Loss-of-Function Mutations in the Cardiac Calcium Channel Underlie a New Clinical Entity Characterized by ST-Segment Elevation, Short QT Intervals, and Sudden Cardiac Death

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Background—Cardiac ion channelopathies are responsible for an ever-increasing number and diversity of familial cardiac arrhythmia syndromes. We describe a new clinical entity that consists of an ST-segment elevation in the right precordial ECG leads, a shorter-than-normal QT interval, and a history of sudden cardiac death.

Methods and Results—Eighty-two consecutive probands with Brugada syndrome were screened for ion channel gene mutations with direct sequencing. Site-directed mutagenesis was performed, and CHO-K1 cells were cotransfected with cDNAs encoding wild-type or mutant \( \text{CACNB2b} \) \( (\text{Ca}_{\mu 2\beta}) \), \( \text{CACNA2D1} \), \( \text{CACNA1C} \) tagged with enhanced yellow fluorescent protein \( (\text{Ca},1,2) \). Whole-cell patch-clamp studies were performed after 48 to 72 hours. Three probands displaying ST-segment elevation and corrected QT intervals \( \leq 360 \) ms had mutations in genes encoding the cardiac L-type calcium channel. Corrected QT ranged from 330 to 370 ms among probands and clinically affected family members. Rate adaptation of QT interval was reduced. Quinidine normalized the QT interval and prevented stimulation-induced ventricular tachycardia. Genetic and heterologous expression studies revealed loss-of-function missense mutations in \( \text{CACNA1C} \) \( (\text{A}39\text{V} \text{and} \text{G}490\text{R}) \) and \( \text{CACNB2} \) \( (\text{S}481\text{L}) \) encoding the \( \alpha_1 \)- and \( \beta_2 \)-subunits of the L-type calcium channel. Confocal microscopy revealed a defect in trafficking of A39V Ca,1,2 channels but normal trafficking of channels containing G490R Ca,1,2 or S481L Ca,\( \mu 2 \)-subunits.

Conclusions—This is the first report of loss-of-function mutations in genes encoding the cardiac L-type calcium channel to be associated with a familial sudden cardiac death syndrome in which a Brugada syndrome phenotype is combined with shorter-than-normal QT intervals. (Circulation. 2007;115:442-449.)

Key Words: arrhythmia ◼ genetics ◼ electrophysiology ◼ tachycardia ◼ fibrillation

Cardiac arrhythmias are responsible for an estimated 1 million cases of syncope and sudden cardiac death (SCD) among Europeans and Americans each year. Cardiac arrhythmias can be acquired as a consequence of coronary heart disease or may be secondary to familial or inherited syndromes. The past decade has witnessed an explosion of information linking cardiac ion channel mutations with a wide variety of inherited arrhythmia syndromes. The long-QT syndrome has been associated with 10 different genes, in large part owing to the pioneering studies of Keating and coworkers. The LQT8 form of long-QT syndrome, also known as Timothy syndrome, is associated with gain-of-function mutations in cardiac calcium channel activity. The cardiac L-type calcium channel is a protein complex formed by at least 3 subunits, \( \alpha_1 \), \( \beta \), and \( \alpha_2 \). The pore-forming \( \text{Ca},1,2 \) \( \alpha_1 \)-subunit is encoded by \( \text{CACNA1C} \). The \( \beta \)- or \( \text{Ca},\mu 2 \)-subunits

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subunit, encoded by \( \text{CACNB2b} \), modulates calcium channel activity in the human heart and enables trafficking by suppressing an endoplasmic reticulum retention signal in the I-III loop of the \( \alpha_1 \)-subunit.\(^5\)

The short-QT syndrome (SQTS), a clinical entity first described in 2000,\(^6\) has been associated with a gain of function in 3 distinct potassium channels (\( \text{KCNH2}, \text{KCNO1}, \text{and KCNJ2} \)) that leads to abbreviation of the ECG QT interval and the development of malignant arrhythmias.\(^7\)-\(^9\)

Loss-of-function mutations in \( \text{SCN5A} \), the gene that encodes the \( \alpha_1 \)-subunit of the cardiac sodium channel, have been linked to Brugada syndrome, which is characterized by an ST-segment elevation in \( V_1 \) through \( V_3 \) and a shorter-than-normal QT interval caused by loss-of-function mutations in \( \text{CACNB2b} \) to Brugada syndrome, which is characterized by an ST-segment elevation in the local institutional review boards.

Informed consent was obtained according to protocols approved by the local institutional review boards.

The ECG was digitally scanned, magnified 4 to 8 times, and measured with digital calipers. The end of the T wave was defined as the intersection of a tangent, drawn to the descending portion of the T wave, with the isoelectric line. QT intervals were measured in lead II whenever possible.

### Methods

**Patients**

Patients were diagnosed with Brugada syndrome on the basis of established criteria.\(^11,12\) We define short QT as corrected QT (QTc) intervals ≤360 ms for males and ≤370 ms for females, on the basis of published reports.\(^13,14\) At a heart rate of 60 bpm, the predicted QT interval (QTp) is 410 ms and the lower limit of normal is defined as 2 SDs below QTp, or 360 ms. Clinical and genetic studies were performed in accordance with human subject guidelines after written informed consent was obtained according to protocols approved by the local institutional review boards.

**ECG Measurement**

The ECG was digitally scanned, magnified 4 to 8 times, and measured with digital calipers. The end of the T wave was defined as the intersection of a tangent, drawn to the descending portion of the T wave, with the isoelectric line. QT intervals were measured in lead II whenever possible.

**Mutation Analysis**

Genomic DNA was prepared from peripheral blood lymphocytes of patients 1, 2, and 3 and available family members. All known exons of the principal long-QT syndrome genes were amplified with intronic primers and sequenced in both directions to probe for mutations. The following genes were screened: \( \text{SCN5A}, \text{SCN1B}, \text{SCN3B}, \text{KCNH2}, \text{KCNO1}, \text{KCNE1}, \text{KCNE2}, \text{KCNE3}, \text{KCNDD3} \) (K,4,3), \( \text{KCNIP2} \) (KCHiP2), \( \text{KCNJC1} \) (Ca,1,2), \( \text{CACNB2b} \) (Ca,gchi), and \( \text{CACNA2D1} \) (Ca,kv). In addition, \( \text{KCNJ5} \) was probed because of association of this transcriptional factor gene with lesser extent in cardiac muscle, including the aorta, bladder, and uterus.\(^3\) Specific mutations in either splice variant cause a gain of function in Ca,1,2 responsible for 2 forms of Timothy syndrome, a multiorgan disease with severe QT prolongation, arrhythmia, and sudden death.\(^3,4\)

**Electrophysiology**

Voltage-clamp recordings from transfected CHO-K1 cells were made with patch pipettes, fabricated from 1.5-mm OD borosilicate glass capillaries, filled with a solution containing (in mmol/L) 120 CsCl, 2.0 MgCl\(_2\), 10 HEPES, 5 CaCl\(_2\), 2 MgATP, and 10 EGTA, (pH 7.25 with CsOH) that had a resistance of 2 to 4 M\( \Omega \). Extracellular solution contained (in mmol/L) 130 NMDG, 5 KCl, 15 CaCl\(_2\), 1 MgCl\(_2\), 10 HEPES, pH 7.35 with HCl. Current signals were recorded with an Axopatch 200A or MultiClamp 700A amplifier (Axon Instruments Inc, Foster City, Calif), and series resistance errors were reduced by 60% to 70% with electronic compensation. All recordings were made at room temperature.

**Data Acquisition and Analysis**

All signals were acquired at 20 to 50 kHz and analyzed with a personal computer running pCLAMP 9 software (Axon Instruments Inc, Foster City, Calif). Results from pooled data are presented as mean±SEM, and \( n \) represents the number of cells in each experiment. Statistical analysis was performed with ANOVA, followed by a Student-Newman-Keuls test with SigmaStat software. \( P<0.05 \) was considered statistically significant.

**Localization of Ca\(^{2+}\) Channels**

Confocal microscopy was used to assess trafficking of Ca\(^{2+}\) channels tagged with enhanced yellow fluorescent protein (EYFP). Cells were grown on polylisine-coated 35-mm glass culture dishes and studied 3 days after transfection. Experiments were performed on an Olympus Fluoview laser-scanning confocal microscope (Olympus America, Center Valley, Pa), and images were acquired with Fluoview acquisition software. EYFP-labeled cells were analyzed in the XYZ configuration. A region of interest measurement confined to within 2 \( \mu \)m of the plasma membrane was made, and the average pixel intensity within this region of interest was defined as peripheral staining. The average pixel intensity for the remaining portion of the cell was also determined and defined as central staining. The ratio of peripheral to central fluorescence was calculated. Measurements were not normalized to cell area.

**Rate Dependence of the QT Interval**

The rate dependence of the QT interval was evaluated during a standard exercise stress test with a bicycle ergometer or treadmill.

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8A (accession No. Z34815), and \( \text{CACNB2b} \) cloned in pcDNA3 (accession No. AF285239), which were a kind gift from Dr Nikolai Soldatov. Chinese hamster ovary (CHO-K1) cells were grown in Gibco F12 nutrient mixture (Gibco, Invitrogen cell culture, Carlsbad, Calif) in 35-mm culture dishes and placed in a 5% CO\(_2\) incubator at 37°C. The cells were cotransfected with lipofectamine or FuGene6 (Roche Diagnostics, Indianapolis, Ind) with a 1:1:1 molar ratio of WT or mutant human \( \text{CACNA1C}, \text{CACNB2b}, \text{and WT CACNA2D1} \). To assess the influence of WT on expression of the mutant channels, CHO-K1 cells were cotransfected with a combination of mutant and WT \( \text{CACNA1C} \) or mutant and WT \( \text{CACNB2b} \) with the same total molar ratio. Electrophysiological studies were performed after 48 to 72 hours of incubation. \( \text{CACNA1C} \) was transfected as either (EYFP)\(_{\text{NcG17}}\), or pcDNA3-CACNA1C. In the latter case, 0.86 \( \mu \)g of enhanced green fluorescent protein cDNA was added to the transfection mixture. The 2 approaches yielded similar electrophysiological results. It is noteworthy that previous studies have demonstrated that the fusion yellow fluorescent protein (EYFP)\(_{\text{NcG17}}\) did not influence Ca,1,2 channel expression.\(^16\)

Previous studies have shown that transmembrane segment 6 in domain I of Ca,1,2 can be encoded by 2 mutually exclusive exons, and 8A.\(^17\) Exon 8 is highly expressed in the heart and to a much lesser extent in other tissues.\(^4\) By comparison, exon 8A expression is less prominent in heart but more impressive in organs with smooth muscle, including the aorta, bladder, and uterus.\(^3\) Specific mutations in either splice variant cause a gain of function in Ca,1,2 responsible for 2 forms of Timothy syndrome, a multiorgan disease with severe QT prolongation, arrhythmia, and sudden death.\(^3,4\)

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**Results**

Eighty-two consecutive probands with a clinical diagnosis of Brugada syndrome enrolled in our registry were systematically screened for ion channel gene mutations. Seven probands (8.5%) were found to have mutations in genes encoding the \( \alpha_{1} \) and \( \beta_{2} \) subunits of the cardiac L-type calcium channel. In addition to ST-segment elevation and a family history of SCD, 3 of the 7 probands exhibited QTc intervals ≥360 ms. The present study is focused on delineation of the clinical characteristics and genetic basis for this distinct clinical entity.

The first proband (III-6), a 25-year-old white male of European descent, presented with aborted SCD. QTc was 330 ms, and a coved-type ST-segment elevation was observed in V1 and V2 after an ajmaline challenge (Figure 1A). His 23-year-old brother (III-5) was also symptomatic, with syncope since age 21 years. Programmed atrial stimulation induced atrial fibrillation (AF) in both individuals and AV nodal reentrant tachycardia in the brother. The rest of the family was asymptomatic. The proband received an implantable cardioverter defibrillator, and over a 3-year follow-up period, he received only inappropriate shocks, which ceased after a cavotricuspid isthmus ablation. A total of 10 family members were evaluated clinically and genetically, and 6 were characterized as phenotype positive on the basis of the presence of ST-segment elevation ≥2 mm at baseline or after ajmaline and a QTc ≥360 ms in males and ≥370 ms in females (Figure 1B). III-3 showed a prominent r' in V2 at baseline and an ST-segment elevation ≥2 mm in response to ajmaline that resulted in neither a coved nor saddleback morphology; therefore, the designation was +/A. III-7, although genotype negative, showed a positive response to ajmaline; QTc was 414 ms. Tall, peaked T waves were observed in some family members presenting with shorter-than-normal QT.
intervals. QT/heart rate slope was −0.639 ms/bpm for patient 1 (III-6) and −0.869 ms/bpm for the symptomatic brother of patient 1 (III-5).

Patient 2, a 41-year-old white male of Turkish descent, presented with AF and an abbreviated QT interval of 300 ms (QTc = 346 ms). His brother died of sudden cardiac arrest at age 45 years. Ajmaline administration (1 mg/kg) led to a further elevation of the ST segment in leads V1 to V3 (Figure 1C). The QT interval showed little rate dependence, with a QT/heart rate slope of −0.54 ms/bpm (Figure 2). Monomorphic ventricular tachycardia was inducible with 2 extrastimuli. Atrial and ventricular effective refractory periods were 150 and 170 ms at a 430-ms pacing cycle length, respectively. AH and HV intervals and sinus node recovery time were within normal limits. Structural heart disease was ruled out by coronary angiography and right ventricular angiography. Quinidine (750 mg/d for 5 days), administered for control of AF, prolonged QTc to 390 ms. An implantable cardioverter defibrillator was implanted for primary prevention. Programmed ventricular stimulation via the implantable cardioverter defibrillator revealed both a central and peripheral pattern of fluorescence, which suggests that a pool of these current-voltage (I-V) relationship between WT, A39V, and CACNB2b WT and the S481L mutant were used (Figure 4F). CACNB2b WT and the S481L mutant were both expressed in CHO cells and per-
channels exists in intracellular organelles and that the proteins translocate normally to the cell membrane. In contrast, the fluorescence pattern of A39V channels was almost exclusively localized to intracellular organelles. The peripheral:central fluorescence ratio was similar for WT, G490R, and S481L (1.34 ± 0.17, 1.58 ± 0.31, and 0.94 ± 0.1; n = 6) but much smaller for A39V (0.41 ± 0.26; P < 0.05 compared with WT and G490R, n = 6 cells), which indicates that very few A39V channels were localized at the sarcolemma. Coexpression of WT and A39V channels was associated with more peripheral fluorescence (ratio = 1.16 ± 0.10) than A39V alone, which suggests that the mutant channel does not interfere with trafficking of WT channels. Coexpression of WT and S481L Ca\textsubscript{\(\alpha_{1C}\)2b} channels yielded a ratio (1.04 ± 0.10) similar to that of WT or S481L alone. These findings suggest that the loss of current observed with A39V is due to a defect in trafficking of mature Ca\textsubscript{\(\alpha_{1C}\)2b} channels from the endoplasmic reticulum/Golgi complex to the cell membrane, whereas channels formed from G490R Ca\textsubscript{\(\alpha_{1C}\)2} or S481L Ca\textsubscript{\(\alpha_{1C}\)2b} subunits traffic normally.

**Discussion**

Although the Brugada syndrome has thus far been linked to mutations that impede sodium channel expression or function, experimental studies have shown that the electrocardiographic and arrhythmic manifestations of the disease phenotype can be recapitulated in the coronary-perfused canine right ventricular wedge preparation with calcium channel blockers, which points to genes encoding the various subunits of the calcium channel as candidates to explain the disease phenotype. Moreover, calcium channel blockers have been reported to produce an acquired form of the Brugada syndrome in humans. Consistent with these findings, the
present study demonstrates an association between loss-of-function mutations in the \( \alpha_1- \) and \( \beta_2b \)-subunits of the cardiac L-type calcium channel and the Brugada syndrome phenotype.

Evidence in support of mutations in the calcium channel being causal include the following findings: (1) mutations in 2 different subunits of the calcium channel are associated with similar disease phenotypes in probands with a family history of SCD; (2) heterologous expression of mutant channels in CHO cells leads to a major loss of function consistent with the Brugada syndrome phenotype and with a shorter-than-normal QT interval; (3) the 3 mutations are not observed in ethnically matched healthy individuals; and (4) there is a clear genotype-phenotype correlation. The absence of an ST-segment elevation in the 2 daughters of patient 2 may be explained on the basis of the well-known low penetrance for clinical manifestation of the Brugada syndrome in young females.\(^ \text{12} \) The apparently false-positive response to ajmaline in III-7 has been reported previously in patients with Brugada syndrome.\(^ \text{20} \) The LOD score of 2.1 does not reach statistical significance for linkage but represents the maximal theoretical LOD score for this relatively small family. This notwithstanding, cosegregation of the mutation with the disease in the family and the in vitro expression data provide proof of the causative nature of the mutation.

Figure 4. Representative whole-cell Ca\(^{2+} \) currents recorded from CHO cells transfected with WT CACNA1C (A) or A39V (B) and G490R (C) mutant CACNA1C and S481L mutant CACNB2b (D). Currents were elicited with the pulse protocol illustrated in the inset above panel B. E, Current-voltage (I-V) relationship for WT (n=5), A39V (n=7), and G490R (n=10) CaV1.2 channels (exon 8A variant). F, I-V relationship for WT (n=10), A39V (n=12), and G490R (n=25) CaV1.2 channels (exon 8 variant). *\(^ P < 0.05 \) compared with G490R. #\(^ P < 0.05 \) compared with A39V. G, I-V relationship for WT (n=10), S481L (n=7) Cav\(_{\beta_2b} \) channels. *\(^ P < 0.05 \) compared with S481L. H through K, Representative confocal XYZ scans showing localization of EYFP-tagged CaV1.2 channels in CHO cells. H, Cell expressing WT CaV1.2 channels showed marked peripheral and cytoplasmic fluorescence. I, Cells expressing A39V CaV1.2 channels showed fluorescence localized in the perinuclear region of the cell. J, Cell expressing G490R CaV1.2 channels exhibit a fluorescence pattern similar to WT, which suggests that trafficking is not impaired. K, Cells expressing S481L Cav\(_{\beta_2b} \) channels exhibit a fluorescence pattern similar to WT, which suggests that trafficking is not impaired.
Arrhythmogenesis in both Brugada syndrome and SQTS is thought to be due to amplification of heterogeneities in action potential characteristics among the different transmural cell types. In Brugada syndrome, a decrease in \( I_Kr \) or \( I_{Ca} \) or augmentation of any one of a number of outward currents, including \( I_Kr, I_{Ks}, I_{NaCa} \), and \( I_{Na} \), can cause preferential abbreviation of the right ventricular epicardial action potential secondary to all-or-none repolarization of the action potential at the end of phase 1. This leads to loss of the action potential dome and the development of spatial dispersion of repolarization and thus the substrate and trigger for ventricular tachycardia, which is usually polymorphic and less frequently monomorphic. In the short-QT syndromes, preferential abbreviation of either the epicardial or endocardial response amplifies spatial dispersion of repolarization and creates the substrate for reentrant arrhythmias. An increase in outward current\(^-\) or a decrease in inward current, including calcium current, may be responsible.

The present study is the first to associate a cardiac calcium channel mutation with the Brugada syndrome or short QT intervals. Although the QTc intervals in probands in the present study may be defined as “short” on the basis of published reports,\(^1,4,14\) they may not in all cases be considered as representing an SQTS, which thus far has been associated with QTc intervals \( \leq 330 \) ms. Only 1 of the probands in the present study presented with a QTc \( = 330 \) ms (patient 1). It is noteworthy that Brugada syndrome is generally associated with a slight prolongation of the QT interval, particularly in the right precordial leads, presumably due to an accentuation of the action potential notch (without loss of the dome), which prolongs the action potential in right ventricular epicardium.

Viskin and coworkers\(^14\) reported that short QT intervals (QTc of \( \leq 360 \) ms for males and \( \leq 370 \) ms for females) are commonly observed in patients with idiopathic ventricular fibrillation. A less-steep QT-RR relationship is also observed in these patients, similar to the abnormal rate dependence of QT reported in patients in the present study. The slope of the QT/heart rate relation was \(-0.639 \) ms/bpm for patient 1 (III-6) and \(-0.869 \) ms/bpm for the symptomatic brother of patient 1 (III-5), \(-0.540 \) ms/bpm for patient 2, and \(-0.991 \) ms/bpm for patient 3. These values are considerably less steep than those reported by Magnano et al\(^22\) for normal controls (\(-1.37 \) ms/bpm). These distinctions are similar to those reported between SQTS1 patients (\(-0.54 \) ms/bpm) and noncarrier controls (\(-1.29 \) ms/bpm).\(^{23}\)

AF is known to be associated with 20% to 30% of Brugada syndrome cases\(^24\) and with a similar or higher fraction of short-QT cases.\(^25\) The high incidence of AF in the present cohort is therefore not unexpected.

Quinidine has been proposed to be of therapeutic value in the Brugada syndrome\(^26\) and in the SQTS.\(^27\) In the setting of Brugada syndrome, it is the \( I_Kr \) blocking effect of the drug that is salutary, whereas in the SQTS, it is the effect of the drug to block \( I_Kr \) and \( I_{Na} \). Clinical evidence of the effectiveness of quinidine in inducible and spontaneous ventricular fibrillation was reported by Belhassen and coworkers\(^28\) in a prospective study of 25 Brugada syndrome patients. The ability of quinidine to prevent induction of ventricular tachycardia and ventricular fibrillation and its effect to prolong QTc in patient 1 is consistent with these earlier reports.

Among 82 probands with a clinically robust diagnosis of Brugada syndrome in the present registry, 6% (5) presented with a shorter-than-normal QT interval. Three (60%) of these 5 probands carried a calcium channel mutation, which points to genetic heterogeneity for this phenotype. Fifteen percent of probands harbored a putative pathogenic mutation in \( SCN5A \), and 4.9% carried a mutation in calcium channel genes associated with Brugada syndrome and QT intervals \( > 370 \) ms. Expression studies are under way to determine the nature of the defect, if any, in calcium channel function in these other mutations. The fraction of probands with \( SCN5A \) mutations (15%) is similar to that reported by Schulze-Bahr and coworkers (14%).\(^{29}\) Whereas a gain of function in calcium channel current secondary to mutations in \( CACNA1C \) produces a sudden death syndrome associated with prolongation of the QT interval,\(^3,4\) the present findings indicate that a loss of function in calcium channel activity secondary to mutations in \( CACNA1C \) or \( CACNB2b \) can contribute to a sudden death syndrome that consists of a shorter-than-normal QT interval and ST-segment elevation (Brugada syndrome phenotype). A similar mirror image of malignant syndromes has been demonstrated for a loss and gain of function in \( SCN5A \) (Brugada versus LQT3 syndromes),\(^10,30\) \( KCNH2 \) (LQT2 versus SQTL),\(^31\) \( KCNQ1 \) (LQT1 versus SQT2),\(^32\) and \( KCNJ2 \) (Andersen-Tawil syndrome, LQT7 versus SQTS).\(^9\)

\( CACNA1C \)– and \( CACNB2b \)-mediated syndromes may be considered as Brugada syndrome types 3 and 4 (\( GPDI-L \) has been reported by London et al\(^33\) as type 2) or SQTS types 4 and 5, depending on which definition of short QT and which QT correction formula one chooses to employ. Because there is no clear basis on which to select Brugada syndrome over short QT or vice versa, we have chosen to present this as a distinct clinical entity in which these 2 sudden death syndromes are combined.

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Disclosures
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10. Wilde AA, Antzelevitch C, Borggrefe M, Brugada J, Brugada R, Brugada P, Corrado D, Antzelevitch C. Short QT intervals (corrected QT of ≤330 ms) were first identified as a distinct clinical entity associated with sudden cardiac death in 1992. The short-QT syndrome, characterized by abnormal rate adaptation of the QT interval. The present study identifies a new clinical entity associated with sudden cardiac death that combines all of these characteristics. This syndrome is linked to loss-of-function mutations in genes encoding the alpha- and beta-subunits of the cardiac L-type calcium channel. This is the first report of a calcium channel loss of function to be associated with familial sudden cardiac death syndrome. CLINICAL PERSPECTIVE

Brugada syndrome, characterized electrocardiographically as displaying a coved-type (type I) ST-segment elevation, was first identified as a new clinical entity associated with sudden death in 1992. The short-QT syndrome, characterized by corrected QT intervals ≤330 ms, was first identified as a distinct clinical entity associated with sudden cardiac death in 2000. Short QT intervals (corrected QT of ≤360 ms for males and ≤370 ms for females) are also commonly observed in patients with idiopathic ventricular fibrillation. Both short-QT syndrome and idiopathic ventricular fibrillation patients display an abnormal rate adaptation of the QT interval. The present study identifies a new clinical entity associated with sudden cardiac death that combines all of these characteristics. This syndrome is linked to loss-of-function mutations in genes encoding the alpha- and beta-subunits of the cardiac L-type calcium channel.
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