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Novel *ALPK3* mutation in a Tunisian patient with pediatric cardiomyopathy and facio-thoraco-skeletal features

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Abstract

Pediatric cardiomyopathy is a complex disease with clinical and genetic heterogeneity. Recently, the *ALPK3* gene was described as a new hereditary cardiomyopathy gene underlying pediatric cardiomyopathies. Only eight patients carrying mutations in *ALPK3* have been reported to date. Here, we report a 3-year-old male patient with both hypertrophic and dilated cardiomyopathy. The patient presented dysmorphic features and skeletal deformities of hands and feet, pectus excavatum, and cleft palate. The genetic investigation was performed by whole-exome sequencing in the patient and his parents. We identified a novel homozygous mutation in *ALPK3* (c.1531_1532delAA; p.Lys511Argfs*12). Our work extends the phenotypic spectrum of the *ALPK3*-associated cardiomyopathy by reporting additional clinical features. This is the first study of a Tunisian patient with mutation in the *ALPK3* gene. In conclusion, *ALPK3* should be included in the list of genes to be considered in genetic studies for patients affected with pediatric syndromic cardiomyopathy.

Introduction

Hypertrophic cardiomyopathy (HCM) and dilated cardiomyopathy (DCM) are the most common forms of primary cardiomyopathies and the major cause of heart failure and sudden cardiac death [1]. HCM is characterized by increased ventricular wall thickness associated with diastolic dysfunction of ventricular chambers. DCM is defined by dilation and systolic dysfunction of the left ventricle (LV) but right-ventricular involvement was also observed [1, 2]. These two entities occur in children with an annual incidence of 1.13 cases per 100.000 children younger than 18 years and 8.34 cases per 100.000 infants [3]. Moreover, higher incidence was found in boys and infants under 1 year of age for both HCM and DCM [3]. HCM and DCM are the most frequent defects among pediatric probands (51% HCM and 30% DCM) [4]. These findings were consistent with the results of the Pediatric Cardiomyopathy Registry (PCMR) [3, 5]. HCM and DCM have genetic and phenotypic heterogeneity with incomplete penetrance and variable expressivity. Different cardiac phenotypes are caused by mutations in the same gene, and numerous genes can be responsible of the same cardiomyopathy [6]. Furthermore, pediatric cardiomyopathies have both genetic and nongenetic etiologies. The genetic make-up of pediatric cardiomyopathies is more diversified than in the adult population because additional syndromic and metabolic genetic causes can be implicated [7]. Hence, the identification of the mutation spectrum and causal associated-genes are challenging. The advent of next generation sequencing technologies, such as whole-exome sequencing (WES) allowed

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the identification of the genetic basis of pediatric cardio-myopathies. Using this technique and the homozygosity mapping, the alpha-kinase 3 (*ALPK3*) gene was recently discovered as a novel pediatric cardiomyopathy-associated gene [8]. Indeed, homozygous mutations in the *ALPK3* gene were identified in 5 patients with pediatric cardio-myopathy. This study hypothesized that *ALPK3* might control initial induction of differentiation and maturation of cardiomyocytes by regulating the expression of cardiac transcription factors such as *HEY2* and *HAND* [8]. The *ALPK3* gene encodes a 1907 amino acids protein, which contains three functional domains: one α-type protein kinase domain and two immunoglobin-like domains. *ALPK3* appears to be involved in cardiomyocytes differ-entiation and heart development [9]. A recent study using human induced pluripotent stem cell showed that absence of *ALPK3* results in abnormal intracellular calcium [10]. Here, we report a novel homozygous frameshift mutation in the *ALPK3* gene in a 3-year-old boy affected with mixed HCM/DCM phenotype and dysmorphic features.

Materials and methods

This study was conducted according to the principles of the Declaration of Helsinki and to the ethical standards of the first author's institutional review board (Registration num-ber: IRB00005445, FWA00010074).

The parents provided their written informed consent to participate in this study. After informed consent was obtained, peripheral blood samples were collected from the affected child and his parents.

Genomic DNA was extracted from the samples accord-ing to standard techniques. Whole-exome sequencing (WES) was performed for the trio (the affected child, the father and the mother), by the Genomics and Bioinformatics Platform (GBiM) from the UMR 1251/Marseille Medical Genetics facility, using the NimbleGen SeqCap EZ MedExome kit (total design size 47 Mb) according to the manufacturer's protocol (Roche Sequencing Solutions, Madison, USA). The SeqCap EZ MedExome kit targets the entire human exome with enhanced coverage of exons from medically relevant genes in Mendelian diseases. Enriched fragment libraries were sequenced on the Illumina NextSeq 500 platform (Illumina, San Diego, CA, USA) using a 150 bp paired-end sequencing protocol. Raw data were mapped to the built of the human genome (hg19) by using BWA 0.7.5. Variant calling was subsequently performed using GATK and annotation was done with ANNOVAR. All subsequent steps were performed using our in-house soft-ware for variant annotation and segregation VarAFT (http://varaft.eu). WES data from the patient and his parents were analyzed simultaneously and segregated using VarAFT. All

modes of inheritance have been tested during the analysis of the data.

In order to reduce the significant number of variants generated by WES sequencing and to identify relevant variants, a strategy of filtering was adopted. Variants were selected as following: [1] variants with Minor Allele Frequency (MAF) ≥ 1% in the Exome Aggregation Con-sortium database (ExAC) (http://exac.broadinstitute.org/) were removed [2]. The remaining variants were filtered based on their type and genomic localization, thus, synonymous, intronic, variants in intergenic, 3′ and 5′ UTR regions were discarded [3]. The obtained variants' list (including rare, nonsense, missense, splice site, and frameshift INDELs), was then subsequently filtered according to the in silico pathogenicity prediction. Thus, variants predicted as polymorphism according to UMD-Predictor (http://umd-predictor.eu/), SIFT (http://sift.jcvi.org/), PolyPhen-2 (http://genetics.bwh.harvard.edu/pph2/), and Mutation Taster (http://www.mutationtaster.org/) were excluded.

Results

Clinical presentation

The patient, a 3-year-old Tunisian boy, is the only child of apparently healthy first cousins aged 21 (mother) and 28 (father) years. He was born at term by spontaneous vaginal delivery following an uncomplicated pregnancy. His birth weight was 3550 g. The patient was hospitalized at birth for 2 months and a week because of respiratory distress. At 7 days, he was diagnosed with mixed HCM/DCM cardiomyopathy, and began treatment by captopril (25 mg), furosemide (40 mg) and carvedilol (6.25 mg). Echocardio-graphy performed at the age of 3 months revealed levo-cardia, situs solitus, LV dilation and concentric hypertrophy with altered systolic function (end-diastolic diameter (EDD) = 26 mm; end-systolic diameter (ESD) = 24 mm; inter-ventricular septum thickness at end-diastole (IVSd) = 9 mm; ejection fraction (EF) = 35%). The right-ventricular walls were enlarged. A patent foramen ovale with left to right shunt and mild tricuspid insufficiency (systolic pul-monary arterial pressure = 30 mmHg) were also reported. Neither aortic insufficiency nor valvular aortic stenosis were observed. There was no isthmic coarctation of the aorta. Cardiac examination at 6 months showed less dilation of the LV with improvement of the systolic function and concentric hypertrophy of both LV and RV (EDD = 27 mm; ESD = 20 mm; IVSd = 12 mm, EF = 50%). Minimal mitral valve insufficiency was noted. Echocardiographic indices at 8 months were as following: EDD = 26 mm; ESD = 19 mm; IVSd = 12 mm, EF = 52% and the LV posterior wall

Fig. 1 Echocardiographic images. **a** Echocardiography of the patient at the age of 11 months and **b** at 15 months. **c** Echocardiography of the father at the age of 30 years
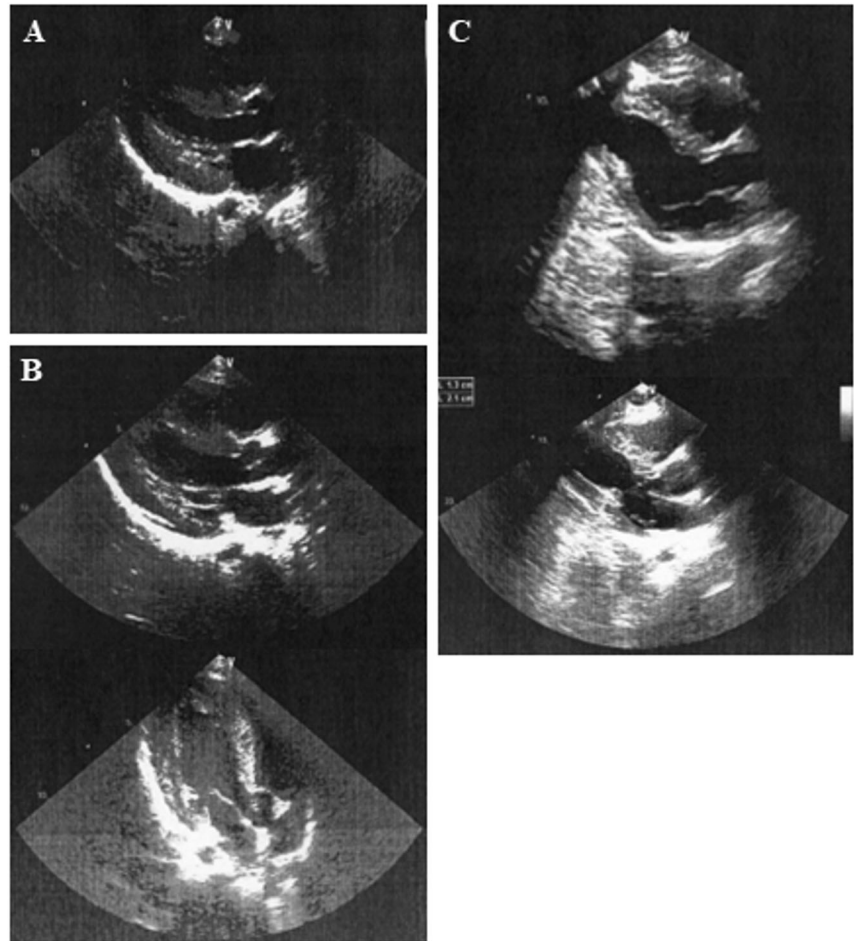
thickness = 12 mm. At 11 months, echocardiography revealed concentric hypertrophy of both ventricles without dilation (Fig. 1a.) (EDD = 27 mm; ESD = 15 mm; IVSd = 18 mm, EF = 74%). At 15 months, echocardiography showed a cardiomyopathy of predominantly hypertrophic LV without obstruction (Fig. 1b.). Abnormalities in left ventricular compliance were also observed and echocardiographic indices were as following: EDD = 25 mm; ESD = 16 mm; IVSd = 15 mm, EF = 65%, and the LV posterior wall thickness = 12 mm. Echocardiographic screening in the father revealed asymmetric septal hypertrophy (septal thickness = 16 mm) and minor congenital mitral anomaly without valvular dysfunction (Fig. 1c). The mother's echocardiography was without abnormalities.

First examination by geneticists at the age of 2 months and a half revealed a weight at 3800 g (<3rd centile), a height at 54 cm (<3rd centile) and a head circumference at 38.5 cm (3rd−15th centile), dysmorphic features including broad forehead, protruding eyes, divergent strabismus, blue sclera, low-set ears, long philtrum, thin lips, cleft palate, microretrognathia, and bilateral camptodactyly of hands and axial hypotonia.

On last examination, at the age of 2 years and 9 months, weight was on the 25th percentile; height and head circumference were on the 50th percentile. He had almost the same dysmorphic features characterized by flat occiput, triangular, and flat face, broad forehead, down-slanting palpebral fissures, protruding eyes, mild ptosis of the left eyelid, blue sclera, low set and backward-rotated small ears, broad nasal ridge and nasal tip, thick ala nasi, short columella, long philtrum, everted lips, cleft palate, microretrognathia, and full cheeks. He also had short neck, sloping shoulders, pectus excavatum, bilateral camptodactyly of hands, bilateral overlapping of the 2nd and 3rd toes, bilateral clinodactyly of the 4th and 5th toes, and knee stiffness. The psychomotor development of the patient was normal.

R-banded chromosome analysis on cultured peripheral blood lymphocytes from the proband was normal 46, XY. Fluorescent In Situ Hybridization (FISH) analysis with MD DiGeorge T-box1 (22q11)/22q13 (SHANK3) kreatech probe was performed but no microdeletion was identified. Creatine phosphokinase, lactate dehydrogenase, serum creatinine, ammonia, and lactates levels and chromatographic analysis of amino and organic acids were normal.

Table 1 List of variants identified after the filtering process according to the autosomal recessive pattern of inheritance

Gene	Ref	Alt	Genotype	Variant type	Amino acid change	rs ID
ADAMTS7	A	G	hom	NA	NM_014272:exon22:c.4740 + 2 T > C	rs773063450
ADH4	CA	–	hom	frameshift deletion	NM_000670:exon6:c.822_823del:p.C274fs	rs29001206
ALPK3	AA	–	hom	frameshift deletion	NM_020778:exon5:c.1531_1532del:p.K511fs	NA
BRD1	G	A	hom	NA	NM_001304808:exon5:c.1657–4 C > T	rs376646773
CCSER1	T	C	hom	NA	NM_001145065:exon3:c.1325–3 T > C	rs116747086
MYO9B	G	A	hom	nonsynonymous SNV	NM_001130065:exon30:c.4894 G > A:p.G1632R	rs745853652
TRMT1	C	T	hom	nonsynonymous SNV	NM_001142554:exon10:c.1310 G > A:p.R437Q	rs770329038

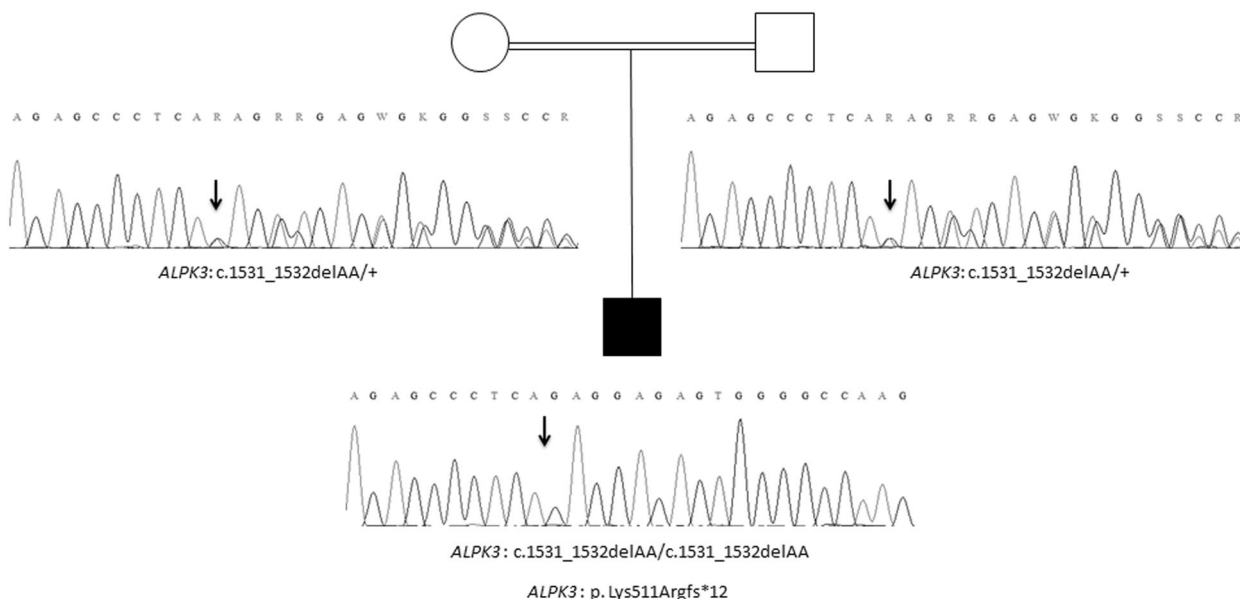*Ref* reference allele, *Alt* alternate allele, *hom* homozygous

Fig. 2 Pedigree of the family. Sanger electropherograms are shown below symbols. (+) indicates the wild-type allele. The arrow indicates the position of the mutation

Whole-exome analysis

Taking into account the large number of genes mutated in inherited cardiac diseases we have performed a WES for the family (trio). WES data were analyzed and segregated using the Variant Annotation and Filtering Tool VarAFT. On average, 92 and 87% of all targeted exome was covered to a depth of 20× and 30×, respectively. All variants identified in our patient using the filtering strategy described above (Material and methods) are listed in Table 1 (homozygous mutations) and Supplementary Table 1 (heterozygous mutations). Based on these lists of variant we prioritized the homozygous frame-shift deletion in exon 5 of the *ALPK3* gene (NM_020778): c.1531_1532delAA; p.Lys511Argfs*12 as a likely causative variant. Indeed, both parents were found heterozygous for this variant (Fig. 2). Moreover, the *ALPK3* c.1531_1532delAA; p.Lys511Argfs*12 is not reported in the following databases: ExAC, dbSNP (https://www.ncbi.nlm.nih.gov/projects/SNP/), NHLBI Exome Sequencing Project (http://evs.gs.washington.edu/EVS/), gnomAD (http://gnomad.broadinstitute.org), 1000 Genomes (http://www.internationalgenome.org), and GME Variome (http://igm.ucsd.edu/gme/). In order to exclude the possibility that the *ALPK3* p.Lys511Argfs*12 deletion could be a frequent variant specific of the Tunisian population, our in-house database, gathering WES data from 70 Tunisian individuals (140 chr) was queried and the variant was not present.

Discussion

We report a 3-year-old boy born to consanguineous parents of Tunisian origin and affected with mixed HCM/DCM, dysmorphic features, pectus excavatum, and skeletal deformities of both hands and feet.

Fig. 3 A schematic representation of the *ALPK3* gene. Blue boxes represent exons. Purple boxes represent untranslated regions (3′ and 5′ UTR). Mutations reported previously are indicated in blue color. Mutation identified in this study is indicated in red color. The three domains—Immunoglobulin-like (Ig-like, red boxes) and Alpha-kinase (green box) domains are also indicated

Through an autosomal recessive model of inheritance analysis, we identified a novel frameshift deletion in *ALPK3* not previously described in any frequency datasets. The *ALPK3* c.1531_1532delAA variant is predicted to result in a premature stop codon (p.Lys511Argfs*12) leading to nonsense-mediated mRNA decay. To our knowledge, this novel variant in *ALPK3* c.1531_1532delAA; is the sixth mutation identified in patient with pediatric cardiomyopathy, as only five mutations in *ALPK3* have been reported to date: c.4736–1 G > A, c.3781 C > T, c.5294 G > A, c.3792 G > A, and c.2018delC (Fig. 3) [8, 10, 11].

The human *ALPK3* gene (OMIM*617608) encodes the alpha-kinase 3 protein and is mainly expressed in heart and skeletal muscle. In 2001, Hosoda et al. identified the *ALPK3* gene, also named *MIDORI* (murine Myocyte Induction Differentiation Originator) using the differential display technique in the mouse P19CL6 cell line system and demonstrated that its expression is enriched in the forming heart during early development.

Different studies suggested that *ALPK3* is involved in the organization of myofibrils and the assembly of intercalated discs [8, 10, 12]. Indeed, a recent study using CRISPR/cas9 editing in a proband-derived iPSC line confirmed that the bi-allelic loss of function mutation in *ALPK3* is pathogenic. Moreover, heterozygous correction of *ALPK3* allowed the full restoration of the wild-type phenotype [10]. The loss of function of *ALPK3* disrupts also membrane repolarization by extending the extracellular field potential duration. Calcium mishandling was also noted, which could underlie the cardiac hypertrophy and arrhythmia [10].

Mixed HCM/DCM phenotype was noted among children [6], in particular in patients mutated in the *ALPK3* gene [8, 10, 11]. Previous studies have reported cases with progression of HCM to DCM [13–15]. Our patient displayed initially a mixed HCM/DCM phenotype that has evolved into a concentric hypertrophy of both left and right ventricles. Çağlayan et al. reported a 2½-year-old male patient carrying a homozygous frameshift mutation in *ALPK3* (c.2018delC; p.Gln675Serfs*30) with a progression of DCM to HCM [11]. Moreover, three patients harboring mutations in *ALPK3* displayed significant right-ventricular dysfunction [8]. On the cardiac level, the phenotype of our patient is consistent with that of patients carrying mutations in *ALPK3* previously described [8, 10, 11].

In our study, both parents were found heterozygous for the *ALPK3* c.1531_1532delAA; p.Lys511Argfs*12 mutation. Echocardiography of the mother did not show any cardiac dysfunction. However, the father presented hypertrophy of the inter-ventricular septum and minor congenital mitral anomaly. These observations are consistent with previous studies which found that heterozygous carriers of *ALPK3* mutations displayed either no evidence of cardiomyopathy or later-onset cardiomyopathy or an atypical distribution of hypertrophy [8, 10].

Hence, the c.1531_1532delAA; p.Lys511Argfs*12 in *ALPK3* at a homozygous state is the likely pathogenic mutation underlying the cardiac phenotype of our patient. Furthermore, we hypothesized that *ALPK3* gene could be responsible of the dysmorphic and skeletal features of our patient. Low-set ears and high arched palate were the unique dysmorphic features described in one patient harboring *ALPK3* mutation [11]. The clinical presentation of our patient is more diversified including cleft palate, pectus excavatum, bilateral camptodactyly, bilateral clinodactyly, and knee stiffness. Tissues expression of all identified variants (Table 1 and Supplementary Table 1) using GTEx database as well as related OMIM diseases did not reveal an association with skeletal deformities, pectus excavatum and cleft palate, except the *ALPK3* variant. Indeed, previous studies in the mouse revealed that *ALPK3* is expressed in the fetal and adult heart, as well as branchial arch and skeletal muscles [9, 12]. Similarly, a high level of *ALPK3* transcript was detected in cardiac and skeletal muscles in humans [10].

In conclusion, our study reinforces the implication of *ALPK3* in pediatric cardiomyopathy and sheds light on the syndromic nature of the disease. Therefore, we have extended the mutational and phenotypic spectrum of *ALPK3*-related disease by reporting a novel homozygous mutation associated with additional clinical features.

Compliance with ethical standards

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