#### Clinical Characteristics, Genetic Findings and Arrhythmic Outcomes of Patients with

# Catecholaminergic Polymorphic Ventricular Tachycardia from China

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### **Abstract**

**Introduction**: Catecholaminergic polymorphic ventricular tachycardia (CPVT) is a rare cardiac ion channelopathy. This study examined the clinical characteristics, genetic basis, and arrhythmic outcomes of CPVT patients from China.

**Methods**: PubMed and EMBASE were systematically searched for case reports or series reporting on CPVT patients from China until February 19<sup>th</sup>, 2022 using the keyword "Catecholaminergic Polymorphic Ventricular Tachycardia" OR "CPVT", with the location limited to "China" OR "Hong Kong" or "Macau" in EMBASE, with no language or publication type restriction. Clinical characteristics, genetic findings, and primary outcome of spontaneous ventricular tachycardia/ventricular fibrillation (VT/VF) were analyzed.

**Results**: A systematic search of the PubMed and Embase databases yielded 1049 and 47 articles, respectively. After the exclusion of overlapping cohorts, a total of 58 unique cases from 15 studies (median presentation age: 8 [5.0-11.8] years old) were included. All patients except for one presented at or before 19 years of age. 56 patients (96.6%) were initially symptomatic. Premature ventricular complexes (PVCs) were present in 44 of 51 patients (86.3%) and VT in 52 of 58 patients (89.7%). Genetic tests were performed on 54 patients (93.1%) with a yield of 87%. *RyR2*, *CASQ2*, *TERCL*, and *SCN10A* mutations were found in 35 (71.4%), 12 (24.5%), one (0.02%) patient, and one patient (0.02%) respectively. 54 patients were treated with beta-blockers, eight received flecainide, five received amiodarone, two received verapamil and one received propafenone. Sympathectomy (n=10) and implantable-cardioverter defibrillator implantation (n=8) were performed. On follow-up, 13 patients developed VT/VF.

**Conclusion**: This is the first systematic review of CPVT patients from China. Most patients had symptoms on initial presentation, with syncope as the presenting complaint. *RyR2* mutation accounts for more than half of the CPVT cases, followed by *CASQ2*, *TERCL* and *SCN10A* mutations.

# Introduction

Cardiac ion channelopathies increases a patient's risk of developing of spontaneous ventricular tachycardia/fibrillation (VT/VF) and sudden cardiac death (SCD) (1-6). Amongst different cardiac channelopathies, such as Brugada syndrome (BrS), catecholaminergic polymorphic ventricular tachycardia (CPVT) is a less prevalent condition in Asia (7, 8). It is typically caused by mutations in either the ryanodine receptor 2 (*RyR2*) gene (9) or the calsequestrin 2 (*CASQ2*) gene (10, 11), but mutations in other genes such as calmodulin (*CALM*) have been implicated (12-14). Patients with CPVT usually present in the first two decades of life, with symptoms manifested after exercises or when in distress, resulting in bidirectional VT (15). Globally, Western countries have mainly contributed to population-based data on CPVT. To our knowledge, the largest registry had reported 237 CPVT patients, which was created by the Pediatric and Congenital Electrophysiology Society of the United States. (16, 17). In another multinational study, 101 CPVT patients who mainly come from France was reported (18), complementing smaller registry and case series studies by the same group (19, 20). In another study, 21 CPVT patients with CALM gene mutations were reported (12).

By contrast, limited data from Asia have been studied in comparison. Taking Japan as an example, 78 patients with CPVT were enrolled in the multi-centre registry (21). Other studies from Japan identified 30 (22) and 29 patients (23) with CPVT respectively. However, to date, no national registry has been established in China, and descriptions on CPVT patients have been limited to case reports or case series (11, 24-26). Moreover, as many of these studies were written in Chinese, researchers beyond China may have limited accessibility due to language barriers. Recently, our team conducted a situation analysis of the local CPVT burden in Hong Kong through a systematic literature search. This study, an extension of our previous work, has the aim of synthesizing evidence on the clinical characteristics, genetic basis, and arrhythmic outcomes of CPVT patients from China.

## Methods

# Patient Cohort and Data Collection

PubMed and Embase were systematically searched for case reports or case series that described CPVT patients from China until February 19<sup>th</sup>, 2022, which allowed a primary synthesis of cases for analysis. Keywords of the search included "Catecholaminergic Polymorphic Ventricular Tachycardia" OR "CPVT", with the country of author limited to "China" OR "Hong Kong" or "Macau" in EMBASE, with no language or publication type restriction. Diagnosis of CPVT was established based on the exercise

treadmill test, adrenaline challenge test, or genetic testing as defined by the individual papers. Where overlapping cohorts were described, data were extracted from the publication with the largest cohort. The individual cases were analyzed according to diagnostic criteria proposed by the 2013 Heart Rhythm Society (HRS)/ European Heart Rhythm Association (EHRA) / Asia-Pacific Heart Rhythm Society (APHRS) expert consensus statement (Supplementary Table 1) (27). All genetic variants described in the studies were searched in the genetic database ClinVar to determine their possible pathogenicity and novelty, and VARSOME for further prediction. Mutation hotspots for RyR2 were also identified according to the criteria set by Priori and Chen (28).

# Data Extraction and Statistical Analysis

The following clinical data were extracted from the published studies: 1) sex, 2) age of presentation, 3) age of diagnosis, 4) family history of SCD or CPVT, 5) initial symptoms, initial presentation with 6) syncope, 7) palpitations, 8) chest pain or 8) seizures, the presence of 10) premature ventricular complexes (PVCs) or 11) VT/VF detected on electrocardiography, Holter studies or exercise stress testing, 12) genetic testing, 13) methods of testing, 14) genetic results and 15) interpretation of the variants, 16) performance of electrophysiological study (EPS) and their respective results; 17) performance of echocardiogram and cardiac magnetic resonance imaging and results; 18) presence of bradycardic complications; 19) the presence of arrhythmias other than premature ventricular complexes (PVCs) /VT/VF, 20) prescription of pharmacological agents and 21) implantation of implantable cardioverter-defibrillator (ICD). Categorical variables were summarized as frequency (%) and continuous variables were expressed as median (Q1-Q3). All statistical analysis was performed using IBM SPSS Statistics 27.

#### **Results**

### Baseline Characteristics and Predictors

A systematic search of the PubMed and Embase databases yielded 1049 and 47 articles respectively. After the exclusion of overlapping cohorts, a total of 58 unique cases from eight cities of China by 15 studies were included (11, 25, 29-41). CPVT cases were reported in the following cities: Beijing (n=22) (11, 29-31), Hong Kong (n=16) (25), Guangzhou (n=7) (32, 37), Nanjing (n=6) (33), Shanghai (n=4) (34, 35, 38, 40), Chengdu (n=1) (36), Shenzhen (n=1) (39) and Xi'an (n=1) (41). Their clinical characteristics and test results are shown in **Table 1**. 21 patients fulfilled at least two criteria and 41 patients fulfilled one criterion of the 2013 HRS/EHRA/APHRS expert consensus statement

(Supplementary Table 1). 22 (37.9%) patients were female and all patients were of Han Chinese origin. All patients except for one presented at or before 19 years of age. The median age of presentation and diagnosis were 8.0 (5.0-11.8) and 10.1 (8.3-13.0) years old respectively, with a median delay of 16 (3.0-46.8) months. 56 patients (96.6%) were initially symptomatic. PVCs were present in 44 out of 51 patients and VT was present in 52 out of 58 patients. An abnormal echocardiogram was found in four patients. Duan *et al.* reported a patient with mild mitral and tricuspid regurgitation with a subsequent finding of a mildly dilated left ventricle on follow-up (36). Ge *et al.* reported a patient with a mildly dilated left ventricle (29). Lin *et al.* reported a patient with a thinner apical myocardium of the left ventricle (37). Abnormality on echocardiogram was also found in a patient conducted by Lee *et al.* but findings were not reported in the study (25). Genetic tests were performed on 54 patients (93.1%) with a yield of 87%. *RyR2, CASQ2, TERCL*, and *SCN10A* mutations were found in 35 (71.4%), 12 (24.5%), one (0.02%) patient, and one patient (0.02%) respectively (**Table 2**).

Pharmacological and non-pharmacological treatments for this cohort are summarized in **Table 3**. 54 patients were treated with β-blocker, eight patients received flecainide, five patients received amiodarone, two received verapamil and two received propafenone. Sympathectomy (n=10) and ICD implantation (n=8) were performed. On follow-up, 13 patients developed incident VT/VF.

# Discussion

To the best of our knowledge, the present study is the first systematic review of published cases of CPVT patients from China. The main findings are that: 1) RyR2 mutations account for over half of the CPVT cases, 2) 24 *RyR2* variants, eight *CASQ2* variants, two *TERCL* variants and one *SCN10A* variant were described, 3) β-blocker are used in 93.1% of the cases, followed less frequently by flecainide, amiodarone, verapamil and propafenone, and 4) 17.2% patients underwent cardiac sympathectomy and 13.8% received ICDs.

SCD is an important clinical problem globally, with congenital and acquired causes (42-45). Regarding the phenotype of congenital cardiac ion channelopathies, CPVT is characterized by exercise-induced bidirectional VT. Significant delays from the date of initial presentation to the date of diagnosis of around six months have been reported in international registry studies on North American and European patients (17, 46). By contrast, the epidemiology and characteristics of studies in Asia are limited. In China, cases of CPVT have been limited to small case reports or case series.

The incidence of adverse outcomes in CPVT patients has been examined in multiple studies, which have focused on syncopal events and SCD (18, 19, 47, 48). Existing evidence suggests that subjects who are initially symptomatic, who constituted the majority of the cohort represented in this systematic review, as well as those who are younger at diagnosis with no administration of β-blocker therapy, have a significantly higher susceptibility to cardiac events, including syncope, aborted cardiac arrest, and/or SCD (18). Regarding electrocardiographic parameters, their effectiveness in risk prediction for VT/VF in patients with CPVT remains uncertain due to a relative shortage of literature assessing such aspects. For assessing SCD as an outcome, although some studies have demonstrated significant differences in QRS durations of the recorded PVCs between patients who remained alive and those who suffered SCD during follow-up, whereas most of the other ECG variables, such as heart rate and QTc interval, failed to demonstrate any notable variations with time (18).

Regarding the genetic basis, this study identified 24 *RyR2* variants. Of these, 13 have been reported outside China: c.490C>T (49), c.2410C>T (RCV000639160.2), c.6886G>A (RCV000465586.1), c.7202G>A (50), c.7258A>G (51), c.7420A>G (52), c.10046C>T (53, 54), c.11836G>A (55, 56), c.12272C>T (RCV00182811.1), c.12475C>A (57), c.13933T>C (58), c.14159T>C (RCV000182842.2), c.14848G>A (56). Since *RyR2* variants have been reported in previous animal studies to be associated with a disruption in calcium homeostasis and a reduction in conduction velocity, functional studies should also be conducted to identify how such variants could lead to the generation of electrophysiological substrates (59-61).*CASQ2*, in comparison, accounts for a fewer proportion of CPVT cases. In our study, 8 variants were reported. Three have been reported from publications arising from outside China: c.97C>T (63), c.98G>A (64), and c.748C>T (RCV000694480.2), with five novel mutations. The two *TERCL* variants as well as one *SCN10A* variant reported in our study are also novel mutations. Finally, *CALM2* has also been implicated in CPVT but our study did not identify mutations in this gene.

## Strengths and limitations

The major strengths of the present study include a comprehensive extraction and integration of data which allows easier interpretation by researchers beyond China and comprehensive analysis of clinical characteristics, genetic basis, and arrhythmic outcomes of CPVT patients from China. This study also forms a basis for further studies in comparing CPVT between China and other Asian or non-Asian populations. However, the major limitation is that data were extracted from case reports or case series. Without a national registry, cases reported may not include all the domains that were assessed in this

current study, therefore the data may not reflect the actual picture of CPVT patients from China, especially regarding arrhythmic events on follow-up.

#### Conclusion

This is the first systemic review of CPVT patients from China. Most patients had symptoms on initial presentation, with syncope as the presenting complaint. RyR2 mutation accounts for more than half of the CPVT cases, followed by CASQ2, TERCL and SCN10A mutations.

**Authors' Contributions**: Sharen Lee, Justin Leung, and Gary Tse: study conception, data acquisition, database building, statistical analysis, manuscript drafting, manuscript revision

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Table 1. Baseline clinical and demographic characteristics of CPVT patients from China.

Parameter	Median (Q1-Q3) / frequency (%)
Female	22 (37.9)
Presentation Age (years)	8.0 (5.0-11.8)
Diagnosis Age (years)	10.1 (8.3-13.0)
Presentation to Diagnosis (months)	16 (3.0-46.8)
Family History of CPVT/SCD	14 (24.1)
Initially symptomatic	56 (96.6)
Initial syncope	54 (93.1)
Initial VT/VF/SCD	15 (25.9)
Initial palpitations	12 (20.7)
Initial chest pain	7 (12.1)
Initial seizure	17 (29.3)
PVC	44 (75.9)
VT/VF	52 (89.7)
VT/VF post-presentation	13 (22.4)
Echocardiogram	43 (74.1)
Abnormal echocardiogram	4 (9.3)
Cardiac MRI performed	5 (8.6)
Abnormal cardiac MRI	0 (0)
Genetic Test	54 (93.1)
Positive Genetic Test	47 (87)
Adrenaline Challenge	9 (15.5)
Positive Adrenaline Challenge	9 (100)
Exercise Tolerance Test	46 (79.3)
Positive Exercise Tolerance Test	44 (97.8)
EPS	3 (5.2)
Positive EPS	3 (100)
Holter Study	43 (74.1)
Arrhythmia in Holter Study	34 (81)

CPVT: catecholaminergic polymorphic ventricular tachycardia; SCD: sudden cardiac death; VT: ventricular tachycardia; VF: ventricular fibrillation; PVC: premature ventricular complex; MRI: magnetic resonance imaging; EPS: electrophysiological study

**Table 2. Genetic test results.** 

	Gene	Mutation	Region in	Coding	Mutation	Mutation	Pathogenicity	Prediction	Reported	Reference
RyR2			Genome	Effect	type	Hotspots for RyR2			Mutation	
RyR2	RvR2	c.229C>T	Exon 3	P77S	Substitution		VUS	VUS		Ge 2017
RyR2		c.490C>T						Likely	No: (49)	
RyR2	RyR2				Substitution	Domain I			Novel mutation	
RyR2         c.554C^A         Exon 37         A.1855D         Substitution         Non-hotspot         VUS         VUS         Novel mutation         Zhaag 2019           RyR2         c.6577G^T         Exon 45         E2296K         Substitution         Domain II         VUS         VUS         Novel mutation         Rb 2020           RyR2         c.7202G^A         Exon 45         E2296K         Substitution         Domain II         VUS         VUS         Nov. (50)         Lee 2021           RyR2         c.7220G^A         Exon 48         R2420G         Substitution         Domain II         VUS         VUS         Nov. (50)         Lee 2021           RyR2         c.7240A>G         Exon 49         R2474G         Substitution         Domain II         VUS         VUS         Nov. (52)         Lee 2021           RyR2         c.7580T>G         Exon 69         8334PL         Substitution         Domain III         VUS         VUS         Nov. (52)         Lee 2021           RyR2         c.1046C>T         Exon 69         8334PL         Substitution         Non-hotspot         VUS         VUS         Nov. (53, 54)         Lee 2021           RyR2         c.12014A>T         Exon 69         Exon 69         Substitution					Substitution					
RyR2         c.6577G−T         Exon 43         V21931         Substitution         Non-hotspot         VUS         VUS         Novel mutation         She 2020           RyR2         c.6886G>A         Exon 45         E2296K         Substitution         Domain II         VUS         VUS         RCV000465586.1         Hou 2019           RyR2         c.7202c>A         Exon 48         R2420G         Substitution         Domain II         VUS         No: (50)         Lee 2021           RyR2         c.7420A>G         Exon 49         R2474G         Substitution         Domain II         VUS         Likely         No: (52)         Lee 2021           RyR2         c.7580T>G         Exon 69         R2474G         Substitution         Domain II         VUS         VUS         No: (53)         Lee 2021           RyR2         c.10046C>T         Exon 69         S3349L         Substitution         Domain III         VUS         VUS         No: (53, 54)         Lee 2021           RyR2         c.12014A>T         Exon 90         E4005V         Substitution         Domain III         VUS         VUS         No: (53, 54)         Lee 2021           RyR2         c.12475C>T         Exon 90         A4091V         Substitution         Domain II										
RyR2         c.6886G-A         Exon 45         E2296K         Substitution         Domain II         VUS         RCV00046586.1         Hou 2019           RyR2         c.722G>A         Exon 47         R2401H         Substitution         Domain II         Likely Pathogenic Pathogenic Pathogenic         No: (51)         Ge 2017           RyR2         c.725RA>G         Exon 48         R2420G         Substitution         Domain II         VUS         VUS         No: (51)         Ge 2017           RyR2         c.7420A>G         Exon 69         R2474G         Substitution         Domain II         VUS         VUS         No: (52)         Lee 2021           RyR2         c.1046C>T         Exon 69         S3349L         Substitution         Domain III         Pathogenic         No: (53, 54)         Lee 2021           RyR2         c.1183GE>A         Exon 90         Exon 98         G3946S         Substitution         Domain III         VUS         VUS         No: (55, 56)         Ge 2017           RyR2         c.12014A>T         Exon 90         E4005V         Substitution         Domain III         VUS         VUS         No: (57, 56)         Ge 2017           RyR2         c.12475C>A         Exon 90         Q4159K         Substitution										
RyR2   c.7202G-A   Exon 48   R2401H   Substitution   Domain II   Likely pathogenic   Pathogenic   Pathogenic   Pathogenic   RyR2   c.7258A-G   Exon 48   R2420G   Substitution   Domain II   VUS   VUS   No: (51)   Ge 2017										
RyR2         c.7258A>G         Exon 48         R2420G         Substitution         Domain II         VUS         VUS         No: (S1)         Ge 2017           RyR2         c.7420A>G         Exon 49         R2474G         Substitution         Domain II         VUS         Likely Pathogenic         No: (S2)         Lec 2021           RyR2         c.7580T>G         Exon 50         1_2527W         Substitution         Domain II         VUS         VUS         Novel mutation         Duan 2018           RyR2         c.1836G>A         Exon 69         \$3349L         Substitution         Domain III         Pub Que         VUS         No: (\$3, 54)         Lee 2021           RyR2         c.1836G>A         Exon 88         G3946S         Substitution         Domain III         VUS         VUS         No: (\$5, 56)         Ge 2017           RyR2         c.12475C>A         Exon 90         E4005V         Substitution         Domain III         VUS         VUS         No: (\$7)         Lee 2021           RyR2         c.12475C>A         Exon 90         A4091V         Substitution         Domain III         VUS         VUS         No: (\$7)         Lee 2021           RyR2         c.139331>C         Exon 99         L4720P         Substitut										
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $							Pathogenic		No: (50)	
	RyR2	c.7258A>G	Exon 48	R2420G	Substitution	Domain II	VUS	VUS	No: (51)	Ge 2017
RyR2         c.10046C>T         Exon 69         \$3349L         Substitution         Non-hotspot         VUS         VUS         No: (53, 54)         Lee 2021           RyR2         c.11836G>A         Exon 88         G3946S         Substitution         Domain III         Pathogenic         No: (55, 56)         Ge 2017, Lee 2021           RyR2         c.12014A>T         Exon 90         E4005V         Substitution         Domain III         VUS         VUS         Novel mutation         Yang 2021           RyR2         c.12272C>T         Exon 90         A4091V         Substitution         Domain III         VUS         VUS         Nov(57)         Lee 2021           RyR2         c.12475C>A         Exon 90         Q4459K         Substitution         Domain III         VUS         VUS         Nov (57)         Lee 2021           RyR2         c.13933T>C         Exon 96         W4645R         Substitution         Domain IV         VUS         VUS         Nov (58)         Ge 2017           RyR2         c.14570T>G         Exon 101         14857S         Substitution         Domain IV         VUS         VUS         Novel mutation         Ge 2017           RyR2         c.14834A>G         Exon 105         Q4945R         Substitution	RyR2	c.7420A>G	Exon 49	R2474G	Substitution	Domain II	VUS		No: (52)	Lee 2021
	RyR2	c.7580T>G	Exon 50	L2527W	Substitution	Domain II	VUS	VUS	Novel mutation	Duan 2018
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	RyR2	c.10046C>T	Exon 69		Substitution	Non-hotspot	VUS	VUS	No: (53, 54)	Lee 2021
RyR2         c.12014A>T         Exon 90         E4005V         Substitution         Domain III         VUS         VUS         Novel mutation         Yang 2021           RyR2         c.12272C>T         Exon 90         A4091V         Substitution         Domain III         VUS         RCV00182811.1         Yang 2021           RyR2         c.12475C>A         Exon 90         Q4159K         Substitution         Domain III         VUS         Likely Pathogenic           RyR2         c.13933T>C         Exon 96         W4645R         Substitution         Domain IV         VUS         VUS         No: (58)         Ge 2017           RyR2         c.14570T>C         Exon 99         L4720P         Substitution         Domain IV         VUS         VUS         No: (58)         Ge 2017           RyR2         c.14570T>G         Exon 101         14857S         Substitution         Domain IV         VUS         VUS         Novel mutation         Ge 2017           RyR2         c.14543A2>G         Exon 105         E4950K         Substitution         Domain IV         VUS         VUS         Novel mutation         Ge 2017           RyR2         c.14861C>G         Exon 105         A4954G         Substitution         Domain IV         VUS		c.11836G>A			Substitution		Pathogenic	Pathogenic		
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	RyR2	c.12014A>T	Exon 90	E4005V	Substitution	Domain III	VUS	VUS	Novel mutation	
RyR2c.12475C>AExon 90Q4159KSubstitutionDomain IIIVUSLikely PathogenicNo: (57)Lee 2021RyR2c.13933T>CExon 96W4645RSubstitutionDomain IVVUSVUSNo: (58)Ge 2017RyR2c.14159T>CExon 99L4720PSubstitutionDomain IVVUSVUSRCV000182842.2Lee 2021RyR2c.14570T>GExon 10114857SSubstitutionDomain IVVUSVUSNovel mutationGe 2017RyR2c.14593C>AExon 102L48651SubstitutionDomain IVVUSVUSNovel mutationGe 2017RyR2c.14843A>GExon 105C4945RSubstitutionDomain IVVUSVUSNovel mutationGe 2017RyR2c.14844G>AExon 105E4950KSubstitutionDomain IVVUSVUSNovel mutationGe 2017RyR2c.14861C>GExon 105A4954GSubstitutionDomain IVVUSVUSNovel mutationLee 2021CASQ2c.97C>TExon 1R33XSubstitutionNot applicableLikely pathogenicNo: (63)Gao 2018, pathogenicCASQ2c.98G>AExon 1R33QSubstitutionNot applicableVUSVUSNo: (64)Li Q 2019CASQ2c.748C>TExon 1R25XSubstitutionNot applicableVUSPathogenicNovel mutationLi Q 2019CASQ2c.748C>TExon 7R250CSubstitutionNot app	RyR2		Exon 90	A4091V	Substitution	Domain III	VUS	VUS	RCV00182811.1	Yang 2021
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	RyR2		Exon 90	Q4159K	Substitution	Domain III	VUS			Lee 2021
RyR2         c.14159T>C         Exon 99         L4720P         Substitution         Domain IV         VUS         VUS         RCV000182842.2         Lee 2021           RyR2         c.14570T>G         Exon 101         14857S         Substitution         Domain IV         VUS         VUS         Novel mutation         Ge 2017           RyR2         c.14530T>A         Exon 105         C4945R         Substitution         Domain IV         VUS         VUS         Novel mutation         Ge 2017           RyR2         c.14834A>G         Exon 105         C4945R         Substitution         Domain IV         UIS         VUS         Novel mutation         Ge 2017           RyR2         c.14861C>G         Exon 105         E4950K         Substitution         Domain IV         VUS         UIS         Novel mutation         Lee 2021           RyR2         c.14861C>G         Exon 105         A4954G         Substitution         Domain IV         VUS         VUS         Novel mutation         Lee 2021           CASQ2         c.97C>T         Exon 1         R33X         Substitution         Not applicable VUS         VUS         No: (63)         Gao 2018, Li Q 2019           CASQ2         c.28G>A         Exon 1         R33Q         Substitution	RvR2	c.13933T>C	Exon 96	W4645R	Substitution	Domain IV	VUS		No: (58)	Ge 2017
RyR2c.14570T>GExon 101I4857SSubstitutionDomain IVVUSVUSNovel mutationGe 2017RyR2c.14593C>AExon 102L48651SubstitutionDomain IVVUSVUSNovel mutationGe 2017RyR2c.1484G>AExon 105Q4945RSubstitutionDomain IVLikely benignVUSNovel mutationGe 2017RyR2c.1484G>AExon 105E4950KSubstitutionDomain IVVUSLikely PathogenicNo: (56)Lee 2021RyR2c.14861C>GExon 105A4954GSubstitutionDomain IVVUSVUSNovel mutationLee 2021CASQ2c.97C>TExon 1R33XSubstitutionNot applicableLikely PathogenicNo: (63)Gao 2018, Li Q 2019CASQ2c.98G>AExon 1R33QSubstitutionNot applicableVUSVUSNo: (64)Li Q 2019CASQ2c.932+1G>AIVSSplice site MutationNot applicableVUSPathogenicNovel mutationGeo 2017CASQ2c.748C>TExon 7R250CSubstitutionNot applicableVUSPathogenicNovel mutationLi Q 2019CASQ2c.748C>TExon 11E359Rfs*Deletion and mutationNot applicableVUSPathogenicNovel mutationLi Q 2019CASQ2c.1074_1075delExon 11E359Rfs*Deletion and insertionNot applicableVUSPathogenicNovel mutationLi Q 2019CASQ2c.117					Substitution					
RyR2         c.14834A>G         Exon 105         Q4945R         Substitution         Domain IV         Likely benign         VUS         Novel mutation         Ge 2017           RyR2         c.14848G>A         Exon 105         E4950K         Substitution         Domain IV         VUS         Likely No: (56)         Lee 2021           RyR2         c.14861C>G         Exon 105         A4954G         Substitution         Domain IV         VUS         Novel mutation         Lee 2021           CASQ2         c.97C>T         Exon 1         R33X         Substitution         Not applicable Likely Pathogenic         Pathogenic No: (63)         Gao 2018, Li Q 2019           CASQ2         c.98G>A         Exon 1         R33Q         Substitution Not applicable VUS         VUS         VUS         No: (64)         Li Q 2019           CASQ2         c.532+1G>A         IVS         Splice site Not applicable VUS         Pathogenic Novel mutation         Novel mutation         Li Q 2019           CASQ2         c.748C>T         Exon 7         R250C         Substitution Not applicable VUS         VUS         Pathogenic Novel mutation         Novel mutation         Li Q 2019           CASQ2         c.748C>T         Exon 11         E359Rfs* Deletion and insection         Not applicable VUS         Pathogenic Nove	RyR2	c.14570T>G	Exon 101	I4857S	Substitution	Domain IV	VUS	VUS	Novel mutation	Ge 2017
RyR2         c.14848G>A         Exon 105         E4950K         Substitution         Domain IV         VUS         Likely Pathogenic         No: (56)         Lee 2021           RyR2         c.14861C>G         Exon 105         A4954G         Substitution         Domain IV         VUS         VUS         Novel mutation         Lee 2021           CASQ2         c.97C>T         Exon 1         R33X         Substitution         Not applicable Pathogenic         Likely Pathogenic         No: (63)         Gao 2018, Li Q 2019           CASQ2         c.98G>A         Exon 1         R33Q         Substitution         Not applicable VUS         VUS         No: (64)         Li Q 2019           CASQ2         c.244C>T         Exon 1         Q82X         Substitution         Not applicable VUS         Pathogenic         Novel mutation         Ge 2017           CASQ2         c.532+IG>A         IVS         Splice site Not applicable VUS         VUS         Pathogenic         Novel mutation         Li Q 2019           CASQ2         c.748C>T         Exon 7         R250C         Substitution         Not applicable VUS         VUS         Pathogenic Novel mutation         Novel mutation         Li Q 2019           CASQ2         c.1074_1075del issociation         Exon 11         E359Rfs*	RyR2		Exon 102	L4865I	Substitution	Domain IV	VUS	VUS	Novel mutation	Ge 2017
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	RyR2	c.14834A>G	Exon 105	Q4945R	Substitution	Domain IV	Likely benign	VUS	Novel mutation	Ge 2017
CASQ2       c.97C>T       Exon 1       R33X       Substitution       Not applicable Pathogenic Pathogenic       Likely Pathogenic Li Q 2019       Pathogenic Li Q 2019         CASQ2       c.98G>A       Exon 1       R33Q       Substitution Not applicable VUS       VUS       No: (64)       Li Q 2019         CASQ2       c.244C>T       Exon 1       Q82X       Substitution Not applicable VUS       Pathogenic Novel mutation       Novel mutation       Ge 2017         CASQ2       c.532+1G>A       IVS       Splice site mutation       Not applicable VUS       Pathogenic Novel mutation       Novel mutation       Li Q 2019         CASQ2       c.748C>T       Exon 7       R250C       Substitution Not applicable VUS       VUS       Pathogenic Novel mutation       Novel mutation       Li Q 2019         CASQ2       c.1074_1075del insC       Exon 11       E359Rfs* Deletion and inscrition       Not applicable VUS       Pathogenic Novel mutation       Novel mutation       Li Q 2019         CASQ2       c.1175_1178del Exon 11       D392Vfs* Deletion Not applicable VUS       Pathogenic Novel mutation       Novel mutation       Li Q 2019         TECRL       c.587C>T       Exon 6       R196Q       Substitution Not applicable VUS       VUS       Novel mutation       Xie 2019         TECRL       c.918+3T > G<	RyR2	c.14848G>A	Exon 105	E4950K	Substitution	Domain IV	VUS		, ,	Lee 2021
CASQ2 c.98G>A Exon 1 R33Q Substitution Not applicable VUS         VUS VUS No: (64)         Li Q 2019           CASQ2 c.244C>T Exon 1 Q82X Substitution Not applicable VUS         Pathogenic Novel mutation Ge 2017           CASQ2 c.532+1G>A IVS         Splice site mutation         Not applicable VUS         Pathogenic Novel mutation Not applicable VUS         Novel mutation Not applicable	RyR2	c.14861C>G	Exon 105	A4954G	Substitution	Domain IV	VUS	VUS	Novel mutation	Lee 2021
CASQ2c.98G>AExon 1R33QSubstitutionNot applicableVUSVUSNo: (64)Li Q 2019CASQ2c.244C>TExon 1Q82XSubstitutionNot applicableVUSPathogenicNovel mutationGe 2017CASQ2c.532+1G>AIVSSplice site mutationNot applicableVUSPathogenicNovel mutationLi Q 2019CASQ2c.748C>TExon 7R250CSubstitutionNot applicableVUSPuthogenicNovel mutationGao 2018, Li Q 2019CASQ2c.838+1G>AIVSSplice site mutationNot applicableVUSPathogenicNovel mutationLi Q 2019CASQ2c.1074_1075del insCExon 11E359Rfs* Deletion and insertionNot applicableVUSPathogenicNovel mutationLi Q 2019CASQ2c.1175_1178delExon 11D392Vfs* DeletionNot applicableVUSPathogenicNovel mutationLi Q 2019ACAG84TECRLc.587C>TExon 6R196QSubstitutionNot applicableVUSVUSNovel mutationXie 2019TECRLc.587C>TExon 6R196QSubstitutionNot applicableVUSVUSNovel mutationXie 2019TECRLc.918+3T>GIVSSplice site mutationNot applicableVUSVUSNovel mutationXie 2019	CASQ2	c.97C>T	Exon 1	R33X	Substitution	Not applicable		Pathogenic	No: (63)	
CASQ2 c.748C>T Exon 7 R250C Substitution Not applicable VUS Pathogenic Novel mutation Li Q 2019  CASQ2 c.838+1G>A IVS Splice site Not applicable VUS Pathogenic Novel mutation Li Q 2019  CASQ2 c.838+1G>A IVS Splice site Not applicable VUS Pathogenic Novel mutation Li Q 2019  CASQ2 c.1074_1075del Exon 11 E359Rfs* Deletion and Not applicable VUS Pathogenic Novel mutation Li Q 2019  insC 12 insertion  CASQ2 c.1175_1178del Exon 11 D392Vfs* Deletion Not applicable VUS Pathogenic Novel mutation Li Q 2019  ACAG 84  TECRL c.587C>T Exon 6 R196Q Substitution Not applicable VUS VUS Novel mutation Xie 2019  TECRL c.918+3T > G IVS Splice site Not applicable VUS VUS Novel mutation Xie 2019  mutation	CASQ2	c.98G>A	Exon 1	R33Q	Substitution	Not applicable	VUS	VUS	No: (64)	
mutationCASQ2c.748C>TExon 7R250CSubstitutionNot applicableVUSVUSRCV000694480.2Gao 2018, Li Q 2019CASQ2c.838+1G>AIVSSplice site mutationNot applicableVUSPathogenicNovel mutationLi Q 2019CASQ2c.1074_1075delExon 11E359Rfs* Deletion and insectionNot applicableVUSPathogenicNovel mutationLi Q 2019CASQ2c.1175_1178delExon 11D392Vfs* DeletionNot applicableVUSPathogenicNovel mutationLi Q 2019ACAG84TECRLc.587C>TExon 6R196QSubstitutionNot applicableVUSVUSNovel mutationXie 2019TECRLc.918+3T > GIVSSplice site mutationNot applicableVUSVUSNovel mutationXie 2019	CASQ2	c.244C>T	Exon 1	Q82X	Substitution	Not applicable	VUS	Pathogenic	Novel mutation	Ge 2017
CASQ2 c.838+1G>A IVS Splice site mutation  CASQ2 c.1074_1075del Exon 11 E359Rfs* Deletion and insc liquid liquid insc liquid l	CASQ2	c.532+1G>A	IVS		•	Not applicable	VUS	Pathogenic	Novel mutation	Li Q 2019
mutationCASQ2c.1074_1075del insCExon 11E359Rfs* Deletion and insCNot applicable VUSPathogenic Novel mutationNovel mutationLi Q 2019CASQ2c.1175_1178del Exon 11D392Vfs* DeletionNot applicable VUSPathogenic Novel mutationLi Q 2019ACAG84TECRLc.587C>TExon 6R196QSubstitutionNot applicable VUSVUSNovel mutationXie 2019TECRLc.918+3T > GIVSSplice site Mot applicable VUSVUSNovel mutationXie 2019	CASQ2	c.748C>T	Exon 7	R250C	Substitution	Not applicable	VUS	VUS	RCV000694480.2	
CASQ2c.1074_1075del insCExon 11E359Rfs* Deletion and insCNot applicable VUSPathogenic Novel mutationNovel mutationLi Q 2019CASQ2c.1175_1178del SCExon 11D392Vfs* Deletion Not applicable VUSPathogenic Novel mutationNovel mutationLi Q 2019ACAG84TECRLc.587C>TExon 6R196QSubstitution Not applicable VUSVUSNovel mutationXie 2019TECRLc.918+3T > GIVSSplice site mutationNot applicable VUSVUSNovel mutationXie 2019	CASQ2	c.838+1G>A	IVS		•	Not applicable	VUS	Pathogenic	Novel mutation	Li Q 2019
CASQ2c.1175_1178del ACAGExon 11D392Vfs* 84DeletionNot applicable Not applicable VUSVUSPathogenic 	CASQ2	_	Exon 11		Deletion and	Not applicable	VUS	Pathogenic	Novel mutation	Li Q 2019
TECRLc.587C>TExon 6R196QSubstitutionNot applicableVUSVUSNovel mutationXie 2019TECRLc.918+3T > GIVSSplice site mutationNot applicableVUSVUSNovel mutationXie 2019	CASQ2	c.1175_1178del	Exon 11	D392Vfs*		Not applicable	VUS	Pathogenic	Novel mutation	Li Q 2019
TECRL c.918+3T > G IVS Splice site Not applicable VUS VUS Novel mutation Xie 2019 mutation	TECRL		Exon 6		Substitution	Not applicable	VUS	VUS	Novel mutation	Xie 2019
					Splice site					
	SCN10A	c.4086G>C	Exon 22	Q1362H		Not applicable	VUS	VUS	Novel mutation	Zhang 2019

Table 3. Management for CPVT patients in China.

Treatment	Frequency (%)			
β-blocker	54 (93.1)			
Verapamil	2 (3.4)			
Amiodarone	5 (8.6)			
Flecainide	8 (13.8)			
Propafenone	2 (3.4)			
Sympathectomy	10 (17.2)			
ICD implantation	8 (13.8)			