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Clinical genetic testing in four highly suspected pediatric restrictive cardiomyopathy cases

Min Zheng^{1†}, Hong Huang^{2†}, Xu Zhu¹, Harvey Ho³, Liling Li¹ and Xiaojuan Ji^{1*}

Abstract

Background: Restrictive cardiomyopathy (RCM) presents a high risk for sudden cardiac death in pediatric patients. Constrictive pericarditis (CP) exhibits a similar clinical presentation to RCM and requires differential diagnosis. While mutations of genes that encode sarcomeric and cytoskeletal proteins may lead to RCM, infection, rather than gene mutation, is the main cause of CP. Genetic testing may be helpful in the clinical diagnosis of RCM.

Methods: In this case series study, we screened for *TNNI3*, *TNNT2*, and *DES* gene mutations that are known to be etiologically linked to RCM in four pediatric patients with suspected RCM.

Results: We identified one novel heterozygous mutation, c.517C>T (substitution, position 517 C → T) (amino acid conversion, p.Leu173Phe), and two already known heterozygous mutations, c.508C>T (substitution, position 508, C → T) (amino acid conversion, p.Arg170Trp) and c.575G>A (substitution, position 575, G → A) (amino acid conversion, p.Arg192His), in the *TNNI3* gene in three of the four patients.

Conclusion: Our findings support the notion that genetic testing may be helpful in the clinical diagnosis of RCM.

Keywords: Restrictive cardiomyopathy, *TNNI3*, Mutation, Constrictive pericarditis

Background

Restrictive cardiomyopathy (RCM) is a rare cardiomyopathy in which the cardiac walls are rigid and the heart is restricted from stretching and filling properly, thus presenting a high risk for cardiac death in pediatric patients [1]. To diagnose RCM, it is crucial to rule out constrictive pericarditis (CP), another cardiac disorder that has

similar clinical presentations and imaging manifestations but different pathophysiological alterations, prognoses, and treatments [2]. For example, in RCM, diastolic dysfunction is caused by abnormal elastic properties of the myocardium and/or intercellular matrix, whereas in CP, diastolic dysfunction is caused by external pericardial constraints [2]. The treatments for RCM and CP are also different. Currently, there are no curative treatments for RCM and the prognosis is generally very poor [3]. Cardiac transplantation is the only effective treatment [3], while CP can often be remedied surgically.

As mentioned above, differentiating RCM from CP in clinical diagnosis can be challenging [2], and many clinical cases have been diagnosed by thoracotomy, which is invasive and associated with high mortality [4]. There are a number of mutations in genes encoding sarcomeric and cytoskeletal proteins, including *TNNI3*, *ACTC*, *β-MHC*,

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TNNT2, *TNNC1*, *DES*, *MYH*, *MYL3*, and *CRYAB*, that have been reported to be etiologically linked to RCM [5]. These gene mutations are distinct from CP or infiltration of cardiac muscle that are usually caused by other pathogenic factors. Thus, it has been suggested that genetic screening of genes encoding sarcomeric proteins could be an important tool to clinically diagnose RCM [6].

In this case series study, we screened gene mutations in *TNNI3*, *TNNT2*, and *DES*, which have been shown to be pathogenic for RCM, in four pediatric patients with suspected RCM and whose transthoracic echocardiography (TTE) presented a similar restricted ventricular filling pattern.

Methods

Ethical approval

This study was approved by the Ethics Committee of Children's Hospital of Chongqing Medical University (074/2013), all methods were carried out in accordance with relevant guidelines and regulations. Informed consent was obtained from the parents of the pediatric patients.

Patients

Four pediatric patients with suspected RCM were admitted to our hospital and underwent TTE examination, which revealed typical signs of a restrictive filling pattern with abnormal E/A ratios and isovolumic relaxation times. The clinical data of these four patients, including family history, disease onset time, clinical symptoms, physical signs, and the results of TTE and other diagnostic information, were obtained from our hospital database. TTE was performed in accordance with the recommendations by the American Society of Echocardiography [7, 8].

Variant analysis

Genomic DNA was extracted from peripheral blood samples using the Whole Blood DNA Mini kit (Yaneng BIO science Co., Ltd, Shenzhen, China) according to the manufacturer's instructions. DNA concentration and purity were analyzed using the Nanodrop ND-2000 (Nanodrop Technologies Company, USA). Primer sequences used for polymerase chain reaction (PCR) in this study as follows: for *DES*8-9: 5'-TGT GCGATGGACCTGTTAC-3' (forward) and 5'-AGG CTCACTCACTGCCAACA-3' (reverse); for *TNNI3*-7: 5'-CCAGGTTATGCCAGTGGTTTTG-3' (forward) and 5'-CCCCTCAGCATCCTCTTTCC-3' (reverse); for *TNNI3*-8: 5'-CTTAGGCATCCAGGGTAGAGT-3' (forward) and 5'-GCAGTAGGCAGGAAGGC-3' (reverse); for *TNNT2*-8: 5'-GGGGCAGTGCTGGAA GAT-3' (forward) and 5'-GCAGTCAAGGAGCAT

CCAGTA-3' (reverse); PCR products were analyzed using Sanger sequencing (a chain termination method) with the ABI 3730XL (Thermo Fisher Scientific Inc., Waltham, MA, USA) and further analyzed using the chromas 2.6.6 DNA sequencing Software (Technelysium Pty Ltd, South Brisbane, Australia).

Data from a control group that consisted of anonymous blood samples from 50 mixed-ancestry individuals of varying ages and genders were obtained from the clinical molecular biological laboratory.

Variants were named based on the nomenclature of the Human Genome Variation Society (<http://www.hgvs.org/mutnomen>). The reference sequences for nucleotides and amino acids were obtained from the National Center of Biotechnology Information (NCBI, <http://www.ncbi.nlm.nih.gov>). Protein IDs encoded by *TNNI3* were obtained from the UniProt Database (<http://www.uniprot.org/>).

Results

General information

Case 1: A 4-year, 5-month-old girl had clinical symptoms of fatigue and exertional shortness of breath. The concentration of serum B-type natriuretic peptide (BNP) was 2070 pg/ml. Abdominal ultrasonography revealed congestive hepatomegaly. Electrocardiogram (ECG) showed bi-atrial enlargement and diffuse ST-T wave changes. The girl eventually died. No family history of RCM or other cardiovascular diseases was reported.

Case 2: A 5-year-old girl had clinical symptoms of exertional fatigue, shortness of breath, and lower extremity edema. The concentration of serum BNP was 2243 pg/ml. Abdominal ultrasonography showed congestive hepatomegaly. ECG indicated ST-T wave changes. At age 6, the girl died suddenly at home. No family history of RCM or other cardiovascular diseases was reported.

Case 3: A 4-month, 21-day-old boy presented with clinical manifestations of cyanosis and late hoarseness. No auxiliary examination results were obtained except for echocardiography. The boy died of heart failure and multiple organ dysfunction soon after admission. No family history of RCM or other cardiovascular diseases was reported.

Case 4: A 7-year, 2-month-old girl was admitted to our hospital with symptoms of coughing and expectoration. The concentration of serum BNP was not obtained. Abdominal ultrasound examination showed congestive hepatomegaly and a large amount of peritoneal effusion. ECG revealed left atrial hypertrophy and a change in ST-T wave. At age 11, the girl died suddenly on her way to school. No family history of RCM or other cardiovascular diseases was reported.

Imaging examination

Case 1: Chest X-ray showed increased heart shadow without calcification of the pericardium (Fig. 1a). Cardiac magnetic resonance imaging (MRI) revealed a bi-atrial enlargement without calcification of the pericardium, thickened pericardium, or endocardium (data not shown). Two-dimensional echocardiography showed that the left and right atria were enlarged, the right ventricle was slightly enlarged, and the left ventricle was normal in size, without calcification of the pericardium, thickened pericardium, or endocardium (Fig. 1g). M-mode echocardiography showed that the left ventricular ejection fraction was less than 55%, and there was no abrupt septal

movement ('notch' or 'bounce' in early diastole, or septal movement toward left ventricle in inspiration) (Fig. 2a). Pulsed Doppler echocardiography showed that the ratio of peak E to peak A velocity of mitral valve flow was less than 1 ($E/A < 1$) and the isovolumic relaxation time (IVRT) was longer than 80 ms (Fig. 2d). Tissue velocity imaging showed that the peak e' and peak a' velocity of mitral annulus decreased with an $e'/a' < 1$ and the peak e' was < 8 cm/s (Fig. 2g).

Case 2: Chest X-ray showed increased heart shadow without calcification of the pericardium (Fig. 1b). Cardiac MRI revealed a bi-atrial enlargement without calcification of the pericardium, thickened pericardium,

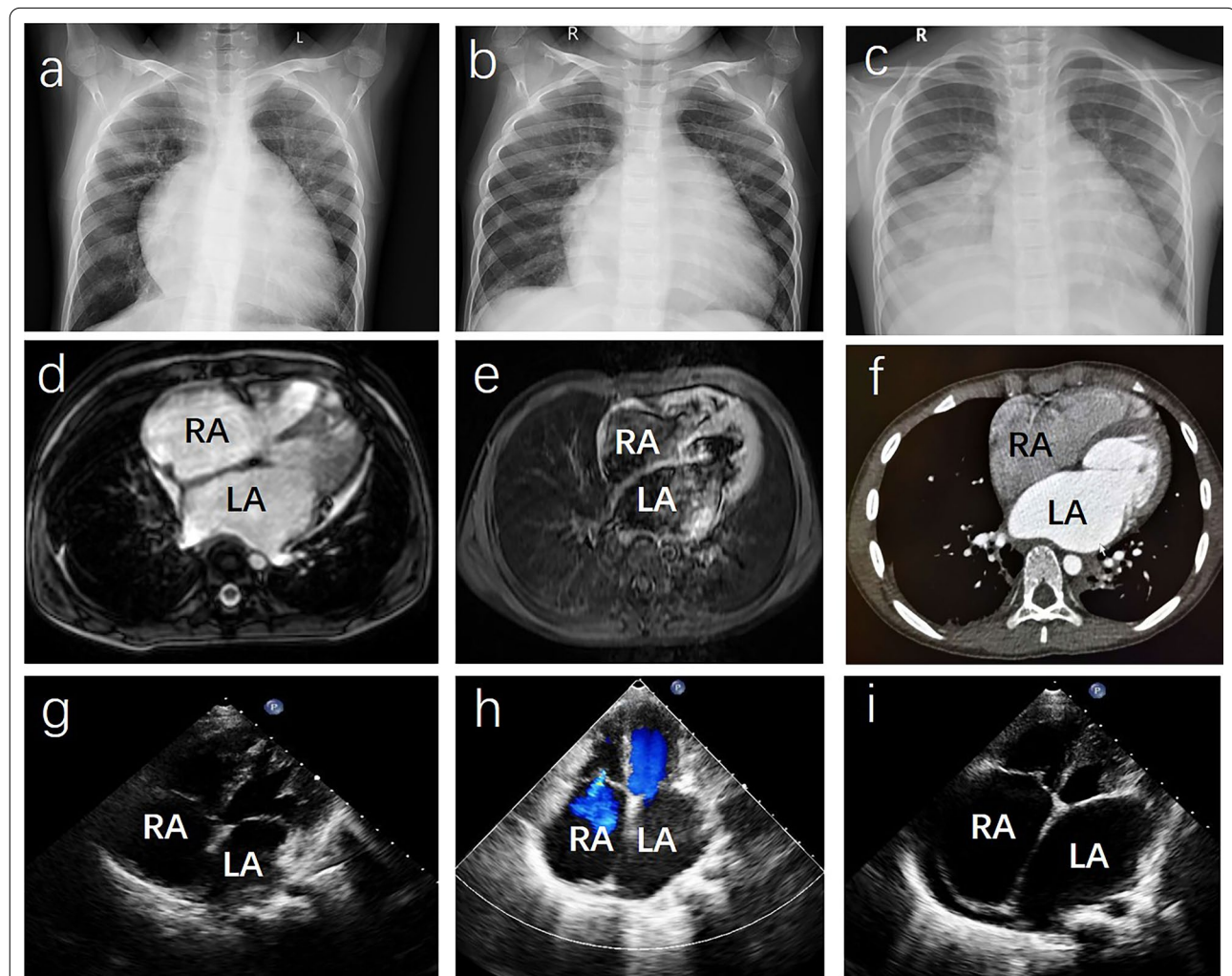
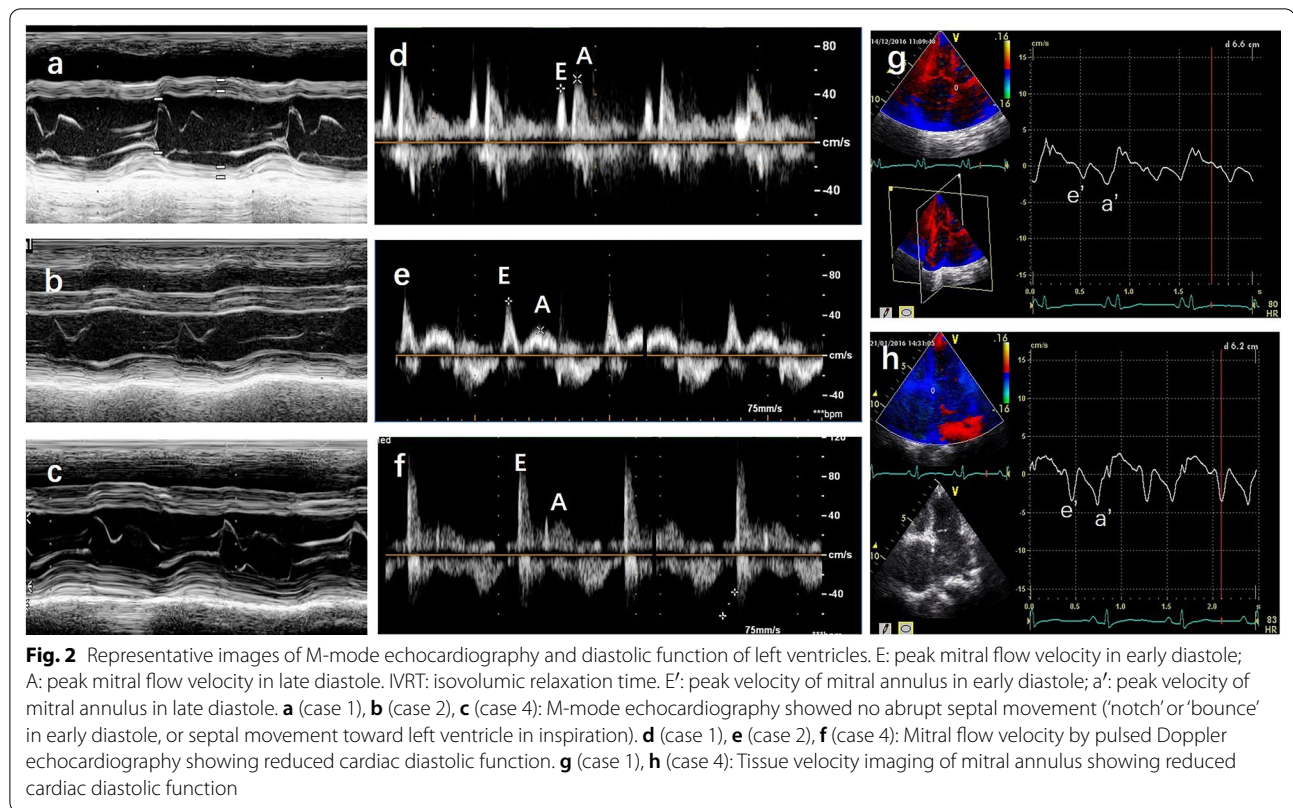


Fig. 1 Representative images of cardiac X-ray, MRI, CTA, and two-dimensional echocardiography. LA left atrium, RA right atrium. **a** (case 1), **b** (case 2), **c** (case 4): Chest X-ray showed increased heart shadow without calcification of the pericardium, thickened pericardium, or endocardium. **d** (case 2), **e** (case 4): Cardiac MRI showed bi-atrial enlargement without calcification of the pericardium, thickened pericardium, or endocardium. **f** (case 4): Cardiac CTA showed bi-atrial enlargement without calcification of the pericardium, thickened pericardium, or endocardium. **g** (case 1), **h** (case 2), **i** (case 4): Two-dimensional echocardiography showed dilation of the left and right atria with normal ventricular sizes, without calcification of the pericardium, thickened pericardium, or endocardium



or endocardium (Fig. 1d). Two-dimensional echocardiography showed dilation of the left and right atria with normal ventricular sizes, without calcification of the pericardium, thickened pericardium, or endocardium (Fig. 1h). M-mode echocardiography showed that the ventricular septum and left ventricular wall were slightly thickened and the left ventricular ejection fraction was less than 55%, and there was no abrupt septal movement ('notch' or 'bounce' in early diastole, or septal movement toward left ventricle in inspiration) (Fig. 2b). Pulsed Doppler echocardiography showed that the peak E and peak A velocity of mitral valve flow decreased significantly ($E/A > 2$) and the IVRT was longer than 80 ms (Fig. 2e). Unfortunately, tissue velocity images were not obtained for this case.

Case 3: No auxiliary examination results were obtained except for echocardiography. Two-dimensional echocardiography showed dilation of the left and right atria with normal ventricular sizes, without calcification of the pericardium, thickened pericardium, or endocardium. M-mode echocardiography showed that the left ventricular ejection fraction was less than 55%, and there was no abrupt septal movement ('notch' or 'bounce' in early diastole, or septal movement toward left ventricle in inspiration). Pulsed Doppler

echocardiography showed that the ratio of peak E to peak A velocity of mitral valve flow was more than 2 ($E/A > 2$) and the IVRT was longer than 80 ms. Unfortunately, tissue velocity images were not obtained and the TTE images of this case were lost.

Case 4: Chest X-ray showed increased heart shadow without calcification of the pericardium (Fig. 1c). Cardiac MRI (Fig. 1e) and cardiac computer tomography angiography (CTA) (Fig. 1f) showed bi-atrial enlargement without calcification of the the pericardium, thickened pericardium, or endocardium. Two-dimensional echocardiography showed dilation of the left and right atria with normal ventricular sizes, without calcification of the pericardium, thickened pericardium, or endocardium. (Fig. 1i).M-mode echocardiography showed that the left ventricular ejection fraction was greater than 55%, and there was no abrupt septal movement ('notch' or 'bounce' in early diastole, or septal movement toward left ventricle in inspiration) (Fig. 2c). Pulsed Doppler echocardiography showed that the ratio of peak E to peak A velocity of mitral valve flow was more than 2 ($E/A > 2$) and the IVRT was longer than 80 ms (Fig. 2f). Tissue velocity imaging showed that the peak e' and peak a' velocity of mitral annulus decreased with an $e'/a' < 1$, and the peak e' was < 8 cm/s (Fig. 2h).

TNNI3 mutations

Sanger sequencing using double orientation primers identified three *TNNI3* mutations in cases 1, 2, and 3, including one novel and two already known mutations (Fig. 3). These missense mutations included a heterozygous mutation at the nucleotide position 508 (c.508C>T) in case 1, resulting in the substitution of arginine with tryptophan at amino acid position 170 (p.Arg170Trp), a heterozygous mutation at position 575 (c.575G>A) in case 2, resulting in the substitution of arginine with histidine at amino acid position 192 (p.Arg192His), and a novel heterozygous mutation at position 517 (c.517C>T) in case 3, resulting in the substitution of leucine with

phenylalanine at amino acid position 173 (p.Leu173Phe). No mutations were identified in case 4, the parents and the elder sister of case 1, or the control group.

All these mutations were not found in 1000Genomes, ESP and EXAC databases, but were revealed by REVEL, SIFT, Polyphen2 and Mutation Taster prediction tools to have a high probability of damaging effect. c.508C>T and c.575G>A were reported in ClinVar in association with cardiomyopathy. Thus, according to ACMG guidelines [9], c.508C>T and c.575G>A were classified as pathogenic variants, while c.517C>T was classified as an uncertain significance variant.

TNNT2 and DES mutations

No mutations were found in *TNNT2* and *DES* in the four patients or in the control group.

Discussion

RCM is a myocardial disorder characterized by elevated myocardial stiffness that leads to restrictive diastolic dysfunction. RCM is also associated with limited unilateral or bilateral ventricular filling resulting from myocardial interstitial fibrous hyperplasia from cardiomyopathy that decreases diastolic volume [10]. RCM patients present with variable clinical manifestations. Patients with end-stage right heart failure are mainly characterized by systemic blood stasis (such as in the jugular vein), hepatomegaly, ascites, lower limb edema, and increased venous pressure [11, 12], whereas some patients may have symptoms linked to left heart failure such as dyspnea, hemoptysis and wet rales at the bottom of the lung, low cardiac output, syncope, and even thromboembolism or sudden death [13]. Other non-specific manifestations of RCM include fatigue, shortness of breath, impaired activity tolerance, and slow physical development [11–13].

RCM may be diagnosed in accordance with the following criteria: 1) a restrictive left ventricular filling pattern in the absence of obviously known causes, and 2) exclusion of CP. A differential diagnosis between RCM and CP may be made by medical history, as well as physical and auxiliary examinations including TTE, chest X-ray, MRI, cardiac catheterization, myocardial biopsy, and blood tests. The main indicators used for differential diagnosis of RCM and CP are shown in Table 1 [14–18].

However, it should be noted that distinguishing CP from RCM diagnosis according to the abovementioned diagnostic criteria can be challenging. In difficult cases, genetic testing may be considered when cardiologists have established a clinical index of suspected RCM based on a patient's clinical records, family history, and electrocardiographic/echocardiographic phenotypes. Indeed, a recent genetic study on pediatric RCM patients suggested that 75% of RCM patients exhibited genetic mutations

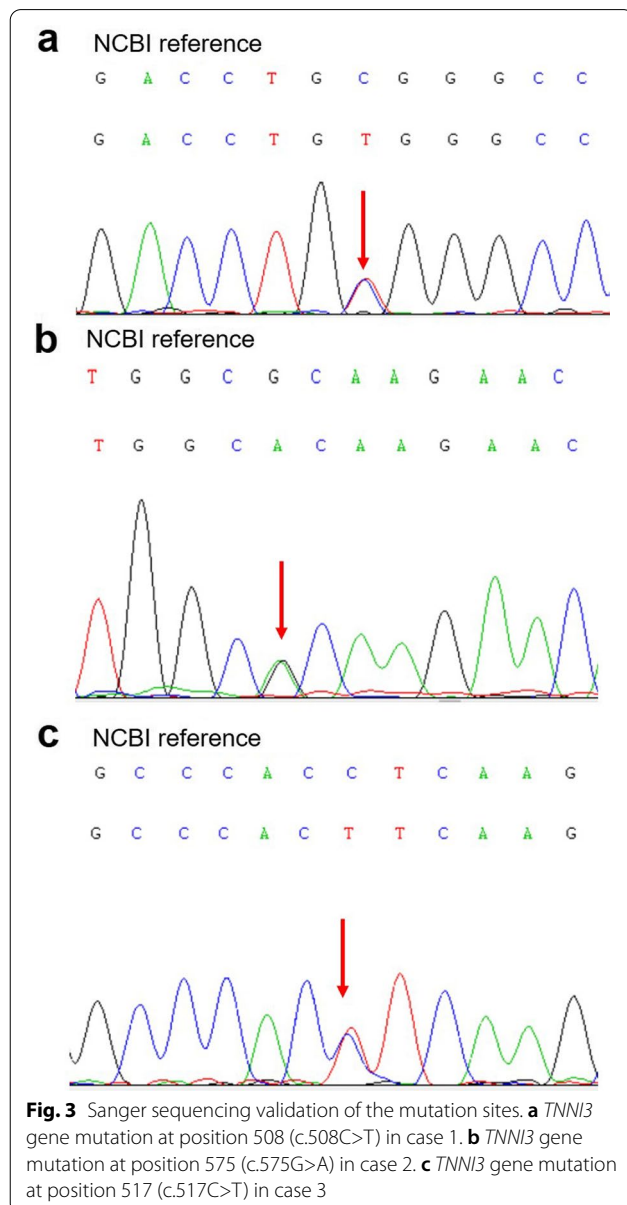


Table 1 Major indicators for differential diagnosis between RCM and CP

	RCM	CP
Pericardial calcification (TTE, Chest X-ray, CT, MRI)	Rare	+
Thickened pericardium (TTE, Chest X-ray, CT, MRI)	0	+
Thickened endocardium (TTE, CT, MRI)	Sometimes	0
Abrupt septal movement ('notch' or 'bounce') in early diastole (TTE)	0	+
Septal movement toward left ventricle in inspiration (TTE)	0	+
Left and right atrial enlargement (TTE, CT, MRI)	+	+
the tissue velocity of mitral annulus (TTE)	< 8 cm/s	> 8 cm/s
systolic area index (Cardiac catheterization)	0.92 ± 0.19	1.4 ± 0.2
End-diastolic pressure difference between left and right ventricles (Cardiac catheterization)	> 5 mmHg	< 5 mmHg
the ratio of right ventricular end-diastolic pressure to systolic pressure (Cardiac catheterization)	0.35 ± 0.14	0.50 ± 0.13
Radionuclide retention in atrium, Delayed radionuclide imaging of right ventricle (Radionuclide examination)	+	0
myocardial interstitial fibrosis (Endomyocardial biopsy)	+	Rare
B-type natriuretic peptide	Can be higher than 800 pg/ml	Most between 100~200 pg/ml

RCM restrictive cardiomyopathy, CP constrictive pericarditis, CT computed tomography, MRI magnetic resonance imaging, TTE transthoracic echocardiography

[19]. Genetic testing is not only important in differentiation between RCM and CP as mentioned above, but also critical in obtaining the final diagnosis of other cardiac diseases such as hypertrophic cardiomyopathy, inherited heart diseases in athletes [20], and sudden cardiac death [21, 22].

Mutations of a number of genes encoding for sarcomeric and cytoskeletal proteins are associated with the etiology of RCM with an incident rate of 33–66% (Table 2) [1, 6, 11, 23–35]. *TNNI3* was the first sarcomere gene reported to be pathogenic for RCM when mutated [11]. In contrast, CP is a disease of the pericardium resulting from chronic inflammation and/or scarring, and familiar CP is extremely rare. A homozygous deletion mutation in exon 6 of the proteoglycan 4 gene (*PRG4*), c.884_885delAG, was reported to be etiologically correlated to familiar CP [10], but this remains to be further corroborated.

In the present study, we genetically investigated four pediatric cases whose TTE revealed a similar RCM pattern, including bi-atrial enlargement with normal ventricular chamber sizes and abnormal diastolic functions. We identified three missense mutations in the *TNNI3* gene: p.Arg170Trp (case 1), p.Arg192His (case 2), and p.Leu173Phe (case 3). The first two mutations have been reported to be etiologically linked to RCM [36–39], but the p.Leu173Phe mutation was novel. Although it is currently unclear whether this novel p.Leu173Phe mutation is pathogenic for RCM, we noted that a number of missense mutations around Leu173, such as p.R170R, p.A171T, and p.K178E, have been reported to cause RCM [40]. Hence, we propose that this novel p.Leu173Phe

Table 2 Genetic mutations associated with RCM

Gene loci	Gene name
ACTC1 [29]	α-Cardiac actin
BAG3 [30]	BCL2-associated athanogene 3
CRYAB [31]	αB-crystallin
DES [32]	Desmin
GLA	α-Galactosidase
MYH7 [11]	β-Myosin heavy chain 7
MYL2	Myosin regulatory light chain 2,slow
MYL3	Myosin light chain 3, slow
MYPN [35]	Myopalladin
TNNI3 [1, 6, 34]	Cardiac troponin I, type 3
TNNT2 [1]	Cardiac troponin T, type 2
TPM1	α-Tropomyosin 1
TTN [35]	Titin
TTR	Transthyretin
MYBPC3 [23]	cMyBP-C
FLNC [24, 25]	filamin C
MYPN [26]	myopalladin
LMNA [28]	Lamin A
ABCC9 [27]	Sur2A

mutation is pathogenic for RCM, although functional studies are warranted to verify our hypothesis in the future.

Mechanistically, *TNNI3* mutations are associated with impaired diastolic functions due to myofibril Ca²⁺ hypersensitivity [12, 41], thus negatively affecting the actin–troponin–tropomyosin complex interaction [42]. It has been hypothesized that changes in actin-binding affinity

to troponin C, and the ability to inhibit thin filaments during diastole caused by certain *TNNI3* mutations, lead to an altered interaction within the actin–troponin–tropomyosin complex, causing severe diastolic dysfunction [42]. Hence, the *TNNI3* mutations found in this case series study may cause reduced cardiac diastolic function. Therefore, the children carrying *TNNI3* missense mutations, combined with their clinical history and results from auxiliary examinations, could have been diagnosed with RCM.

Conclusion

We report here that *TNNI3* mutations, including one novel missense mutation, p.Leu173Phe, and two already known mutations, p.Arg170Trp and p.Arg192His, were identified in three of four highly suspected pediatric RCM cases. Our findings contribute to the knowledge about the genetic basis of RCM and support the notion that genetic testing could be helpful in the clinical diagnosis of RCM, especially when exclusion of CP is difficult.

Abbreviations

RCM: Restrictive cardiomyopathy; CP: Constrictive pericarditis; TTE: Transthoracic echocardiography; ECG: Electrocardiogram; BNP: B-type natriuretic peptide; MRI: Magnetic resonance imaging; CTA: Tomography angiography; IVRT: Isovolumic relaxation time; E/A: The ratio of peak E to peak A velocity of mitral valve flow.

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Not applicable.

Author contributions

XJ designed the study and the data collection instruments, collected data, reviewed and revised the manuscript. MZ collected data, drafted the initial manuscript, and reviewed and revised the manuscript. HH designed the data collection instruments, coordinated and supervised data collection, and collected data. XZ and LL designed the study and collected data. HHO reviewed and revised the manuscript. All authors approved the final manuscript as submitted and agree to be accountable for all aspects of the work. All authors read and approved the final manuscript.

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Availability of data and materials

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Declarations

Ethics approval and consent to participate

This study was approved by the Ethics Committee of Children's Hospital of Chongqing Medical University (074/2013). Informed consent to participate was obtained from the parents of the pediatric patients.

Consent for publication

Written informed consent was obtained from the parents of the pediatric patients for publication of this Case report and any accompanying images. A copy of the written consent is available for review by the Editor of this journal.

Competing interests

The authors declare that they have no competing interests.

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References

- Hayashi T, Tanimoto K, Hirayama-Yamada K, Tsuda E, Ayusawa M, Nunoda S, et al. Genetic background of Japanese patients with pediatric hypertrophic and restrictive cardiomyopathy. *J Hum Genet*. 2018;63(9):989–96. <https://doi.org/10.1038/s10038-018-0479-y>.
- Garcia MJ. Constrictive pericarditis versus restrictive cardiomyopathy? *J Am Coll Cardiol*. 2016;67(17):2061–76. <https://doi.org/10.1016/j.jacc.2016.01.076>.
- Kucera F, Fenton M. Update on restrictive cardiomyopathy. *Paediatr Child Health*. 2017;27(12):567–71. <https://doi.org/10.1016/j.paed.2017.10.002>.
- Bicer M, Ozdemir B, Kan I, Yuksel A, Tok M, Senkaya I. Long-term outcomes of pericardiectomy for constrictive pericarditis. *J Cardiothorac Surg*. 2015;10:177. <https://doi.org/10.1186/s13019-015-0385-8>.
- Muchtar E, Blauwet LA, Gertz MA. Restrictive cardiomyopathy: genetics, pathogenesis, clinical manifestations, diagnosis, and therapy. *Circ Res*. 2017;121(7):819–37. <https://doi.org/10.1161/CIRCRESAHA.117.310982>.
- Mouton JM, Pellizzon AS, Goosen A, Kinnear CJ, Herbst PG, Brink PA, et al. Diagnostic disparity and identification of two *TNNI3* gene mutations, one novel and one arising de novo, in South African patients with restrictive cardiomyopathy and focal ventricular hypertrophy. *Cardiovasc J Afr*. 2015;26(2):63–9. <https://doi.org/10.5830/CVJA-2015-019>.
- Mitchell C, Rahko PS, Blauwet LA, Canaday B, Finstuen JA, Foster MC, et al. Guidelines for performing a comprehensive transthoracic echocardiographic examination in adults: recommendations from the American Society of Echocardiography. *J Am Soc Echocardiogr*. 2019;32(1):1–64. <https://doi.org/10.1016/j.echo.2018.06.004>.
- Lai WW, Geva T, Shirali GS, Frommelt PC, Humes RA, Brook MM, et al. Guidelines and standards for performance of a pediatric echocardiogram: a report from the Task Force of the Pediatric Council of the American Society of Echocardiography. *J Am Soc Echocardiogr*. 2006;19(12):1413–30. <https://doi.org/10.1016/j.echo.2006.09.001>.
- Richards S, Aziz N, Bale S, Bick D, Das S, Gastier-Foster J, et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med*. 2015;17(5):405–24. <https://doi.org/10.1038/gim.2015.30>.
- Arbustini E, Di Toro A, Giuliani L, Favalli V, Narula N, Grasso M. Cardiac phenotypes in hereditary muscle disorders: JACC state-of-the-art review. *J Am Coll Cardiol*. 2018;72(20):2485–506. <https://doi.org/10.1016/j.jacc.2018.08.2182>.
- Kapoor M, Das S, Biswas A, Seth S, Bhargava B, Rao VR. Mutations in hot-spot region of MYH7 gene exon 23 associated with restrictive cardiomyopathy. *Cardiogenetics*. 2017;7(1):66. <https://doi.org/10.4081/cardiogenetics.2017.6358>.
- Ding WH, Han L, Xiao YY, Mo Y, Yang J, Wang XF, et al. Role of whole-exome sequencing in phenotype classification and clinical treatment of pediatric restrictive cardiomyopathy. *Chin Med J (Engl)*. 2017;130(23):2823–8. <https://doi.org/10.4103/0366-6999.219150>.
- Sabato LA, Mendes LA, Cox ZL. Restrictive cardiomyopathy associated with long-term use of hydroxychloroquine for systemic lupus erythematosus. *J Pharm Pract*. 2017;30(5):571–5. <https://doi.org/10.1177/0897190016655726>.

14. Qamruddin S, Alkharabsheh SK, Sato K, Kumar A, Cremer PC, Chetrit M, et al. Differentiating constriction from restriction (from the Mayo Clinic Echocardiographic Criteria). *Am J Cardiol.* 2019;124(6):932–8. <https://doi.org/10.1016/j.amjcard.2019.06.002>.
15. Parakh N, Mehrotra S, Seth S, Ramakrishnan S, Kothari SS, Bhargava B, et al. NT pro B type natriuretic peptide levels in constrictive pericarditis and restrictive cardiomyopathy. *Indian Heart J.* 2015;67(1):40–4. <https://doi.org/10.1016/j.ihj.2015.02.008>.
16. Ackerman MJ, Priori SG, Willems S, Berul C, Brugada R, Calkins H, et al. HRS/EHRA expert consensus statement on the state of genetic testing for the channelopathies and cardiomyopathies: this document was developed as a partnership between the Heart Rhythm Society (HRS) and the European Heart Rhythm Association (EHRA). *Europace.* 2011;13(8):1077–109. <https://doi.org/10.1093/europace/eur245>.
17. Talreja DR, Nishimura RA, Oh JK, Holmes DR. Constrictive pericarditis in the modern era: novel criteria for diagnosis in the cardiac catheterization laboratory. *J Am Coll Cardiol.* 2008;51(3):315–9. <https://doi.org/10.1016/j.jacc.2007.09.039>.
18. Habib G, Bucciarelli-Ducci C, Caforio ALP, Cardim N, Charron P, Cosyns B, et al. Multimodality imaging in restrictive cardiomyopathies: an EACVI expert consensus document In collaboration with the "Working Group on myocardial and pericardial diseases" of the European Society of Cardiology Endorsed by The Indian Academy of Echocardiography. *Eur Heart J Cardiovasc Imaging.* 2017;18(10):1090–121. <https://doi.org/10.1093/ehjci/jex034>.
19. Ware SM, Wilkinson JD, Tariq M, Schubert JA, Sridhar A, Colan SD, et al. Genetic causes of cardiomyopathy in children: first results from the pediatric cardiomyopathy genes study. *J Am Heart Assoc.* 2021;10(9):e017731. <https://doi.org/10.1161/jaha.120.017731>.
20. Limongelli G, Nunziato M, D'Argenio V, Esposito MV, Monda E, Mazzaccara C, et al. Yield and clinical significance of genetic screening in elite and amateur athletes. *Eur J Prev Cardiol.* 2020. <https://doi.org/10.1177/2047487320934265>.
21. Monda E, Sarubbi B, Russo MG, Caiazza M, Mazzaccara C, Magrelli J, et al. Unexplained sudden cardiac arrest in children: clinical and genetic characteristics of survivors. *Eur J Prev Cardiol.* 2020. <https://doi.org/10.1177/2047487320940863>.
22. Monda E, Lioncino M, Rubino M, Caiazza M, Cirillo A, Fusco A, et al. The risk of sudden unexpected cardiac death in children: epidemiology, clinical causes, and prevention. *Heart Fail Clin.* 2022;18(1):115–23. <https://doi.org/10.1016/j.hfc.2021.07.002>.
23. Wu W, Lu CX, Wang YN, Liu F, Chen W, Liu YT, et al. Novel phenotype-genotype correlations of restrictive cardiomyopathy with myosin-binding protein C (MYBPC3) gene mutations tested by next-generation sequencing. *J Am Heart Assoc.* 2015;4(7):66. <https://doi.org/10.1161/JAHA.115.001879>.
24. Kiselev A, Vaz R, Knyazeva A, Khudiakov A, Tarnovskaya S, Liu J, et al. De novo mutations in FLNC leading to early-onset restrictive cardiomyopathy and congenital myopathy. *Hum Mutat.* 2018;39(9):1161–72. <https://doi.org/10.1002/humu.23559>.
25. Roldan-Sevilla A, Palomino-Doza J, de Juan J, Sanchez V, Dominguez-Gonzalez C, Salguero-Bodes R, et al. Missense mutations in the FLNC gene causing familial restrictive cardiomyopathy. *Circ Genom Precis Med.* 2019;12(3):e002388. <https://doi.org/10.1161/CIRCGEN.118.002388>.
26. Huby AC, Mendsaikhon U, Takagi K, Martherus R, Wansapura J, Gong N, et al. Disturbance in Z-disk mechanosensitive proteins induced by a persistent mutant myopalladin causes familial restrictive cardiomyopathy. *J Am Coll Cardiol.* 2014;64(25):2765–76. <https://doi.org/10.1016/j.jacc.2014.09.071>.
27. Neagoe O, Ciobanu A, Diaconu R, Mirea O, Donoiu I, Militaru C. A rare case of familial restrictive cardiomyopathy, with mutations in MYH7 and ABCC9 genes. *Discoveries.* 2019;7(3):99. <https://doi.org/10.15190/d.2019.12>.
28. Paller MS, Martin CM, Pierpont ME. Restrictive cardiomyopathy: an unusual phenotype of a lamin A variant. *ESC Heart Fail.* 2018;5(4):724–6. <https://doi.org/10.1002/ehf2.12294>.
29. Kaski JP, Syrris P, Burch M, Tome-Esteban MT, Fenton M, Christiansen M, et al. Idiopathic restrictive cardiomyopathy in children is caused by mutations in cardiac sarcomere protein genes. *Heart.* 2008;94(11):1478–84. <https://doi.org/10.1136/hrt.2007.134684>.
30. Schänzer A, Rupp S, Gräf S, Zengeler D, Jux C, Akintürk H, et al. Dysregulated autophagy in restrictive cardiomyopathy due to Pro209Leu mutation in BAG3. *Mol Genet Metab.* 2018;123(3):388–99. <https://doi.org/10.1016/j.ymgme.2018.01.001>.
31. Brodehl A, Gaertner-Rommel A, Klauke B, Grewe SA, Schirmer I, Peterschroder A, et al. The novel alphaB-crystallin (CRYAB) mutation p.D109G causes restrictive cardiomyopathy. *Hum Mutat.* 2017;38(8):947–52. <https://doi.org/10.1002/humu.23248>.
32. Pruszczyk P, Kostera-Pruszczyk A, Shatunov A, Goudeau B, Dрамиńska A, Takeda K, et al. Restrictive cardiomyopathy with atrioventricular conduction block resulting from a desmin mutation. *Int J Cardiol.* 2007;117(2):244–53. <https://doi.org/10.1016/j.ijcard.2006.05.019>.
33. Purevjav E, Arimura T, Augustin S, Huby A-C, Takagi K, Nunoda S, et al. Molecular basis for clinical heterogeneity in inherited cardiomyopathies due to myopalladin mutations. *Hum Mol Genet.* 2012;21(9):2039–53. <https://doi.org/10.1093/hmg/dds022>.
34. Ruan Y, Lu C, Zhao X, Liang R, Lian H, Routledge M, et al. Restrictive cardiomyopathy resulting from a troponin I type 3 mutation in a Chinese family. *Chin Med Sci J.* 2016;31(1):1–7. [https://doi.org/10.1016/s1001-9294\(16\)30015-3](https://doi.org/10.1016/s1001-9294(16)30015-3).
35. Peled Y, Gramlich M, Yoskovitz G, Feinberg MS, Afek A, Polak-Charcon S, et al. Titin mutation in familial restrictive cardiomyopathy. *Int J Cardiol.* 2014;171(1):24–30. <https://doi.org/10.1016/j.ijcard.2013.11.037>.
36. Kostareva A, Kiselev A, Gudkova A, Frishman G, Ruepp A, Frishman D, et al. Genetic spectrum of idiopathic restrictive cardiomyopathy uncovered by next-generation sequencing. *PLoS ONE.* 2016;11(9):e0163362. <https://doi.org/10.1371/journal.pone.0163362>.
37. Cimiotti D, Fujita-Becker S, Mohner D, Smolina N, Budde H, Wies A, et al. Infantile restrictive cardiomyopathy: cTnl-R170G/W impair the interplay of sarcomeric proteins and the integrity of thin filaments. *PLoS ONE.* 2020;15(3):e0229227. <https://doi.org/10.1371/journal.pone.0229227>.
38. Mogensen J, Kubo T, Duque M, Uribe W, Shaw A, Murphy R, et al. Idiopathic restrictive cardiomyopathy is part of the clinical expression of cardiac troponin I mutations. *J Clin Investig.* 2003;111(2):209–16. <https://doi.org/10.1172/jci200316336>.
39. Gomes AV, Liang J, Potter JD. Mutations in human cardiac troponin I that are associated with restrictive cardiomyopathy affect basal ATPase activity and the calcium sensitivity of force development. *J Biol Chem.* 2005;280(35):30909–15. <https://doi.org/10.1074/jbc.M500287200>.
40. Cimiotti D, Budde H, Hassoun R, Jaquet K. Genetic restrictive cardiomyopathy: causes and consequences—an integrative approach. *Int J Mol Sci.* 2021. <https://doi.org/10.3390/ijms22020558>.
41. Achal M, Trujillo AS, Melkani GC, Farman GP, Ocorr K, Viswanathan MC, et al. A restrictive cardiomyopathy mutation in an invariant proline at the myosin head/rod junction enhances head flexibility and function, yielding muscle defects in drosophila. *J Mol Biol.* 2016;428(11):2446–61. <https://doi.org/10.1016/j.jmb.2016.04.021>.
42. Kostareva A, Gudkova A, Sjöberg G, Mörner S, Semernin E, Krutikov A, et al. Deletion in TNNI3 gene is associated with restrictive cardiomyopathy. *Int J Cardiol.* 2009;131(3):410–2. <https://doi.org/10.1016/j.ijcard.2007.07.108>.

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