Drug-Induced Long-QT Syndrome Associated With a Subclinical SCN5A Mutation

Naomasa Makita, MD, PhD*; Minoru Horie, MD, PhD*; Takeshi Nakamura, MD; Tomohiko Ai, MD, PhD; Koji Sasaki, MD; Hisataka Yokoi, MD; Masayuki Sakurai, MD; Ichiro Sakuma, MD, PhD; Hideo Otani, MD, PhD; Hirofumi Sawa, MD, PhD; Akira Kitabatake, MD, PhD

**Background**—Subclinical mutations in genes associated with the congenital long-QT syndromes (LQTS) have been suggested as a risk factor for drug-induced LQTS and accompanying life-threatening arrhythmias. Recent studies have identified genetic variants of the cardiac K+ channel genes predisposing affected individuals to acquired LQTS. We have identified a novel Na+ channel mutation in an individual who exhibited drug-induced LQTS.

**Methods and Results**—An elderly Japanese woman with documented QT prolongation and torsade de pointes during treatment with the prokinetic drug cisapride underwent mutational analysis of LQTS-related genes. A novel missense mutation (L1825P) was identified within the C-terminus region of the cardiac Na+ channel (SCN5A). The L1825P channel heterologously expressed in tsA-201 cells showed Na+ current with slow decay and a prominent tetrodotoxin-sensitive nonactivating component, similar to the gain-of-function phenotype most commonly observed for SCN5A-associated congenital LQTS (LQT3). In addition, L1825P exhibited loss of function Na+ channel features characteristic of Brugada syndrome. Peak Na+ current density observed in cells expressing L1825P was significantly diminished, and the voltage dependence of activation and inactivation was shifted toward more positive and negative potentials, respectively.

**Conclusions**—This study demonstrates that subclinical mutations in the LQTS-related gene SCN5A may predispose certain individuals to drug-induced cardiac arrhythmias. (Circulation. 2002;106:1269-1274.)

**Key Words:** long-QT syndrome ▪ drugs ▪ genetics ▪ torsade de pointes ▪ ion channels

Congenital long-QT syndrome (LQTS) is a rare inherited disorder of cardiac repolarization that predisposes affected individuals to life-threatening arrhythmias. The molecular basis of LQTS is the prolongation of action potential duration attributable to defects in several ion channel genes encoding delayed rectifier K+ currents (I_K) or Na+ current (I_Na)1. The cardiac Na+ channel α subunit gene SCN5A is responsible for a subgroup of LQTS (LQT3).2,3 idiopathic ventricular fibrillation (IVF), or Brugada syndrome (BrS).4,5 The cellular mechanism for QT prolongation in most LQT3 is attributed to defects in Na+ channel function, the heterologously expressed Na+ channel current with slow decay and a prominent tetrodotoxin-insensitive nonactivating component, similar to the gain-of-function phenotype most commonly observed for SCN5A-associated congenital LQTS (LQT3). In addition, L1825P exhibited loss of function Na+ channel features characteristic of Brugada syndrome. Peak Na+ current density observed in cells expressing L1825P was significantly diminished, and the voltage dependence of activation and inactivation was shifted toward more positive and negative potentials, respectively.

**Conclusions**—This study demonstrates that subclinical mutations in the LQTS-related gene SCN5A may predispose certain individuals to drug-induced cardiac arrhythmias. (Circulation. 2002;106:1269-1274.)

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subclinical mutations or polymorphisms in SCN5A may predispose to life-threatening drug-induced arrhythmias.

**Methods**

**Patient**

A 70-year-old woman was admitted to the hospital because of recurrent syncope. She had been treated with acebutolol (200 mg/d) and pirmenol (200 mg/d) for hypertension and frequent premature ventricular contractions, respectively. Her ECG while taking these medications exhibited complete right bundle-branch block (CRBBB) and a normal QT interval (QTc, 435 ms, Figure 1A). Soon after the addition of cisapride (5 mg/d) because of bowel transit dysfunction, she experienced general malaise and syncope. ECG telemetry on admission showed severe bradycardia (junctional rhythm, heart rate ∼30 bpm) with QT prolongation (QTc, 480 ms) and repetitive TdP (Figure 1B). Time course of QT interval. Emergency pacing was performed (pacing rate, 80 bpm) at the first day. Marked QT prolongation was observed (QTc, 731 ms). It was shortened the next day after withdrawal of drugs (QTc, 594 ms). QT interval was normalized at the sixth day (QTc, 417 ms). D, ECG recordings on V2 lead during treadmill exercise test before exercise and at the maximum exercise are shown. Heart rate was increased from 66 to 93 bpm, and the QTc was prolonged from 408 to 457 ms.

**Figure 1.** Electrocardiographic findings of the patient. A, ECG recording obtained from the proband during treatment with acebutolol and pirmenol before prescription of cisapride. Normal sinus rhythm (heart rate, 73 bpm) with complete right bundle-branch block was evident, and the QT interval was within normal limits (QTc, 435 ms). B, ECG telemetry on admission showed severe bradycardia after prescription of cisapride (junctional rhythm, heart rate ∼30 bpm) with QT prolongation (QTc, 480 ms) and repetitive TdP. C, Time course of QT interval. Emergency pacing was performed (pacing rate, 80 bpm) at the first day. Marked QT prolongation was observed (QTc, 731 ms). It was shortened the next day after withdrawal of drugs (QTc, 594 ms). QT interval was normalized at the sixth day (QTc, 417 ms). D, ECG recordings on V2 lead during treadmill exercise test before exercise and at the maximum exercise are shown. Heart rate was increased from 66 to 93 bpm, and the QTc was prolonged from 408 to 457 ms.
Molecular Genetics

Genomic DNA was extracted from peripheral blood leukocytes by a standard method. All exons of SCN5A were amplified by polymerase chain reaction (PCR) using primers designed by Wang et al.\(^3\) and analyzed by single-strand conformational polymorphism (SSCP), as previously reported.\(^3\) Genetic screening of KCNQ1, HERG, KCNE1, and KCNE2 was carried out as previously described.\(^11\),\(^14\) The PCR product showing an aberrant conformer was subcloned into pGEMTeasy (Promega), and multiple independent clones were sequenced using an ABI Prism 310 genetic analyzer (Applied Biosystems).

Site-Directed Mutagenesis and Electrophysiology

Wild-type (WT) human heart sodium channel α subunit (hH1) cDNA was subcloned into the pRcCMV plasmid (Invitrogen). Site-directed mutagenesis of hH1 was performed by an overlap-extension PCR strategy, as described.\(^15\) A 183-bp HincII/SacII fragment (No. 5290-5473 of hH1) of the mutant PCR fragment was subcloned back into the pRcCMV-WT plasmid to generate a mutant plasmid pRcCMV-L1825P. Correct assembly of the mutant was verified by restriction analysis, and the mutated regions generated by PCR were sequenced completely to identify clones without polymerase errors. The human cell line tsA-201 was transiently transfected with either pRcCMV-WT or pRcCMV-L1825P using standard calcium phosphate method in combination with a bicistronic plasmid pCD8-IRES-hH1 with Dynabeads (Dynal).

Na’ currents were recorded 24 to 72 hours after transfection using the whole-cell patch-clamp technique and analyzed, as we described elsewhere.\(^16\) The holding potential was −120 mV unless otherwise stated, and details of each pulse protocol are given schematically in the Figures and explained in the Results section. In some experiments, cells were superfused with bath solution containing either cisapride (0.01% in DMSO), pirmenol, tetrodotoxin, or mexiletine to determine their pharmacological effects. Functional expression studies were performed on multiple independent recombinants. Results are presented as mean±SEM, and statistical comparisons were made using the unpaired Student’s t test. Statistical significance was assumed for P<0.05. Cisapride and pirmenol were obtained from Welfide Co and Dainippon Pharmaceutical Inc, respectively.

Results

Molecular Genetics

Initial SSCP analysis was performed to screen for genetic variations in the LQTS-related K’ channel genes KCNQ1, HERG, KCNE1, and KCNE2. Because aberrant conformers were not detected in these genes, we screened SCN5A. An aberrant SSCP conformer was identified in exon 28 of the proband. DNA sequencing confirmed a T to C transition leading to amino acid substitution of proline for leucine1825 (L1825P; Figure 2B) located within the C-terminal region of hH1 (Figure 2C). The amino acid residue corresponding to L1825 of hH1 was highly conserved among different Na’ channel isoforms (Figure 2D). This sequence variation was not observed in 200 normal chromosomes, consistent with a disease-related mutation. Heterozygous state of the proband and the WT sequence of the proband’s sister were confirmed by direct sequencing of the genomic DNA (data not shown).

Functional Analysis of the L1825P Mutation

Because the basal QT-interval of the patient was normal, it was expected that functional defects exhibited by the L1825P mutant channel, if any, might be minor when heterologously expressed in mammalian cells. Contrary to this assumption, the recombinant L1825P channel showed profound biophysical abnormalities. Figure 3A illustrates representative whole-cell current traces from cells expressing WT or L1825P Na’ channels in the presence of coexpressed hβ1, Current density of L1825P channel measured at test pulse potential of −20 mV was approximately one third of WT (WT, 459±99 pA/pF, n=13; L1825P, 136±21 pA/pF, n=12; P<0.001). L1825P showed a robust persistent late current and slower current decay. The amplitude of the persistent late current after 200 ms of depolarization at −20 mV was ∼8-fold larger in L1825P (WT, 0.3±0.05% of the peak current, n=15; 2.56±0.27%, n=22; P<0.001), and it was almost completely abolished by either 30 μmol/L tetrodotoxin (Figure 3B) or 10 μmol/L mexiletine but was not affected by higher temperature at 34°C (data not shown). Macroscopic current decay fit with a biexponential function revealed that the fraction of slowly inactivating component (A_s) was significantly larger and the time constants for both fast and slow components (τ_s, τ_p) were significantly larger in L1825P relative to WT at all
test pulse voltages between −40 and 30 mV (Figure 3C). These data suggest that the onset of inactivation was significantly slowed and was incomplete in L1825P.

The voltage dependence of steady-state inactivation of L1825P showed a significant hyperpolarizing shift (V1/2: WT, −91.0±1.3 mV; L1825P, −102.0±1.1 mV; n=13; L1825P, −102.0±1.1 mV; n=16; P<0.001) (Figure 4A). Conversely, voltage dependence of activation of L1825P significantly shifted toward depolarizing direction (V1/2: WT, −47.2±1.1 mV; L1825P, −38.3±0.74 mV; P<0.001). Slope factors for both inactivating and activating were significantly larger in L1825P (kact: WT, 6.93±0.23 mV; L1825P, 8.78±0.23 mV, P<0.001; kact: WT, −6.08±0.26 mV; L1825P, −8.48±0.16 mV; P<0.001) (Figure 4A). Large negative shift of steady-state inactivation and positive shift of activation do not alter the point at which 2 curves cross; however, they do result in larger window current than WT, probably attributable to noninactivating Na+ channel even at higher prepulse potentials (Figure 4B). Recovery from inactivation was assessed by a standard double-pulse protocol using a recovery potential of −120 mV. Although the time constants of either fast or slow recovery components were comparable between WT (n=12) and L1825P (n=16) (τf: WT, 10.8±2.0 ms; L1825P, 9.5±0.4 ms; τf: WT, 154±28 ms; L1825P, 181±27 ms), the fraction of the slow component (A5) was significantly larger in L1825P (WT, 0.16±0.02; L1825P, 0.25±0.02; P<0.01), indicating that the recovery from inactivation was significantly slower in L1825P (Figure 4C). The severe abnormalities in activation and fast inactivation gating properties exhibited by L1825P will potentially result in greater reduction in Na+ channel availability during excitation.

In addition to the dysfunction of activation and fast inactivation, some mutant Na+ channels associated with IVF/BrS show defects in inactivation kinetics intermediate between fast and slow inactivation, referred to as IIM, which is now recognized as an important biophysical feature underlying certain Na+ channelopathies.17 We analyzed the onset of slow inactivation by prolonging the prepulses to from 1 ms to 10 s followed by a brief repolarization to allow channels to recover from fast inactivation before the test pulse. Distinct from the BrS mutation T1620 mol/L18 or the LQT3/BrS mutant channel 1795insD19 that have enhanced IIM, the time course of the onset of slow inactivation of L1825P was virtually identical to WT (Figure 4D).

Although L1825P channel shows slower open-state inactivation, a population of Na+ channels enters an inactivated state without channel opening by a mechanism called closed-state inactivation. Closed-state inactivation greatly affects the availability of the channels at voltages near the resting membrane potentials, thereby controlling the Na+ current amplitude of the action potential. The time course of the development of closed-state inactivation at −100 mV was significantly facilitated in L1825P (Figure 4E). These data suggest that a substantial fraction of L1825P channels are inactivated at voltages near the resting potential.

To test whether the IKr blocker cisapride has direct effects on Na+ channels, 1 μmol/L cisapride, a sufficient concentration to block If,20 was applied to the bath solution. However, cisapride did not change the peak Na+ current in either WT or L1825P channels (% control; WT, 99.8±3.6%, n=6; L1825P, 88.8±4.3%, n=8; NS). Cisapride failed to change the kinetics or the amplitude of the persistent Na+ current in either WT or L1825P, confirming that cisapride-induced QT prolongation in the proband was mediated through mechanisms other than direct effects on cardiac Na+ channels. We also examined the effect of the Na+ channel blocker pirmenol, which the proband had been actively taking by the time she developed TdP. However, 10 μmol/L pirmenol did not affect the persistent late current of L1825P, whereas it
blocked the peak Na⁺ current of L1825P to the extent comparable to WT (% control; WT, 95.7±4.0%, n=5; L1825P, 86.4±3.7%, n=4, NS). Therefore, it is unlikely that pirmenol had been reducing persistent Na⁺ current of L1825P, thereby protecting against QT prolongation before cisapride exposure.

Discussion

Drug-induced LQTS is a prevalent life-threatening disorder with uncertain etiologies but shares substantial clinical features with congenital LQTS. It has been inferred that a subset of individuals with normal or borderline QT-interval may carry subclinical mutations in LQTS disease genes and are susceptible to life-threatening arrhythmias on drug exposure. In fact, several lines of evidence have suggested genetic variations of LQTS-related K⁺ channel genes. Our study suggests that Na⁺ channel mutations can predispose apparently stable patients to life-threatening arrhythmias when treated with agents that inhibit K⁺ channels.

Rodent et al. hypothesized repolarization reserve as a potential mechanism underlying susceptibility to drug-induced LQTS. The cardiac action potential is orchestrated by a fine balance between inward and outward currents expressed in myocardial cells. The action potential duration is prolonged by either an increase of inward currents or a decrease of outward currents. Because the outward currents consist of multiple distinct K⁺ currents, such as I₆, I₇, or I₉, K⁺ channel dysfunction attributable to mutations or polymorphisms could be potentially compensated by other K⁺ currents, and thereby the repolarization is tolerated (repolarization reserve). To extrapolate this hypothesis, it is assumed that repolarization reserve allows the dysfunction of the L1825P mutation to be tolerated until the time of drug exposure. However, administration of cisapride blocked I₆ and exhausted the repolarization reserve, leading to manifest the action potential prolongation and TdP. There are several lines of evidence supporting the existence of functional interplay between Na⁺ and outward K⁺ currents in the in vivo myocardium. Using a canine perfused ventricular wedge model, Shimizu et al. have shown that mexiletine reduced transmural dispersion of repolarization and prevented TdP in the LQT2 model as well as in LQT3. Moreover, K⁺ channel opener nicorandil prevents TdP in congenital or acquired models of LQT1, LQT2, and LQT3. The functional association between gain of function of I₆ and loss of function of I₉ attributable to cisapride may be responsible for the manifestation of drug-induced QT prolongation in the present case.

Moreover, QT-prolonging drugs usually require multiple risk factors, such as hypokalemia, female sex, or slow heart rate to manifest life-threatening arrhythmias. In the present case, bradycardia, presumably induced by acebutolol, was the additional risk factor to trigger QT prolongation and TdP. Another explanation is that the contribution to persistent Na⁺ current of L1825P to the cardiac action potential duration may be relatively small, because the persistent current is offset by the concomitant loss of function phenotype (Figures 4A, 4D, and 4E). Alternatively, biophysical dysfunctions of the L1825P allele could be functionally compensated by the WT allele. Furthermore, manifestation of LQTS is variable and seems to be determined in genotype-specific, mutation-specific, or individual-specific manners, and up to 75% of the
gene carriers show normal QT interval. It is speculated that the present case could be a congenital LQTS with an SCN5A mutation that exhibits reduced penetrance. Moreover, contribution of other genes, such as P450 3A4, a major metabolizing enzyme of cisapride, remains to be examined.

Mutations in SCN5A result in multiple arrhythmic syndromes, including LQT3, IVF/BrS, an inherited cardiac conduction defect, and sudden infant death syndrome, constituting a spectrum of disease entities termed cardiac Na+ channelopathies. Heterologously expressed L1825P and 1795insD channels exhibit biophysical properties strikingly similar to an SCN5A mutation 1795insD found in an unusual LQT3 family, in which affected individuals exhibited rate-dependent QT prolongation and ST elevation. The L1825P and 1795insD mutations, both located at the C-terminal of the Na+ channel, share the following biophysical properties: (1) prominent prolongation and ST elevation. The L1825P and 1795insD mutations, both located at the C-terminal of the Na+ channel, share the following biophysical properties: (1) prominent persistent late Na+ current; (2) negative shift of steady-state inactivation; and (3) decreased current density. These results suggest that LQT3 and IVF/BrS are closely related Na+ channelopathies with overlapping phenotypes and that L1825P is another example of a mutation that can explain this clinical overlap. Nonetheless, clinical manifestations of these 2 mutations are not identical. Exercise-induced ST elevation observed in 1795insD was not evident in L1825P despite the fact that both channels exhibited BrS-like properties. This phenotypic difference in ST elevation may be attributed to the difference in the kinetics of INa, the physiological mechanism for the rate-dependent ST elevation in 1795insD, but it was not evident in L1825P.

In summary, we propose that subclinical mutations in the LQTS-related gene SCN5A may predispose the subset of individuals to life-threatening arrhythmias during drug therapy.

Acknowledgments

This study was supported in part by research grants 13670685 (to Dr Makita) and 12670663 (to Dr Horie) from the Ministry of Education, Culture, Sports, Science and Technology, Japan, the research grant for cardiovascular diseases (13A-1) (Drs Makita and Horie) from the Ministry of Health, Labour and Welfare, Japan, and Takeda Memorial Foundation (to Dr Horie). We thank A. Aida and M. Kasai for technical assistance for the experiments and Dr A.L. George for critical reading of the manuscript.

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Circulation. 2002;106:1269-1274; originally published online August 12, 2002;
doi: 10.1161/01.CIR.0000027139.42087.B6
Circulation is published by the American Heart Association, 7272 Greenville Avenue, Dallas, TX 75231
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Print ISSN: 0009-7322. Online ISSN: 1524-4539

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World Wide Web at:
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