Biophysical Properties of 9 KCNQ1 Mutations Associated With Long-QT Syndrome

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Background—Inherited long-QT syndrome is characterized by prolonged QT interval on the ECG, syncope, and sudden death caused by ventricular arrhythmia. Causative mutations occur mostly in cardiac potassium and sodium channel subunit genes. Confidence in mutation pathogenicity is usually reached through family genotype-phenotype tracking, control population studies, molecular modeling, and phylogenetic alignments; however, biophysical testing offers a higher degree of validating evidence.

Methods and Results—By using in vitro electrophysiological testing of transfected mutant and wild-type long-QT syndrome constructs into Chinese hamster ovary cells, we investigated the biophysical properties of 9 KCNQ1 missense mutations (A46T, T265I, F269S, A302V, G316E, F339S, R360G, H455Y, and S546L) identified in a New Zealand–based long-QT syndrome screening program. We demonstrate through electrophysiology and molecular modeling that 7 of the missense mutations have profound pathological dominant-negative loss-of-function properties, confirming their likely disease-causing nature. This supports the use of these mutations in diagnostic family screening. Two mutations (A46T, T265I) show suggestive evidence of pathogenicity within the experimental limits of biophysical testing, indicating that these variants are disease-causing via delayed- or fast-activation kinetics. Further investigation of the A46T family has revealed an inconsistent cosegregation of the variant with the clinical phenotype.

Conclusions—Electrophysiological characterization should be used to validate long-QT syndrome pathogenicity of novel missense channelopathies. When such results are inconclusive, great care should be taken with genetic counseling and screening of such families, and alternative disease-causing mechanisms should be considered. (Circ Arrhythmia Electrophysiol. 2009;2:417-426.)

Key Words: long QT ■ mutations ■ arrhythmia ■ ion channels ■ sudden cardiac death

Long-QT syndrome (LQTS) is a potentially fatal arrhythmic syndrome typically associated with a prolonged QT interval on the surface 12-lead ECG. It represents a diverse range of disorders associated with prolonged ventricular repolarization. Current estimates are that LQTS mutation carriers can be present in 1 in 1000 to 5000. Recent advances in the molecular basis of LQTS have revealed a greater than expected incidence within families with causative potassium and sodium cardiac ion channel genes. More recently, LQTS and the allelic SCN5A disorder, Brugada syndrome, have been strongly associated with a proportion of sudden unexpected death syndrome cases, including in infancy.

Clinical Perspective on p 426

To date, 10 genes have proven association with LQTS: LQT1 (KCNQ1) and LQT2 (HERG) encode α-subunits of the voltage-gated K+ channel, Iβ1 and Iβ2, respectively; LQT3 (SCN5A) encodes the α-subunit of a voltage-gated Na+ channel.
channel; LQT5 (KCNE1) and LQT6 (KCNE2) code for the β-subunit of IKr and IKr, respectively; and LQT4 (Ankyrin-B) is a member of a membrane adapter protein family. Recently, the Andersen (KCNJ1) and Timothy (Cav1.2) syndrome genes have been suggested as loci for LQT7 and LQT8, respectively.15 We demonstrate that 7 of the missense mutations have been suggested as loci for LQT7 and LQT8, respectively.8,9

The locations of the newly identified mutations were assessed in 300 control chromosomes as well as data from other screening studies and database sites. Various Genebank databases were aligned with LQTS gene families and homologs at the point of mutation to assess the degree of evolutionary conservation.

Site-Directed KCNQ1 Mutagenesis and Transient Transfection in Chinese Hamster Ovary Cells

The human KCNQ1 DNA was originally provided by Dr Mark Keating (currently at Novartis Institute of Biomedical Research, Cambridge, Mass). Individual KCNQ1 mutation constructs were made using a QuickChange XL site-directed mutagenesis kit and manufacturer instructions (Stratagene Inc. La Jolla, Calif). The human KCN1 channel auxiliary subunit KCNIE1/RES-pEGFP construct was a gift from Dr Al George at Vanderbilt University. All inserts were sequenced to ensure that only the desired mutation was obtained. Wild-type or mutated KCNQ1 constructs and KCN1 (at 1:1 μg ratio) were transiently cotransfected into cultured Chinese hamster ovary cells with Fugene6 transfection reagent (Roche Applied Science, Indianapolis, Ind). A plasmid encoding the enhanced green fluorescent protein (pEGFP) linked to KCN1 was used to identify transected cells for the voltage clamp studies. Cells were grown for 48 hours after transfection before study.

Whole-Cell Voltage Clamp Studies and Solutions

Whole-cell voltage clamping was performed at room temperature with 3 to 5 mol/LΩ patch microelectrodes and an Axopatch 200A amplifier (Molecular Devices, Sunnydale, Calif). The cell chamber (extracellular) solution contained (in mmol/L) NaCl 145, KCI 4.0, MgCl2 1.0, CaCl2 1.8, glucose 10, and HEPES 10; the pH was 7.4, adjusted with NaOH. The pipette (intracellular) solution contained (in mmol/L) KCl 110, MgCl2 1.0, ATP-K2 5.0, BaPTA-K5 5.0, and HEPES 10; the pH was 7.2, adjusted with KOH. Data acquisitions were done by use of pClamp9.2 (Axon Instruments Inc), sampled at 1 kHz, and low-pass—filtered at 5 kHz. Activating current was elicited with 5-second depolarizing pulses to +60 mV from a holding potential of −80 mV at a 10-mV increments, and tail current was recorded on return to −40 mV. Pulses were delivered every 30 seconds. To mimic a “physiological” action potential duration, a single 400-ms pulse to +20 mV and back to −40 mV for another 100 ms from the holding potential of −80 mV was used to compare the initial IKs magnitudes in wild-type and several particular KCNQ1 mutant channels in some experiments. To determine the membrane potential of the channels activated, I-V relationships were established by fitting data to the Boltzmann equation: 

\[ I = \frac{I_{\text{max}}}{1 + \exp\left(\frac{V-V_{50}}{k}\right)} \]

where \( I_{\text{max}} \) is the maximal current, \( V \) is the testing potential, \( V_{50} \) is the membrane potential at which 50% of the channels are activated, and \( k \) is the slope factor. Current densities (pA/pF) were obtained after normalization to cell surface area calculated by Membrane Test (OUT 0) in pClamp9.2. The steady-state activating current at the end of a 5-second depolarizing pulse to +60 mV and the peak deactivating tail current at −40 mV were measured for comparisons of wild type (WT) with mutated IKs densities. The time constants (τa, ms) for activating IKs currents in WT and any mutations with obvious channel gating changes were obtained by using the Chebyshev method to fit individual activating current traces to the monoexponential function: 

\[ A_1 \exp\left(-t/(\tau_a)\right) + C \]

Statistical Analysis

Data are expressed as mean ± SEM. For comparisons among means of several groups, ANOVA was used, with post hoc pairwise comparisons by Duncan test if significant differences among means were detected. If only 2 groups were being compared, Student’s t test was used. A probability value of <0.05 is considered statistically significant.

Structural Modeling

The locations of the newly identified KCNQ1 mutations were investigated using the recently published homology model of the transmembrane regions of the open and closed KCNQ1 channel in...
tetrameric form. All models were visualized using the molecular graphics program Chimera (http://www.cgl.ucsf.edu/chimera/).

Results

LQTS Cases
All 9 patients with 5 novel and 4 literature-recurrent KCNQ1 mutations selected for functional analysis had Romano-Ward syndrome, an autosomal dominant hereditary disorder characterized by a prolonged QT interval on the ECG, syncope, and sudden death. The heart rate–corrected QT interval (QTc) ranged from 480 to 660 ms (average, 534 ± 20 ms). Eight patients were of European descent, and 1 was of Maori descent. The presenting clinical features are indicated in Table 1. Three cases were identified from follow-up of sudden unexpected death in a first-degree family member.

Novel KCNQ1 Mutations in LQTS
Between 2001 and 2005, 48 gene-positive probands were identified in an LQTS screening program in New Zealand: 25 had KCNQ1 mutations, 9 of which (in 2004) had not been reported in the literature (see Table 1). Subsequently, 4 of the variants (A46T, A302V, G316E, and S546L) have been reported by other LQTS screening programs but without any supporting electrophysiological data, whereas there are alternative amino acid substitutions or frameshifts recorded at positions 265 (T265fs +22X), 302 (A302T), and 360 (R360T). Therefore, all 9 variants described here are novel observations based on receptor properties recorded by in vitro functional electrophysiology. Sequence analysis revealed that these mutations are located in a variety of domain regions in KCNQ1 (Figure 1): the N terminus (A46T), S5 (T265I), the S5 and P loop linker (F296S), the P loop (A302V and G316E), S6 (F339S), and the C terminus (R360G, H455Y, and S546L).

Population studies confirmed that these sequence variations were not represented in unrelated controls, and phylogenetic alignment of KCNQ1 homologs confirmed that the mutations have occurred at conserved sites. Mutation constructs of KCNQ1 were prepared using a QuikChange XL site-directed mutagenesis kit and submitted for electrophysiological characterization.

Seven KCNQ1 Mutations Are Loss-of-Function Channels
To compare the biophysical properties of normal IKs with those of the KCNQ1 subunit mutations, we used single 5-second pulsing to +60 mV from a holding potential of −80
mV to elicit the $I_{Ks}$ current. The tail current was recorded on return to $-40 \text{ mV}$. WT KCNQ1 and the auxiliary subunit KCNE1 were first coexpressed to generate an outward potassium current typical to cardiac $I_{Ks}$ current (Figure 2A). Individual KCNQ1 mutations were then studied with KCNE1 coexpression for comparison. As illustrated in Figure 2 and Figure 3A and B, 7 of the 9 KCNQ1 mutations generated a reduced $I_{Ks}$ current when coexpressed with KCNE1. The $I_{Ks}$ magnitudes by the other 2 mutations (A46T and T265I) were similar to normal $I_{Ks}$, except that A46T-$I_{Ks}$ showed a fast activation (Figure 2B): the time constants for activation at $60 \text{ mV}$ were 1717.3 ± 192.4 ms (WT) and 977.6 ± 68.9 ms (A46T-$I_{Ks}$, $P<0.01$, n=6 cells for each group), respectively. The half-maximal voltage ($V_{0.5}$) of $I_{Ks}$ activation was not different among WT, A46T, T265I, G316E F339S, and H455Y ($P<0.05$) (Figure 3C). However, the $V_{0.5}$ for the mutation F296S was $10 \text{ mV}$ more negative than WT-$I_{Ks}$ ($P<0.05$), whereas the $V_{0.5}$ for S546L was significantly shifted toward a more positive direction ($+20 \text{ mV}$ greater than WT-$I_{Ks}$, $P<0.01$). Because of very small $I_{Ks}$ magnitude from A302V and R360G, the current-voltage curves for the 2 mutations were not established to generate the $V_{0.5}$ values.

Enhanced Initial $I_{Ks}$ Currents and Loss of the Delay Phase of the $I_{Ks}$ in Particular KCNQ1 Mutations

In our experiments with a 5-second pulse protocol, we found that 2 KCNQ1 mutations (A46T and H445 years) activated more rapidly without an initial delay at the very beginning phase of the $I_{Ks}$ (Figure 2, B and I). In addition, T265I appears to have a longer delay before the current activation (Figure 2C). Accordingly, we applied a single 500-ms pulse protocol that mimics a physiological action potential duration. In this protocol, a 400-ms depolarization pulse to $+20 \text{ mV}$ with a 100-ms repolarization to $-40 \text{ mV}$ was used. The current magnitudes at 100th- and 400th-ms points were measured for comparisons. As illustrated in Figure 4A, WT-$I_{Ks}$ showed an initial delay at first $\approx 50$-ms before activation (rising phase in dotted box). The mutations A46T-$I_{Ks}$ and H455Y-$I_{Ks}$ lost this initial current delay with a rapid activation/rising phase (Figure 4, B and E). However, the mutation T265I-$I_{Ks}$ displayed a longer delay ($\approx 150$ ms) before activation (Figure 4D). The summarized data on the current magnitudes at 100th- and 400th-ms points are presented in Figure 4, C and F.

Given the fact that the $I_{Ks}$ channel is highly upregulated by β-adrenergic stimulation and that the mutation A46T was located in the N terminus of the KCNQ1 channel, we further compared the effects of a β-receptor agonist isoproterenol (1 µmol/L) on WT-$I_{Ks}$ and this mutant. The experimental results in Figure 4 (G through I) showed that the β-stimulation increased the current in both WT and A46T to a similar extent, implying that the A46T mutation did not influence the β-stimulation–mediated phosphorylation of the KCNQ1 channel. Previously, we and others have already

![Figure 2. $I_{Ks}$ for WT (A) and mutated KCNQ1 constructs (B through J) in the presence of KCNE1 in Chinese hamster ovary cells. Raw $I_{Ks}$ traces were obtained by using the voltage-clamp protocol at room temperature. Cells were clamped to a holding potential of $-80 \text{ mV}$. Activating $I_{Ks}$ was elicited with a 5-second pulse from $-80$ to $+60 \text{ mV}$, and deactivating tail current was recorded on repolarization to $-40 \text{ mV}$ for another 5 seconds.](http://circep.ahajournals.org/doi/fig/10.1161/CIRCARRHYTHMIA.109.980795)
demonstrated that several amino acid residues in the N terminus (S27) and C terminus (S468 and T470) are critical phosphorylation sites of the KCNQ1 channel.19,20

Two Mutations Have Suggestive Outcomes

There is inconclusive but suggestive evidence for functional consequences of 2 variants in this study (A46T and T265I) representing challenges for the clinical interpretation of the genotype. The mutation C794T (with resulting T265I) was found in a 40-year-old woman who presented after resuscitated sudden death during sleep (Figure 5A). She had been taking sibutramine, a medication to aid with weight loss, for approximately 3 weeks before her presentation, and her case has been previously reported.16 Her QTc was 600 to 660 ms, and she went on to have an intracardiac cardioverter-defibrillator inserted. A previous ECG was also abnormal, with prolonged QTc of 500 ms. Subsequent ECGs have had QTc values in the upper normal range. She has 4 children who all have prolonged QTc intervals, 1 of whom has a history of syncope on exertion. Cascade testing in 3 younger children has identified the same mutation as the proband, whereas the oldest child has declined genetic testing. The proband’s mother and 3 siblings have all had ECGs with normal QTc intervals. Her father has a prolonged QTc of 0.48 seconds and is gene-positive.

The mutation G136A (with resulting A46T) has previously been reported by Napolitano et al.10 In our cohort, it was detected in a 57-year-old woman after presentation with acute syncope while taking cisapride (Figure 5B). She had a history of syncope at times of stress. Her initial QTc interval was 620 ms, whereas subsequent ECGs have revealed QTc intervals of 400 to 470 ms. Her presenting episode of collapse occurred in the days after the unexpected death of her son, who had died suddenly, during gentle activity, at 37 years of age. He also had a history of syncope, but there were no prior ECGs. The postmortem examination revealed no cause, but no DNA was available for posthumous genetic screening. Despite the proband’s presentation, the acutely prolonged QTc interval, and family history of young sudden death, further investigation of the family to date lends some doubt as to the

Figure 3. Summarized data for WT and mutated IKs currents. A, Steady-state IKs current levels for WT and mutations. Currents were measured at the end of a 5-second depolarizing pulse. B, Peak IKs tail current for WT and mutations. Peak tails were measured after a 5-second repolarizing pulse to −40 mV. C, Half-maximal voltage of IKs activation (V0.5, mV) for WT and mutations. After current-voltage relations were obtained, the V0.5 values were obtained after fitting individual data points to the Boltzmann equation: I = I_max/[1 + exp (Vt−V0.5)/k]]. Two mutations (A302V and R360G) expressed tail currents too small to generate a V0.5 value.

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malignancy of this mutation. The proband has 3 other children who all have a history of syncope and have undergone cascade genetic screening. One son (QTc, 380 to 420 ms) and 1 daughter (QTc, 420 to 480 ms) tested positive for this mutation; the other daughter (QTc, 420 to 440 ms) had negative cascade testing. The proband’s 2 living siblings have not presented for assessment but are reportedly asymptomatic. Another sibling died in an accident at age 20 years. With regard to the proband’s parents, her father died at age 71 years, and her mother’s genetic screening was negative. As a result of the poor cosegregation of the mutation with clinical findings in this family, together with the in vitro electrophysiological testing result, we are not using cascade screening as a definitive test for the presence or absence of disease in this family.

Molecular Modeling of the KCNQ1 Mutations
The tertiary positions of mutations T265I, F296S, A302V, G316E, and F339S were examined in relation to the recently published homology model of the transmembrane regions of the protein.17 The N-terminal A46T mutation and the C-terminal R360G, H455Y, and S546L fell outside the current coverage of published models and crystal structures. A crystal structure for the C-terminal region of human KCNQ1 has recently been elucidated,21 but this is restricted to residues 584 to 621 of the C terminus.

As shown in Figure 6A, in the closed state, T265 and F339 are closely located and likely to interact by means of intrachain hydrophobic interactions between S5 and S6. F296 and A302 are also closely located, but on the extramembrane portion of the P loop. Comparison of the closed and open states of the channel (Figure 6A and B) reinforces the importance of the mutated positions. In the open state, the interactions between the residues of each pairing are less intimate, suggesting that engagement and loss of specific hydrophobic interactions are central to the conformational changes in the transmembrane and loop regions required for activity of the channel. We speculate that mutations involving these residues disrupt the fine architecture of the channel and preclude normal opening and closure. G316 is located on the P loop, squarely at the entry to the pore (Figure 6C). The G316E mutation directly restricts the aperture of the pore by introducing a much larger and negatively charged glutamic acid residue to this critical gating position (Figure 6D). It is also possible that the mutation may bring about misfolding of
Figure 5. Pedigrees and clinical data of the gene-positive families with uncertain, ambiguous outcomes. A, Family with KCNQ1 A46T and associated clinical presentation and incidences. B, Family with T265I and associated clinical presentation and incidences. Refer to the figure for the key guide.
the protein, which may subsequently affect its trafficking or tetramerization, although homology modeling of the E316 variant (data not shown) suggests that this is unlikely.

**Discussion**

Many KCNQ1 mutations and rare variants have now been identified in a variety of KCNQ1 domains and regions (http://www.fsm.it/cardmoc), some of which are recurrent in populations whereas some remain private to 1 index case or extended family. This represents a dilemma in the clinical setting because it is difficult to assign pathogenicity to novel variants without several levels of validating evidence, the best of which is the demonstration of biophysical deficits by in vitro electrophysiological experiments. This is a highly specialized and challenging technology platform that is unlikely to cross over to the diagnostic domain; nevertheless, it can provide definitive evidence and clinical confidence that a gene variant can translate into a functional mutation. For this reason, we describe in this study the biophysical characterization of 9 KCNQ1 variants in patients with Romano-Ward syndrome.15,16 The gene-positive patients had unequivocally prolonged QTc intervals, and all but 1 had typical presentation scenarios such as syncpe during exercise, a history of sudden death in the family, or resuscitated cardiac arrest. Within the KCNQ1 subunit structure, these mutations are located in different regional domains: the N terminus (A46T), S5 (T265I), the S5 and P loop linker (F296S), P loop (A302V and G316E), and the C terminus (R360G, H455Y, and S546L). Four variants (A46T, A302V, G316E, and S546L) have subsequently been detected by other LQTS screening programs but without any supporting electrophysiological data, whereas there are alternative amino acid substitutions or frameshifts recorded at positions 265 (T265fs/H11001), 302 (A302T), and 360 (R360T).10,18 Whatever the status and origin of the KCNQ1 variants, the biophysical investigation of their pathogenicity has not been investigated.

The value of discovering the physiological properties of channel variants has contributed much to the understanding of the pathophysiological mechanisms of LQTS.12–14 Cardiac slowly activating delayed rectifier K+ current (IKs) is generated by coassembly of the α-subunit KCNQ1 (KvLQT1) and its auxiliary subunit KCNE1 (minK). The IKs current does not play a major role in regulation of cardiac repolarization under normal physiological conditions. However, mutations in the KCNQ1 gene could cause inherited prolongation of the QT interval by reducing the quality of IKs current, thereby affecting cardiac repolarization. Expression studies have demonstrated that LQTS mutations of genes related with K+ currents can produce loss of channel function by either a net current reduction by altering the channel gating and kinetic
properties, prevention of assembly of functional channel protein, or an abnormal intracellular protein trafficking.

We examined the electrophysiological properties of the 9 KCNQ1 mutations in the presence KCNE1 by heterologous expression in Chinese hamster ovary cells and by using a whole-cell voltage clamp. We found 7 KCNQ1 mutations causing a reduced $I_{KS}$ current density with coexpression of KCNE1, indicating the loss of function in the heterotetrameric state channel. The electrophysiological data for the 7 KCNQ1 mutations with decrease the $I_{KS}$ density suggest several possible mechanisms: (1) a positive shift of the channel activation voltage could lead to a reduction of the current (this effect is more obvious in the mutation S546L); (2) the dominant-negative effect; and (3) failure of the channel protein expression within the cell membrane. The studies relating to the latter 2 effects are separate projects that are being pursued, but irrespective of the specific mechanism involved, it is now possible to label these 7 LQTS genotypes as definitive pathological mutations.

Two other mutations (A46T and T265I) displayed no alterations in the current density, although there is evidence that T265I-IKs displayed a longer delay (=150 ms) before activation, and A46T-IKs (as well as H455Y-IKs) lost initial current delay with a rapid activation/rising phase. In the mutation T265I, a longer initial 100-ms current delay and small current magnitude would be responsible for prolonged QT intervals. Studies have demonstrated that the initial delay phase of $I_{KS}$ channel activation is caused by its $\beta$-subunit KCNE1 via moving the channel through multiple closed states before opening during a depolarization, thereby decreasing the initial current activation. In the cases of A46T-IKs and H455Y-IKs, whether the interaction between the mutation and KCNE1 is affected to some degree remains to be studied further. The mutation-caused loss of delay of the initial $I_{KS}$ activation could be caused by channel accumulation in open states between depolarization pulses. The mutation-caused loss of delay of the initial $I_{KS}$ activation could be associated with more channel accumulations in Zone 1 of closed states that are near-open states in the Markov model of the $I_{KS}$ channel kinetics. The channel accumulation in Zone 1 of closed states between cardiac action potentials provides an “available reserve” that represents an important mechanism for $I_{KS}$ participation in repolarization and its dependence on rate. During the action potential repolarization, especially at fast heart rates, these readily available channels can very quickly open on demand to cause rapid $I_{KS}$ activation and rise, an effect to shorten cardiac action potential duration. Again, the current magnitude at the first 100 ms of $I_{KS}$ activation was larger in the mutation A46T than in WT current (Figure 4C). Therefore, these alterations in $I_{KS}$ properties could explain failure to observe a prolonged QT interval in the A46T patient.

Structural modeling helps us to conceptualize the different functional effects of particular mutations. Mutation of T265 and F339 affect interactions between S5 and S6. This is consistent with the T265I mutation displaying a longer delay (=150 ms) before activation (Figure 4D) as the normal movements of the S5 helix required for efficient opening and closure are impeded by the substitution of threonine by the larger more hydrophobic isoleucine. F339S, on the other hand, involves substitution by a smaller more polar residue, which is less physically impeding but nevertheless remains pathogenic as indicated by the functional assays (Figure 2G).

Although the A302V substitution involves residues of similar size, the observed functional effects may be caused by the external aqueous environment being less forgiving of changes in hydrophobic interactions. Similarly, changes in polarity of exposed extramembrane residues on mutation affect $V_{0.5}$ values, resulting accordingly in more negative (F296S, change to polar) or more positive S546L (change to hydrophobic) values. The G316E mutation appears to obstruct directly the normal aperture of the pore by introducing a much larger and negatively charged glutamic acid side chain to one of the most sensitive gating positions. Modeling and comparison of the heteromeric mutation of 2 of the 4 chains (Figure 6D) with the WT (Figure 6C) reveal the extent to which the pore is likely to be obstructed. It is interesting to note that the mutation also disrupts the second glycine residue in a combinatorial sequence pattern [S/T]xx[S/T]xG[F/Y]G that has been identified in 90% of 134 potassium channel reentrant loops analyzed, which suggests that this glycine residue may also be important for the stable insertion of the P loop within the membrane.

In summary, the biophysical characterization of these 9 KCNQ1 missense mutations has provided unequivocal heterogeneous proof of pathogenicity in 8 variants to support the various clinical and genetics studies. We remain uncertain as to the pathogenicity of A46T, given that the suggestive biophysical evidence and cosegregation studies are inconclusive in part because of resistance to wider family screening. In this family it is possible that the genetic basis of the QT prolongation lies elsewhere, and further molecular screening of the index cases must remain an option. Although cellular electrophysiological testing is unlikely to move easily into the clinical diagnostic area, its clinical value is very important and not in question, given the high proportion of novel genetic variants being discovered presenting a challenge to the clinical and genetic counseling teams. For the time being, a collaborative multidisciplinary approach is needed between clinical and research domains to permit relative and informative proof for cardiologists and genetic counseling teams.

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Disclosures
None.

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5. Wehrens XHT, Vos MA, Doevendans PA, Wellens HJJ. Novel insights in the disease-causing nature of these mutations. These findings support the use of electrophysiological characterization to identify dominant negative/loss-of-function properties in 7 of 9 novel LQTS mutations evaluated in this study, supporting use of biophysical testing to provide evidence for functional pathogenicity of such mutations. The protein coded for by the mutated gene can be expressed in vitro to allow electrophysiological characterization of the resulting ion channels, providing an indication of the mechanisms by which the clinical phenotype is produced. Electrophysiology analysis identified dominant negative/loss-of-function properties in 7 of 9 novel LQTS mutations evaluated in this study, supporting the disease-causing nature of these mutations. These findings support the use of electrophysiological characterization to potentially validate LQTS pathogenicity of novel missense mutations in ion channels. This approach may be helpful in assessing risk and providing genetic counseling and screening of families with novel mutations.

CLINICAL PERSPECTIVE

Long-QT syndrome (LQTS) is characterized by prolonged QT interval on the ECG, syncope, and sudden death caused by ventricular arrhythmia. Inherited LQTS is caused by mutations in cardiac ion channel genes, and mutation screening in LQTS is now a well-established part of genetic service programs around the world. Identification of mutations that are known to cause arrhythmias is useful. The significance of novel mutations is often unclear. Is such a mutation a rare natural variation in the human genetic code or a pathophysiological entity predisposing to sudden death? This study supports the use of biological testing to provide evidence for functional pathogenicity of such mutations. The protein coded for by the mutated gene can be expressed in vitro to allow electrophysiological characterization of the resulting ion channels, providing an indication of the mechanisms by which the clinical phenotype is produced. Electrophysiology analysis identified dominant negative/loss-of-function properties in 7 of 9 novel LQTS mutations evaluated in this study, supporting the disease-causing nature of these mutations. These findings support the use of electrophysiological characterization to potentially validate LQTS pathogenicity of novel missense mutations in ion channels. This approach may be helpful in assessing risk and providing genetic counseling and screening of families with novel mutations.
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