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## Review

## Current topics in catecholaminergic polymorphic ventricular tachycardia

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## ABSTRACT

Catecholaminergic polymorphic ventricular tachycardia (CPVT) is induced by emotions or exercise in patients without organic heart disease and may be polymorphic or bidirectional in nature. The prognosis of CPVT is not good, and therefore prevention of sudden death is of utmost importance. Genetic variants of CPVT include *RyR2*, *CASQ2*, *CALM2*, *TRD*, and possibly *KCNJ2* and *ANK2* gene mutations. Hypotheses that suggest the causes of CPVT include weakened binding of FKBP12.6 and *RyR2*, a store overload-induced  $Ca^{2+}$  release (SOICR), unzipping of intramolecular domain interactions in *RyR2*, and molecular and functional abnormalities caused by mutations in the *CASQ2* gene. The incidence of an *RyR2* anomaly in CPVTs is about 35–79%, whereas anomalies in the *CASQ2* gene account for 3–5% CPVTs. The ping-pong theory, suggesting that reciprocating delayed after depolarization induces bigeminy of the right and left bundle branches, may explain the pathogenesis of bidirectional ventricular tachycardia. Flecainide, carvedilol, left sympathetic nerve denervation, and catheter ablation of the PVC may serve as new therapeutic strategies for CPVT while gene-therapy may be applied to some types of CPVT in the future. Although, not all sudden cardiac deaths in CPVT patients are currently preventable, new medical and interventional therapies may improve CPVT prognosis.

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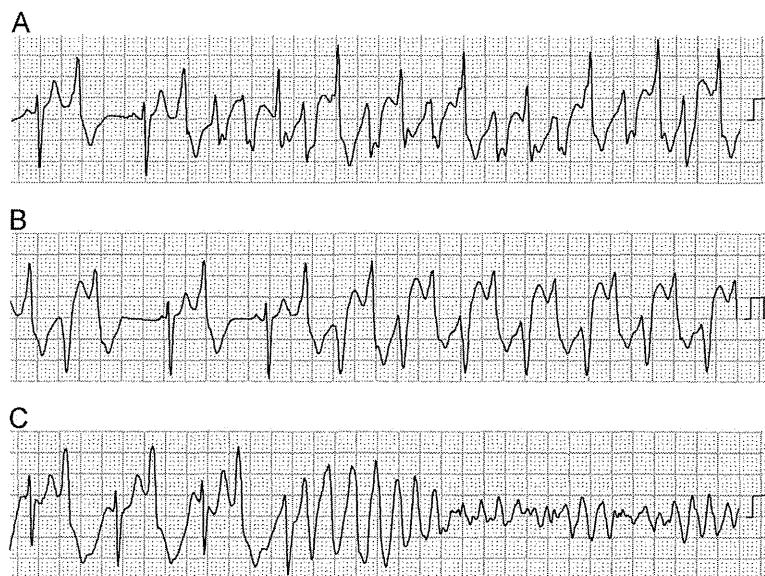
## 1. Introduction

Catecholaminergic polymorphic ventricular tachycardia (CPVT) is induced by emotional stress or exercise in patients without

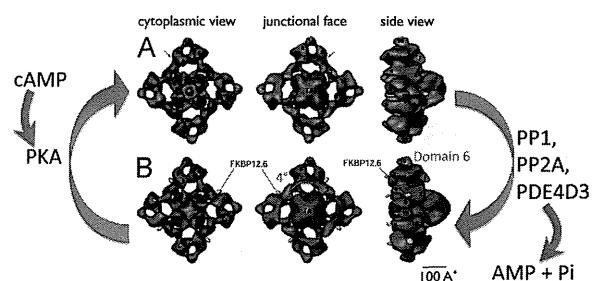
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**Fig. 1.** Typical features of ventricular tachycardia in a patient with CPVT. (A) Polymorphic ventricular tachycardia. (B) Bidirectional ventricular tachycardia. (C) Rapid polymorphic ventricular tachycardia deteriorating into ventricular fibrillation. These electrocardiograms were recorded by Holter monitoring in the CM3 lead in the same patient.



**Fig. 2.** Surface representations of RyR2 3D reconstructions with and without bound FKBP12.6. [7]. (A) High activity state of RyR2. A 3D map of RyR2, obtained by in vitro assembly of purified RyR2 incubated with FKBP12.6 alone. (B) Low activity state of RyR2. A 3D map of RyR2, obtained by incubating RyR2 with FKBP12.6 and an excess of FK506. FKBP12.6 is denoted by the blue dots. The major difference in these structures is observed in domain 6, which extends in the vertical direction (shown by the blue arrow), and the transmembrane assembly is rotated about 4° (shown by the blue arrow in the lower center panel). FKBP12.6: calstabin2, protein kinase A: PKA, phosphatase 1: PP1, phosphatase 2A: PP2A, phosphodiesterase 4D3: PDE 4D3, TA: transmembrane assembly.

organic heart disease and may be polymorphic or bidirectional (Fig. 1) [1–3]. This ventricular arrhythmia sometimes degenerates into rapid polymorphic ventricular tachycardia and ventricular fibrillation (Fig. 1) and may lead to syncope or sudden death. The incidence of CPVT is reported to be as high as 1:10,000, but its real prevalence is unclear.

## 2. Clinical manifestations and prognosis

The first clinical manifestations of CPVT are syncope or aborted sudden cardiac death during exercise or emotional stress and appear during the first or second decade of life [1–3]. CPVT differs from seizures, in that almost all syncopal events are associated with physical activity or emotional stress and do not occur during a resting state.

The prognosis of CPVT is very poor. About 40% patients die within 10 years of diagnosis [3]. Although prognosis in recent times

could be better than previous reports, sudden death and severe brain damage are still reported in CPVT patients.

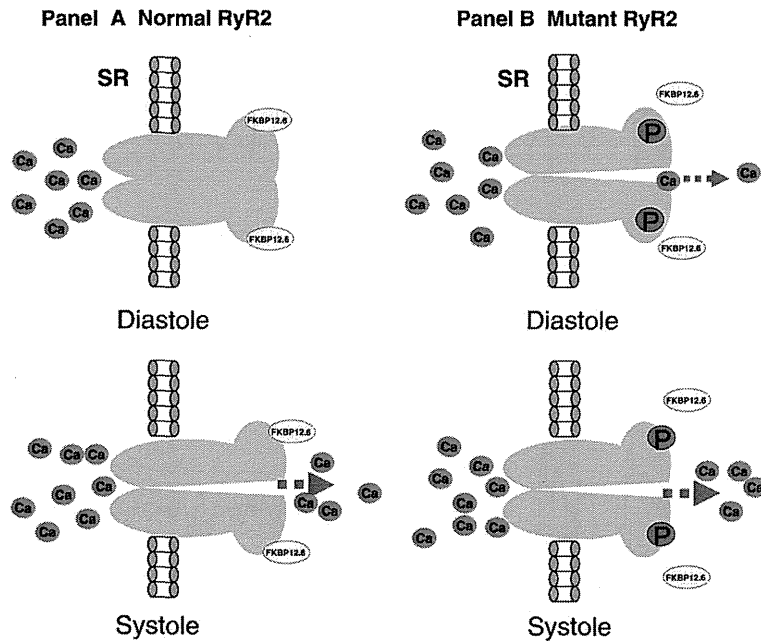
## 3. Diagnosis of CPVT

CPVT patients usually have a normal resting ECG, or just a lower heart rate than is normal for their age [3]. During exercise in these patients, monomorphic premature ventricular contractions (PVCs) increase, then polymorphic, or bidirectional PVC bigeminy appear, followed by bidirectional or polymorphic VT. Exercise induced supraventricular arrhythmias (atrial fibrillation, premature atrial contraction, and atrial tachycardia) are also common in the patients with CPVT [4]. The diagnostic criteria of CPVT are as follows [5]:

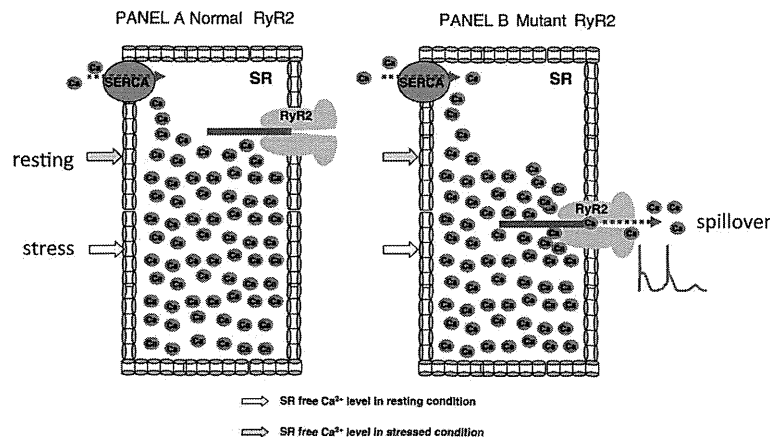
1. CPVT is diagnosed in the presence of a structurally normal heart, normal ECG, and unexplained exercise or catecholamine-induced bidirectional VT, polymorphic ventricular premature beats or VT in individuals < 40 years of age.
2. CPVT is diagnosed in patients (index case or family member) who have a pathogenic mutation.
3. CPVT is diagnosed in family members of a CPVT index case with a normal heart who manifests exercise-induced PVCs or bidirectional/polymorphic VT.
4. CPVT can be diagnosed in the presence of a structurally normal heart and coronary arteries, normal ECG, and unexplained exercise or catecholamine-induced bidirectional VT, polymorphic ventricular premature beats or VT in individuals > 40 years of age.

## 4. Mechanism of CPVT

The major pathogenic mechanism of CPVT is thought to involve the malfunction of RyR2. RyR2 is a large tetrameric protein expressed on the sarcoplasmic reticulum (SR) membrane. RyR2 is anchored to calsequestrin (CASQ2) by satellite proteins such as calmodulin (CaM), FKBP12.6, (calstabin2), protein kinase A (PKA), phosphatase 1 (PP1), and phosphatase 2A (PP2A) bound to the cytoplasmic region and junctin, and triadin (TRD) bound to the luminal side [6].



**Fig. 3.** FKBP12.6 dissociation from mutant *RyR2* in the pathogenesis of CPVT [8]. FKBP12.6 acts as a stabilizer that preserves the closed *RyR2* channel during diastole. Weakened binding affinity with FKBP12.6 may lead to a  $\text{Ca}^{2+}$  leak during diastole.



**Fig. 4.** The store overload-induced  $\text{Ca}^{2+}$  release (SOICR) hypothesis [8]. With normal *RyR2*, the resting and stress levels of free calcium are below the SOICR threshold (panel A). If the SOICR threshold falls below the level of free SR calcium as with mutant *RyR2*, a leak of  $\text{Ca}^{2+}$  will occur and generate a delayed after-depolarization.

A three-dimensional reconstruction of *RyR2* bound to FKBP12.6 is shown in Fig. 2B. When *RyR2* is bound to FKBP12.6, it forms a stable structure with closed pores, the domain 6 of *RyR2* was found to protrude into the luminal side, when observed from the junctional face after the transmembrane assembly (TA) was rotated counterclockwise by about  $4^\circ$  [7]. When unbound to FKBP12.6, *RyR2* assumes an open state (Fig. 2A) [7].

Several pathogenic hypotheses have been reported regarding the causes of CPVT [8]. The first theory suggests the dissociation of FKBP12.6 from *RyR2*. The normal *RyR2* channel is stabilized by FKBP12.6 and closes during diastole. With mutant *RyR2*, the binding affinity with FKBP12.6 is weakened, and phosphorylation of *RyR2* by protein kinase A (PKA) results in dissociation of

FKBP12.6 from *RyR2*, resulting in open channels which may leak  $\text{Ca}^{2+}$  during diastole (Fig. 3).

The second hypothesis is a store overload-induced  $\text{Ca}^{2+}$  release (SOICR) theory [8]. With normal *RyR2*, the resting and stress levels of free  $\text{Ca}^{2+}$  are below the SOICR level. However, with mutant *RyR2*, the SOICR threshold drops below the level of free  $\text{Ca}^{2+}$  in the SR. This may cause a spillover of  $\text{Ca}^{2+}$  from the SR (Fig. 4).

The third hypothesis considers defective intramolecular domain interaction [8]. *RyR2* is stabilized by a tight zipping of the intramolecular structure. If a mutation interferes with this zipping structure, the intramolecular domain interaction is weakened, causing an unzipping of the interdomain structure and leads leaking of  $\text{Ca}^{2+}$  from the SR (Fig. 5).

The fourth hypothesis suggests that the molecular and functional abnormalities are related to mutations in the *CASQ2* gene [8]. *CASQ2* is a  $\text{Ca}^{2+}$  storage protein inside the SR. The functional storage capacity of *CASQ2* or its reduced levels, may lead to increased levels of free  $\text{Ca}^{2+}$  inside the SR, leading to a  $\text{Ca}^{2+}$  leak

during diastole (Fig. 6). It is also known that *CASQ2* stabilizes binding of *RyR2* with *TRD* and the junction.

This  $\text{Ca}^{2+}$  overload activates the forward mode of the  $\text{Na}^+/\text{Ca}^+$  exchanger (NCX), increases the transient inward current ( $I_{ti}$ ), and induces ventricular arrhythmias due to delayed after depolarizations (DADs).

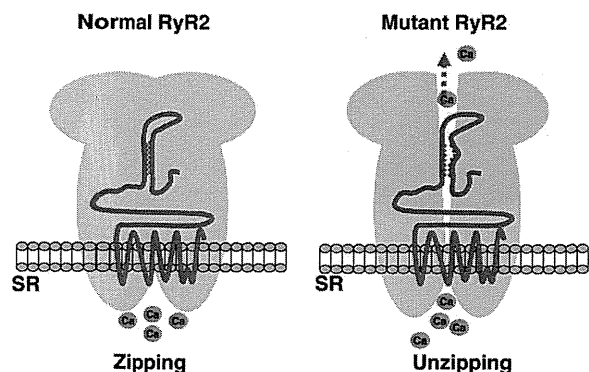


Fig. 5. Defective intramolecular domain interactions in *RyR2* mutations [8]. The N terminal domain and the central domain of *RyR2* interact with a tight “zipping” that serves to stabilize the channel (left panel). A mutation in either domain weakens this interaction (unzipping), which results in leaking of  $\text{Ca}^{2+}$  from *RyR2* (right panel).

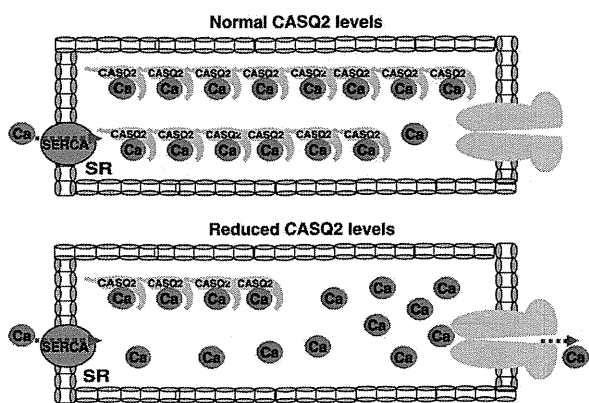


Fig. 6. Molecular and functional abnormalities related to mutations in the *CASQ2* gene [8]. Storage of  $\text{Ca}^{2+}$  in the SR largely depends on the level and function of *CASQ2* (upper panel). Decreased levels or function of *CASQ2* results in increase in the free SR  $\text{Ca}^{2+}$  that may result in a  $\text{Ca}^{2+}$  leak from *RyR2* during diastole (lower panel).

## 5. Subtypes of CPVT

Several subtypes of CPVT have been reported (Table 1). The most common type of CPVT is caused by an anomaly in the *RyR2* gene (CPVT1) [9,10]. This accounts for more than 50% of CPVT cases. In our CPVT cohort, about 79% of the CPVT cases were related to an anomaly in the *RyR2* gene. The inheritance of CPVT1 is autosomal dominant, and sudden death was observed in about 10% of these patients. There were no sex differences noted in this CPVT.

The second most common type of CPVT is caused by a *CASQ2* gene anomaly (CPVT2) [11,12]. The inheritance of CPVT2 is autosomal recessive, and the rate of sudden death is higher than that observed in CPVT1. However, autosomal dominant mutations of *CASQ2* are also reported [13–15].

CPVT3 was reported in a family with showing a 7p22-p14 chromosome anomaly, but the gene responsible has not been identified yet [16]. Recently, calmodulin (*CALM*) [17] and triadin (*TRD*) [18] anomalies have been found to responsible for CPVT4 and CPVT5, respectively.

*CALM* is a protein that involves the calcium dependent  $I_{Ca}$  inactivation of the L-type Ca channel. Further, *CALM* also stabilizes the *RyR2* channel. Thus, a mutation in *CALM* may easily cause  $\text{Ca}^{2+}$  overload. *TRD* is a protein that connects *CASQ2* to *RyR2*, and stabilizes the *RyR2* channel. A mutation in *TRD* may also result in a diastolic leak of  $\text{Ca}^{2+}$  and  $\text{Ca}^{2+}$  overload in the myocytes.

*KCNJ2* encodes the cardiac inward rectifier K channel. A mutation in *KCNJ2* causes the Andersen–Tawil syndrome (LQT7), and is also reported in patients with exercise induced bi-directional VT [19]. Whether or not this type of mutation should be included as a subtype of CPVT is a matter of controversy. Mutations in the *ANK2* gene are well known as a cause of LQT4. Recently, a patient with an *ANK2* mutation was reported to have bi-directional VT [20]. This may be another disease related to CPVT.

A type of adult CPVT has also been reported [21,22]. In this disease, the patients are predominantly female, with CPVT onset at the age of around 40 years, and no sudden death is reported. We believe that this may not be a specific type of CPVT, but rather a mild form of the disease.

In the Japanese CPVT registry, 78 patients (M:F=26:52, age=  $11.2 \pm 8.2$  years) were enrolled. In this registry, only 6% of the cases were familial cases whereas 94% of the cases were sporadic

Table 1  
Subtypes of CPVT.

Subtypes	Juvenile type					Adult type		
	CPVT1	CPVT2	CPVT3	CPVT4	CPVT5	CPVT related diseases		
						ATS	LQT4	
Incidence (%)	50–60	1	< 1	< 1	< 1	< 1	< 1	≈ 30
Inheritance	AD	AR	AR	AD	Sporadic	AD	AD	Sporadic
Onset of symptoms	10 years	7 years	10 years	4 years	2, 26 years	14, 9, 17 years	?	> 20 years (40 years)
Sex	M:F=1:1	M:F=1:1	M:F=1:1	M:F=1:1	M=3	F>M?	?	F>>M
Chromosome locus	1q43	1p13.1	7p22–p14	14q32.11	6q22.31	17q24.3	4q25–26	
Gene	<i>RyR2</i>	<i>CASQ2</i>	?	<i>CALM1</i>	<i>TRD</i>	<i>KCNJ2</i>	<i>ANK2</i>	<i>RyR2</i> ≈ 30%
Protein				CaM		$\text{K}_{ir}2.1\alpha$	Ankyrin-B	
Sudden death (%)	≈ 10	≈ 42	≈ 75	≈ 18	≈ 25	?	?	0

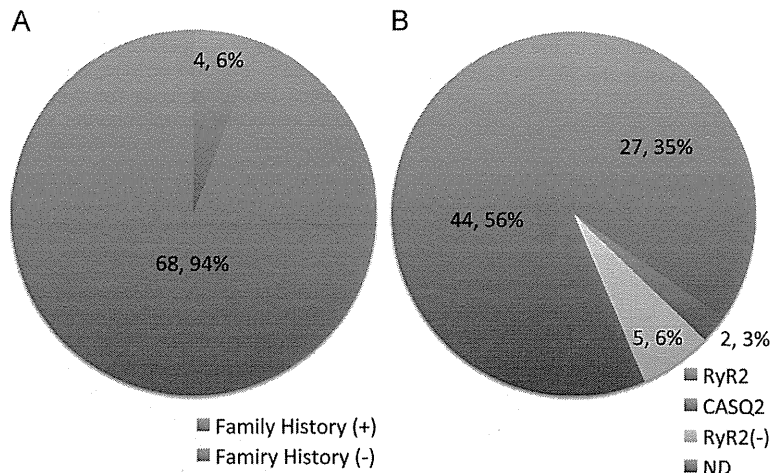


Fig. 7. Family history and gene anomalies in the Japanese registry. (A) Family history in the registry. (B) Gene mutations ND; gene testing was not performed.

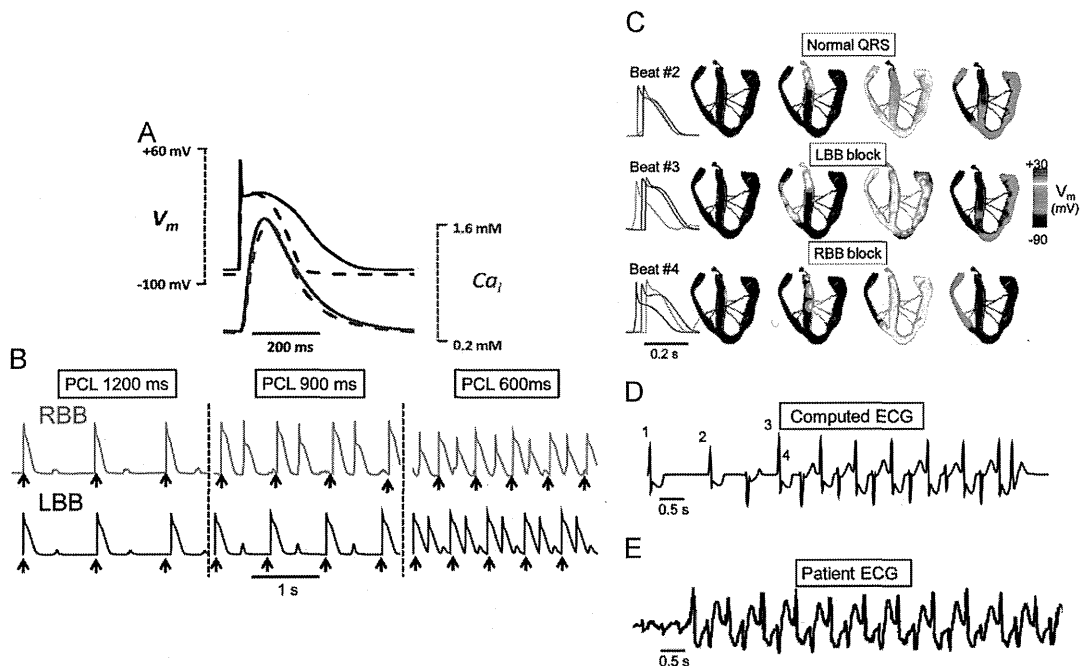


Fig. 8. A possible mechanism for bidirectional ventricular tachycardia: ping-pong in the His-Purkinje system [27]. (A) Comparison of simulated rabbit ventricular (dashed line) and Purkinje (solid line) action potentials (APs) and  $Ca_i$  transients during pacing at 600 ms. (B) Rate dependence of delayed after depolarizations (DADs) and bigeminy in Purkinje cell AP models. For the green trace, the rate threshold for DAD-induced bigeminy was 67 bpm (pacing cycle length [PCL] 900 ms), such that pacing (black arrows) at both 900 and 600 ms induced bigeminy. For the purple trace, the bigeminy rate threshold was 100 bpm (PCL 600 ms), such that pacing at 600 ms, but not 900 ms, induced bigeminy. LBB: left bundle branch; RBB: right bundle branch. (C) Voltage snapshots depicting the activation sequence at BVT onset. Beat #2 is the last paced beat, with normal activation. Beat #3 is the first beat of BVT, due to a DAD-triggered action potential (AP) arising in the right bundle branch (RBB), resulting in a QRS with a left bundle branch (LBB) block pattern. Beat #4 is the second beat of BVT, due to a DAD-triggered AP arising in the LBB and results in a QRS with RBB block pattern. Traces on the right show the timing of APs recorded from the His bundle (red), RBB (green), and LBB (purple). (D) Computed ECG from the simulation in A, showing BVT. (E) ECG recorded in a patient during BVT.

(Fig. 7A). In this cohort, 56% of the patients had not undergone genetic testing. However, of the 46% patients who underwent genetic testing, 79% of the patients had an RyR2 gene anomaly, 6% had a CASQ2 gene anomaly, and in 15% of the patients the specific causative gene anomaly was unknown (Fig. 7B). The estimated RyR2 genotype percentage is reported to range from 35% [23] up to

65% [24,25], and the CASQ2 genotyped patients are estimated to account for approximately 3–5% [25].

The proportions of familial cases reported in other studies were 21.3% [26] and 30% [21]. The lower percentage of familial cases observed in our cohort may be because half of the registered cases are over 15 years old, at which time only information of familial

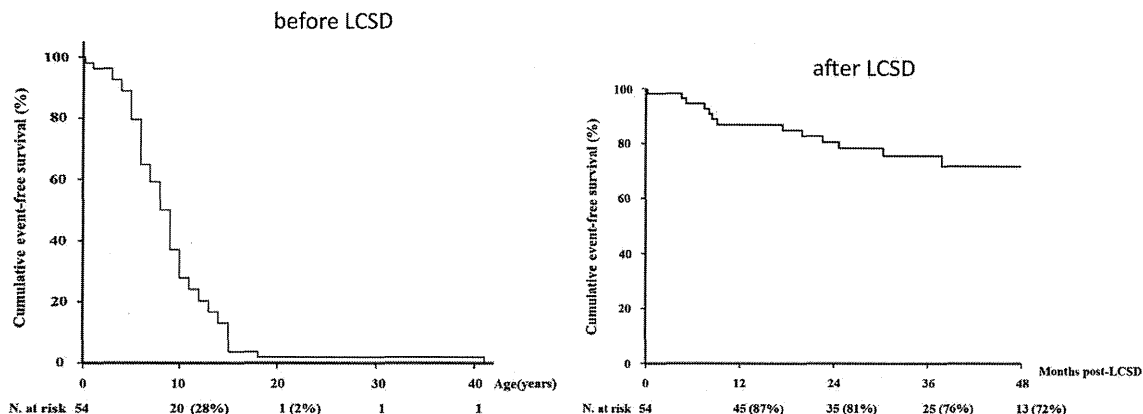


Fig. 9. Kaplan-Meier curve of cumulative survival to a first major cardiac event before and after left cardiac sympathetic denervation (LCSD) in symptomatic patients with CPVT [38]. In 63 patients with CPVT, the cumulated event free survival significantly improved after LCSD.

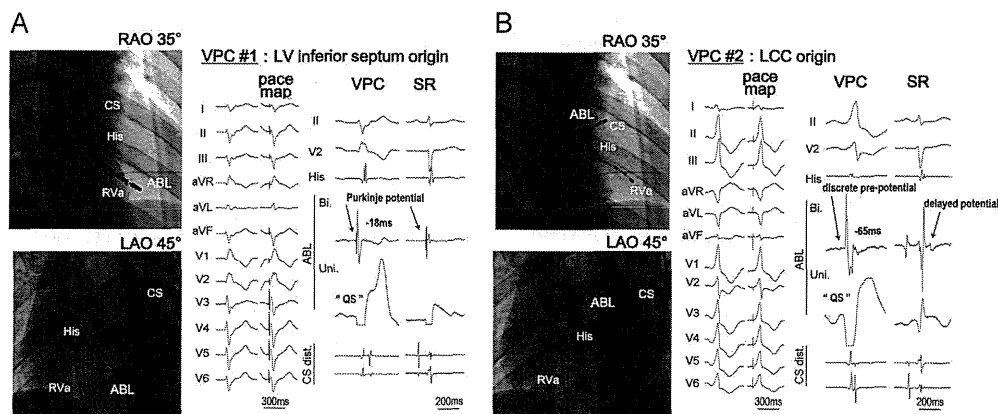


Fig. 10. Pace mapping of PVC in a patient with CPVT [43]. (A) A perfect pace map of the second beat of the CPVT was obtained on the left ventricular septum. Purkinje potential at that point was recorded during the PVC and sinus rhythm. (B) A perfect pace map of the first beat of a PVC was obtained at the left coronary cusp. A discrete pre-potential was recorded during the PVC, and a delayed potential was recorded during sinus rhythm.

history was taken without exercise or genetic testing. This may result in an apparently lower percentage of familial cases. Kawamura et al. have reported that *RyR2* positive CPVT cases are more likely to have clinically diagnosed CPVT-affected family members with bidirectional VT, and sinus bradycardia [26].

## 6. The mechanism of bidirectional VT

Bidirectional VT is the most characteristic feature of CPVT. In the His-Purkinje system, DAD induced bigeminy may differ depending on whether they are induced by the right bundle branch or the left bundle branch. The right bundle branch (RBB) caused a DAD induced bigeminy at a pacing rate of 900 ms (Fig. 8B), whereas the left bundle branch (LBB) induced a bigeminy at a pacing rate of 600 ms (Fig. 8B) [27]. In these situations, the sinus rate exceeded the threshold of the RBB-DAD induced bigeminy rate, and the beat after the sinus beat may have been induced from the RBB, resulting in a LBB block (LBBB) type PVC. The coupling interval of the normal sinus beat to the LBBB type PVC exceeded the threshold of the LBB-DAD induced bigeminy, and the next beat arose from LBB, resulting in a RBB block (RBBB) type PVC. When the coupling interval of the LBBB type PVC and RBBB type PVC exceeded the threshold of the RBB-DAD induced bigeminy, the next beat arose from the RBB followed by a beat

from the LBB, one after the other (Fig. 8C) [27]. This computer simulation suggests a mechanism for the bidirectional VT.

## 7. Therapy for the CPVT

### 7.1. $\beta$ Blockers

The long acting  $\beta$  blocker, nadolol, is preferred for prophylactic treatment of CPVT. Propranolol is also an effective medication. However,  $\beta$  blockers cannot completely suppress the arrhythmic events in CPVT patients [28].

Carvedilol is reported to inhibit the SOICR in an HEK 293 cell culture model. Among various  $\beta$  blockers, only carvedilol inhibits *RyR2* activity [29]. Thus, carvedilol may be an effective  $\beta$  blocker for CPVT, but its  $\beta$  blocking effect may be weak in comparison to the other  $\beta$  blockers. Therefore, the efficacy of carvedilol needs to be further investigated.

### 7.2. Verapamil

Verapamil has also shown beneficial effects in some CPVT patients [30,31]. However, the long-term efficacy of verapamil is still controversial.

### 7.3. Flecainide

Flecainide is an effective medication for CPVT [32–34]. Flecainide treatment shows improvement of ventricular arrhythmias in 74% of the genotype positive CPVT cases [32], and in 92% of the genotype negative CPVT cases [34]. Flecainide is thought to function by direct suppression of the RyR2 receptor. Among the Class I anti-arrhythmic medications, only flecainide and propafenone inhibit RyR2 activity [35]. However, recent report denies the direct suppression of RyR2 by flecainide [36]. That may suggest another mechanism of flecainide, such as inhibition of NCX.

### 7.4. Left cardiac sympathetic denervation

Left cardiac sympathetic denervation is reported to be a useful therapeutic method for suppressing ventricular arrhythmias in CPVT patients [37,38]. In patients with uncontrollable ventricular arrhythmias, left cardiac sympathetic denervation is highly useful in controlling ventricular tachyarrhythmias (Fig. 9). The rate of complications involving Horner syndrome is very low if denervation is performed in the lower half of the T1 sympathetic ganglion through the T4 ganglion [38].

### 7.5. ICD

Implantation of an ICD should be considered in patients in the absence of controlled optimal therapy [39]. However, implantation of an ICD in children still has a number of technical problems [40]. Moreover, inappropriate or painful shocks may increase the risk of further ventricular arrhythmias, and electrical storms that may result in lethal events.

### 7.6. Catheter ablation

Pulmonary vein isolation is reported to be effective in some CPVT patients with atrial fibrillation [41]. Purkinje cells are reported to be more arrhythmogenic than ventricular myocytes in a mutant knockout mouse model of CPVT [42]. The onset of CPVT may be initiated from Purkinje cells. Successful catheter ablation has been reported at the site of Purkinje potentials or discrete prepotentials (Fig. 10) [43].

### 7.7. Gene therapy

The homozygous R33Q knock-in mouse has a dysfunctional CASQ2, which may cause CPVT. In this mouse model, isoproterenol induced DADs, which were markedly reduced after 12 months following infection with an adenoviral vector (serotype 9), that carried the normal CASQ2 gene [44]. This report suggested the possible use of gene therapy for some types of CPVT in the future.

### Conflict of interest

All authors declare no conflict of interest related to this study.

### Acknowledgment

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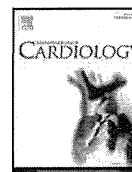
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## Targeted resequencing identifies *TRPM4* as a major gene predisposing to progressive familial heart block type I



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### ABSTRACT

**Background:** Progressive cardiac conduction disease (PCCD) is one of the most common cardiac conduction disturbances. It has been causally related to rare mutations in several genes including *SCN5A*, *SCN1B*, *TRPM4*, *LMNA* and *GJA5*.

**Methods and results:** In this study, by applying targeted next-generation sequencing (NGS) in 95 unrelated patients with PCCD, we have identified 13 rare variants in the *TRPM4* gene, two of which are currently absent from public databases. This gene encodes a cardiac calcium-activated cationic channel whose precise role and importance in cardiac conduction and disease is still debated. One novel variant, *TRPM4*-p.I376T, is carried by the proband of a large French 4-generation pedigree. Systematic familial screening showed that a total of 13 family members carry the mutation, including 10 out of the 11 tested affected individuals versus only 1 out of the 21 unaffected ones. Functional and biochemical analyses were performed using HEK293 cells, in whole-cell patch-clamp configuration and Western blotting. *TRPM4*-p.I376T results in an increased current density concomitant to an augmented *TRPM4* channel expression at the cell surface.

**Conclusions:** This study is the first extensive NGS-based screening of *TRPM4* coding variants in patients with PCCD. It reports the third largest pedigree diagnosed with isolated Progressive Familial Heart Block type I and confirms that this subtype of PCCD is caused by mutation-induced gain-of-expression and function of the *TRPM4* ion channel.

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### 1. Introduction

Progressive cardiac conduction defect (PCCD) was first described in the sixties by Lenègre [1] and Lev [2] as a fibrosis process affecting the

conduction system. It is one of the most common cardiac conduction disturbances characterized by a progressive alteration of cardiac conduction through the His-Purkinje system with right or left bundle branch block (RBBB or LBBB) and widening of QRS complexes, leading to complete atrioventricular block (AVB), syncope and sudden death.

Familial cases of PCCD have been reported with an autosomal dominant inheritance and causally related to rare mutations in genes involved in cardiac impulse propagation (*SCN5A* [3,4], *SCN1B* [5] and *TRPM4* [6,7]), in the structure of the nuclear lamina (*LMNA* [8,9]) and in cell-to-cell communication (*GJA5* [10]).

Among these genes, *TRPM4*, encoding a calcium-activated cationic channel that is expressed in Purkinje fibers and nodal tissue [6,7], has first been linked to progressive familial heart block type I (PFHBI) in two large pedigrees, respectively from South Africa [6] and Lebanon

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[7]. PFHBI is associated with a progressive impairment of the His bundle branches conduction, typically starting with RBBB and then left anterior hemiblock (LAHB) and that may progress to a complete AVB. QRS duration increases with time while PR and QTc intervals remain constant [11–13].

Conduction defects in TRPM4-dependent familial cases were shown to be related to gain-of-function mutations proposed to be caused by a reduction of the deSUMOylation of TRPM4 channels and an impaired endocytosis resulting in stabilization and overexpression of mutant channels at the plasma membrane [6,7]. Since these two seminal reports, eighteen gain- or loss-of-function variants have been identified as causing diverse forms of cardiac conduction defects and/or Brugada syndrome [14–16].

Here, using next generation sequencing (NGS) technologies, we report novel TRPM4 variants including one (c.T1127C; p.I376T) segregating with the third largest reported PCCD family. This missense mutation segregates in 39 relatives of a 4-generation pedigree and was observed to lead to gain-of-expression and function of the mutant channel. These findings strongly support a central role of TRPM4 in cardiac conduction and cardiac conduction disorders.

## 2. Methods

### 2.1. Patient phenotyping

The study was conducted according to the French guidelines for genetic research and approved by the ethic committee of the Nantes University Hospital. A written consent was obtained for each family member who accepted to participate in the study.

The investigation included a physical examination with particular attention to the cardiovascular system and a 12-lead ECG. Heart rate, PR interval, QRS, QTc duration, P and QRS axes were measured automatically at rest (Mac Vu Marquette Inc., Milwaukee, Wisconsin, USA). Conduction defects were defined using the conventional classification [17, 18]. Two expert physicians, blinded to the clinical status, independently and systematically reviewed the ECG parameters.

Because of the prevalence of minor conduction defects in the general population and in order to decrease the risk of misclassification, only the most obviously affected patients were considered as affected. QRS axis was classified as normal when its value was between  $-30^\circ$  and  $+90^\circ$ . PR duration shorter than 210 ms was considered as normal. Patients were considered as affected if they have been implanted with a pacemaker (PM) for PCCD or if they have an ECG showing a major conduction defect (complete AVB, complete RBBB, complete LBBB, parietal block (PB) defined as a QRS wider than 115 ms without morphology of RBBB or LBBB, LAHB or left posterior hemiblock (LPHB)). Given the progressive nature of the disease, only patients older than 45 without any conduction defect were considered as unaffected. All the other patients were considered as undetermined and not included for the evaluation of the ECG parameters. Cardiac morphological diseases were excluded by echocardiography in all patients.

### 2.2. Targeted sequencing

Genomic DNA was extracted from peripheral blood lymphocytes by standard protocols. The DNA yields were assessed by measurements using Quant-IT™ dsDNA Assay Kit, Broad Range (Life Technologies, Q33130). The purity of the DNA was assessed by spectrophotometry (OD 260:280 and 260:230 ratios) using a Nanodrop instrument (Thermo Scientific). DNA integrity was assessed by separation in a E-Gel® 96 Agarose Gels, 1% (Life Technologies, G700801). For multiplex amplification, we used the HaloPlex™ Target Enrichment System (Agilent Technologies, 1–500 kb, ILMFST, 96 reactions, G9901B), Protocol Version D.2 (November, 2012). We applied a custom HaloPlex™ design enabling high-throughput sequencing of the coding regions of 45 genes previously linked to cardiac arrhythmias or conduction defects and/or

sudden cardiac death, including 19 genes known or suspected to be involved in PCCD. In this study we focused solely on the relevant 19 PCCD genes including *SCN5A*, *SCN1B*, *TRPM4*, *GJA5* and *LMNA* that have already been associated with isolated cardiac conduction defects together with *GJA1*, *GJC1*, *SCN10A*, *NKX2-5*, *TBX5*, *SNTA1*, *PRKAG2*, *RYR2*, *EMD*, *BMP2*, *BMPR1A*, *GATA4*, *MSX2* and *TNNI3K* as likely candidate genes. The targeted coding regions (exons)  $\pm 10$  bp correspond to 141 kb of genomic sequence.

Target enrichment and sequencing were performed as previously described [19]. First, 200 ng of gDNA samples were digested in eight different restriction reactions, each containing two restriction enzymes, to create a library of gDNA restriction fragments. These gDNA restriction fragments were hybridized to the HaloPlex probe capture library. Probes are designed to hybridize and circularize targeted DNA fragments. During the hybridization process, Illumina sequencing motifs including index sequences were incorporated into the targeted fragments. The circularized target DNA biotinylated HaloPlex probe complexes were captured on magnetic streptavidin beads. We proceeded to a ligation reaction of the circularized complexes followed by an elution reaction before PCR amplification. The amplified target DNA was purified using AMPure XP bead (Beckman Coulter, A63881). To validate enrichment of target DNA in each library sample by microfluidics analysis, we used the 2200 TapeStation (Agilent Technologies, G2964AA), with D1K ScreenTape (Agilent Technologies, 5067–5361), and D1K Reagents (Agilent Technologies, 5067–5362). We ensured that the majority of amplicons range from 175 to 625 bp. Finally we quantified each library by qPCR using KAPA Library Quantification Kit (Clinisciences, KK4854). Libraries were pooled to an equimolar concentration and DNA was then denatured with NaOH. Finally libraries pool was diluted to a 4 pM final concentration before proceeding to 100 bp paired-end Illumina sequencing on HiSeq.

### 2.3. Detection of rare coding variation in TRPM4

Raw sequence reads were aligned to the human reference genome (GRCh37) using BWAMEM (version 0.7.5a) after removing sequences corresponding to Illumina adapters with Cutadapt v1.2. GATK was used for indel realignment and base recalibration, following GATK DNaseq Best Practices. Variants were called for each sample separately using GATK UnifiedGenotyper (version 2.8) and Samtools mpileup (version 0.1.19), and variants were considered for further analyses if found by both GATK and Samtools with a minimum quality score of 25.

Variants were considered of interest if: 1—They present a potential pathogenicity as predicted by Variant Effect Predictor (Ensembl). Variants were considered as having a potential functional consequence if they were annotated with one or more of the following SO terms for at least one RefSeq transcript: “transcript\_ablation” (SO:0001893), “splice\_donor\_variant” (SO:0001575), “splice\_acceptor\_variant” (SO:0001574), “stop\_gained” (SO:0001587), “frameshift\_variant” (SO:0001589), “stop\_lost” (SO:0001578), “initiator\_codon\_variant” (SO:0001582), “inframe\_insertion” (SO:0001821), “inframe\_deletion” (SO:0001822), “missense\_variant” (SO:0001583), “transcript\_amplification” (SO:0001889); 2—They were rare that is if the minor allele frequency (MAF) was  $<1\%$  compared to the 1000 genomes phase 1 data (379 individuals of European origin, integrated release v3, downloaded from <ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20110521>), to the NHLBI GO Exome Sequencing Project (ESP) data – Exome Variant Server (EVS) (4300 individuals of European origin, ESP6500SI-V2 release, downloaded from <http://evs.gs.washington.edu/EVS>), and to the Exome Aggregation Consortium (ExAC) data (60,706 unrelated individuals including more than 33,300 non-Finnish European individuals, release v1, downloaded from [ftp://ftp.broadinstitute.org/pub/ExAC\\_release](ftp://ftp.broadinstitute.org/pub/ExAC_release)).

In case of missense variants SIFT [20] and PolyPhen-2 (PPH-2) [21] were used to predict the impact of the amino acid substitutions. Filtering was performed using Knime4Bio [22].

#### 2.4. Segregation analysis

Familial segregation analyses were carried out by bidirectional direct sequencing of amplified genomic DNA amplicons with variant-specific primers (forward: CCTCCATCCCTTTGGACAG; reverse: CAGGCCAGGA AAGGTGTCTA) using the “Big Dye Terminator v3.1 Cycle Sequencing Kit” (Applied Biosystems - Life Technologies) following the manufacturer's recommendations. The capillary sequencing was performed on Applied Biosystems 3730 DNA Analyzer using standard procedures provided by Applied Biosystems (Life Technologies).

The RefSeq NM\_017636.3 transcript has been used to compare our sequencing data.

Linkage was assessed between the variant I376K and the disease using standard method comparing likelihood under a recombination fraction of 50% (no linkage) and 0% (full linkage). LOD score [23] calculation was performed with Superlink-Online SNP version 1.1 (<http://cbl-hap.cs.technion.ac.il/superlink-snp/main.php>) [24].

We postulated a rare causal variant (frequency set at 1/10,000) and dominant model with high penetrance (80%). The prevalence is 5% and therefore, the phenocopy rate is 0.0499.

A LOD score higher than 3 is considered as significant for linkage.

#### 2.5. Cell culture and transfection

Human embryonic kidney (HEK293) cells were cultured with DMEM medium supplemented with 4 mM Glutamine, 10% FBS and a cocktail of streptomycin–penicillin antibiotics. For the electrophysiological studies, the cells were transiently transfected with 80 ng of HA-TRPM4 WT or HA-TRPM4 p.I376T in a 35 mm dish mixed with 4  $\mu$ l of JetPEI (Polyplus transfection, Illkirch, France) and 46  $\mu$ l of 150 mM NaCl. The cells were incubated for 24 h at 37 °C with 5% CO<sub>2</sub>. All transfections included 400 ng of cDNA encoding CD8 antigen as a reporter gene. Anti-CD8 beads (Dyna<sup>®</sup>, Oslo, Norway) were used to identify transfected cells, and only CD8-displaying cells were analyzed. Cells were used 24 h after transfection.

For the biochemical studies, HEK 293-cells were transiently transfected with 960 ng of either HA-TRPM4 WT, HA-TRPM4 p.I376T variants or empty vector (pcDNA4TO) in a P100 dish (BD Falcon, Durham, North Carolina, USA) mixed with 30  $\mu$ l of JetPEI (Polyplus transfection, Illkirch, France) and 250  $\mu$ l of 150 mM NaCl. The cells were incubated for 48 h at 37 °C with 5% CO<sub>2</sub>.

#### 2.6. Cell surface biotinylation assay

Following 48 h of incubation, transiently transfected HEK293 cells were treated with EZlink<sup>™</sup> Sulfo-NHS-SS-Biotin (Thermo Scientific, Rockford, Illinois, USA) 0.5 mg/ml in cold 1X PBS for 15 min at 4 °C. Subsequently, the cells were washed twice with 200 mM glycine in cold 1X PBS and twice with cold 1X PBS to inactivate and remove the excess biotin, respectively. The cells were then lysed with 1X lysis buffer (50 mM HEPES pH 7.4; 150 mM NaCl; 1.5 mM MgCl<sub>2</sub>; 1 mM EGTA pH 8.0; 10% Glycerol; 1% Triton X-100; 1X Complete Protease Inhibitor Cocktail (Roche, Mannheim, Germany)) for 1 h at 4 °C. Cell lysates were centrifuged at 16,000 g; 4 °C for 15 min. Two milligram of the supernatant was incubated with 50  $\mu$ l Streptavidin Sepharose High Performance beads (GE Healthcare, Uppsala, Sweden) for 2 h at 4 °C, and the remaining supernatant was kept as the input. The beads were subsequently washed five times with 1X lysis buffer before elution with 50  $\mu$ l of 2X NuPAGE sample buffer (Invitrogen, Carlsbad, California, USA) plus 100 mM DTT at 37 °C for 30 min. These biotinylated fractions were analyzed as TRPM4 expressed at the cell surface. The input fractions, analyzed as total expression of TRPM4, were resuspended with 4X NuPAGE Sample Buffer plus 100 mM DTT to give a concentration of 1 mg/ml and incubated at 37 °C for 30 min.

#### 2.7. Western blot experiments

Protein samples were analyzed on 9% polyacrylamide gels, transferred with the TurboBlot dry blot system (Biorad, Hercules, CA, USA) and detected with anti-TRPM4 (generated by Pineda, Berlin, Germany), anti  $\alpha$ -actin A2066 (Sigma-Aldrich, St. Louis, Missouri, USA) antibodies using SNAP i.d. (Millipore, Billerica, MA, USA). The anti-TRPM4 antibody was generated by Pineda (Berlin, Germany) using the following peptide sequence: NH<sub>2</sub>-CRDKRESDSERLKRTSQKV-CONH<sub>2</sub>. A fraction of the antisera, which was subsequently used in this study, was then affinity purified.

#### 2.8. Cellular electrophysiology

For patch-clamp experiments in whole-cell configuration, glass pipettes (tip resistance, 1.5–3 M $\Omega$ ) were filled with an intracellular solution containing (in mM): 100 CsAsp, 20 CsCl, 4 Na<sub>2</sub>ATP, 1 MgCl<sub>2</sub>, 10 EGTA, and 10 HEPES. The pH was adjusted to 7.20 with CsOH, and the free Ca<sup>2+</sup> concentration at 100  $\mu$ M with CaCl<sub>2</sub> using WEBMAXCLITE program (<http://www.stanford.edu/~cpatton/downloads.htm>). Access resistance ranges was from 3 to 5 M $\Omega$ . Extracellular solution contained (in mM): 156 NaCl, 1.5 CaCl<sub>2</sub>, 1 MgCl<sub>2</sub>, 6 CsCl, 10 glucose and 10 HEPES. The pH was adjusted to 7.40 with NaOH. Patch-clamp recordings were carried-out in the whole-cell configuration at room temperature (23–25 °C). TRPM4 currents were investigated using a ramp protocol. The holding potential was –60 mV. The 400 ms increasing ramp from –100 to +100 mV ends with a 300 ms step at +100 mV then 300 ms at –100 mV. A new ramp was performed every 2 s. Before seal formation, liquid junction potential was compensated to keep the baseline at 0 mV. Using a Digidata 1440 A analog-digital interface (Axon Instruments, Inc.), currents were filtered at 5 kHz and the sampling frequency was at 50 kHz. Current densities were obtained by dividing the peak current recorded at –100 mV by the cell capacitance (17  $\pm$  2 pF and 16  $\pm$  1 pF, respectively transfected with WT and I376T-TRPM4 channels). Of note, capacitances and series resistances were not compensated.

#### 2.9. Data analysis and statistical methods

Currents were analyzed with Clampfit software (Axon Instruments, Inc). Data were analyzed using a combination of pClamp10, Excel (Microsoft) and Prism (Graphpad).

Comparisons between groups were performed with impaired two-tailed Student's t test. Data are expressed as mean  $\pm$  SEM. A p-value <0.05 was considered significant.

### 3. Results

#### 3.1. Mutational screening

Ninety-five patients with PCCD were recruited through the French National Referral Center for Sudden Cardiac Death as previously described [25]. Nineteen genes known or suspected to be involved in conduction defects were sequenced in these patients using the HaloPlex<sup>™</sup> System, resulting in a mean coverage depth of 578 $\times$  per sample: *SCN5A*, *SCN1B*, *TRPM4*, *GJA5* and *LMNA* that have already been associated with isolated cardiac conduction defects together with *GJA1*, *GJC1*, *SCN10A*, *NKX2-5*, *TBX5*, *SNTA1*, *PRKAG2*, *RYR2*, *EMD*, *BMP2*, *BMPR1A*, *GATA4*, *MSX2* and *TNNI3K*. A graphical representation of the mean coverage obtained for the 5 major genes is provided in Supplemental Fig. 1.

When selecting only genetic variants with a potential pathogenicity as predicted by Variant Effect Predictor (see methods) and an MAF below 1% in public databases, we identified a total of 45 variants in 43 patients: 11 novel variants and 34 rare variants (see Supplemental Table 1). Among these variants, 13 have already been associated with cardiac pathologies such as the Brugada syndrome and cardiac