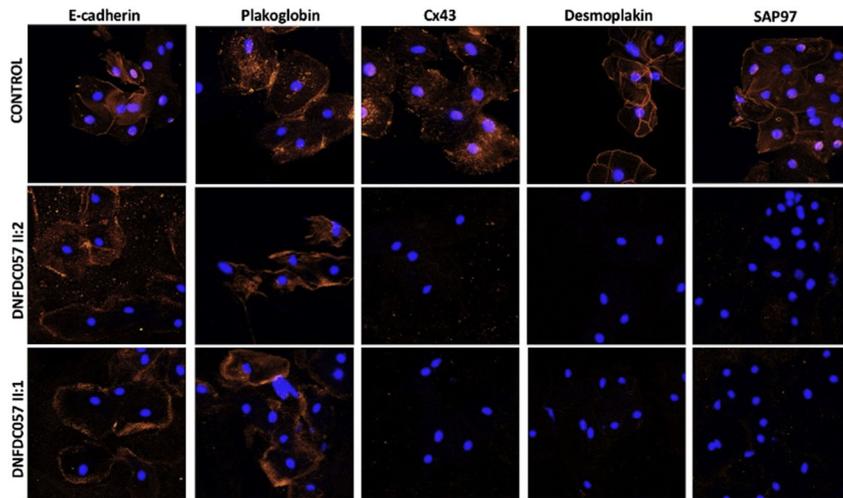


FIGURE 7. Immunohistochemistry of Buccal Mucosa
 Immunostaining of the buccal mucosa in patients DNFDC057-II:1 and II:2 shows normal signals for plakoglobin, and diminished signal for connexin 43 (Cx43), desmoplakin, and SAP97. E-cadherin staining is used as a cell quality control and is normal in all samples.

TABLE 1
Clinical Phenotype Features of FLNC Truncation Carriers and DCM-Affected Individuals

Family	DNFDC057	DNFDC079	DNFDC195	TSFDC029
Individual	II:1	III:1	II:2	II:2
Sex	M	F	M	F
Age at diagnosis, yrs	59	33	39	62
Variation	Frameshift	Stopgain	Splicing	Splicing
Nucleotide change	c.5669-1delG	c.2119C>T	c.2930-1G>T	c.7251+1A>G
AA change	p.G1891Vfs1X	p.Q707X	p.K977fs	p.Y2381Gfs
Secondary mutation				
NYHA functional class	III	III	II	I
Symptoms	DOE, fatigue	Palpitations, SOB	Pre-syncope, SOB	Palpitations
Arrhythmias	PACs, PVCs, NSVT	PVCs, AF, sustained VT (1997)	No arrhythmias	Multiform PVCs
ECG	AVB1, incomplete LBBB	AVB1, LVH	Nonspecific ST changes	PVCs
LVEDD, cm	6.4	5.6	5.4	5.4, inferobasal hypokinesis
LVEF, %	45	10	20	15
CK, U/l [†]	118	106	56	NA
RV	Normal	Mild dilatation	Dilatation	Mild dilatation and dysfunction
Outcome	NYHA functional class II, LVEF 21%, CRT, AICD, LVAD (2016)	Severe LV and RV dysfunction, heart transplant (2009)	Normalized LVEF 60%	NYHA functional class I, LVEF 51%
Follow-up, yrs	11	11	1	6
				15
				14

Family	TSFDC029	TSFDC031	TSFDC043	TSSDC130
Individual	III:6*	III:7	IV:1	II:2
Sex	M	F	M	M
Age at diagnosis, yrs	35	34	27	44
Variation	Splicing	Splicing	Splicing	Splicing
				76
				20
				20

Family	TSFDC029	TSFDC031	TSFDC043	TSSDC130
Nucleotide change	c.7251+1A>G	c.7251+1A>G	c.3791-1G>A	c.805C>T
AA change	p.Y2381Gfs	p.Y2381Gfs	p.G1264fs	p.R269X
Secondary mutation			SCN5A c.5270delT; p.F1757fs	
NYHA functional class	I	II	III	II
Symptoms	Asymptomatic, SCD	Fatigue, palpitations	Fatigue, SOB	Syncope
Arrhythmias	NA	No arrhythmias	PAF, SVT, SAECG	Sustained VT
ECG	Normal	PACs, PVCs (93/24h)	Normal	SB, IV conduction delay, nonspecific ST changes
LVEDD, cm	4.9	5.3	5.7	6.4
LVEF, %	63	45	47	14
CK, U/l [†]	50	80	103	NA
RV	Normal	Normal	NA	Dilatation and dysfunction
Outcome	Cardiomegaly at autopsy	NYHA functional class I	NYHA functional class II, SCD	PM, heart failure death (2008)
	NYHA functional class I	NYHA functional class I, palpitations, LVEF 52%	NYHA functional class I, palpitations, LVEF 40%	Recurrent sustained VT, AICD (1999), NYHA functional class II
Follow-up, yrs	15	15	4	17
				9
				14

Families DNFD057, TSFDC029, and TSFDC031 are previously reported variants (9).

* Individual III:6 died before enrollment; DNA was not available for genetic testing.

[†]Normal CK level is <223 U/l.

AA = amino acid; AF = atrial fibrillation; AICD = automatic implantable cardioverter-defibrillator; AVB = atrioventricular block; CK = creatine kinase; CRT = cardiac resynchronization therapy; DOE = dyspnea on exertion; ECG = electrocardiogram; FS = fractional shortening; IV = intraventricular; LAFB = left anterior fascicular block; LBBB = left bundle branch block; LVAD = left ventricular assist device; LVEDD; left ventricular end-diastolic dimension; LVEF = left ventricular ejection fraction; LVH = left ventricular hypertrophy; NA = not available; NCD = noncardiac death; NYHA = New York Association functional class; PAF = paroxysmal atrial fibrillation; PM = pacemaker; PAC = premature atrial contraction, PVC = premature ventricular contraction; RBBB = right bundle branch block; RV = right ventricle; SAECG = signal-averaged electrocardiography; SB = sinus bradycardia; SCD = sudden cardiac death; SOB = shortness of breath; ST = sinus tachycardia; VT = ventricular tachycardia.