Table 1. Clinical backgrounds of the exercise and control groups

	Exercise group ($n=21$)	Control group ($n=17$)	p
Men/Women	10/11	11/6	0.290
Age (year)	61.9±8.6	64.5±5.9	0.293
Duration of diabetes (year)	9.5±8.1	10.8±7.4	0.52
Previous coronary artery diseases, *n* (%)	9 (42.9)	9 (52.9)	0.536
Current smoker, *n* (%)	4 (19.0)	2 (11.8)	0.536
Therapy for diabetes at baseline, *n* (%)			
Diet only	8 (38.1)	3 (17.7)	0.167
Insulin	3 (14.3)	3 (17.6)	0.778
Sulfonylurea or Glinide	6 (28.6)	7 (41.2)	0.415
Biguanide	5 (23.8)	7 (41.2)	0.252
Thiazolidindione	0 (0)	0 (0)	-
α-glucosidase inhibitor	4 (19.1)	6 (35.3)	0.258
Therapy for diabetes after 3 months, *n* (%)			
Diet only	12 (57.1)	3 (17.7)	0.013
Insulin	1 (4.8)	3 (17.7)	0.198
Sulfonylurea or Glinide	4 (19.1)	7 (41.2)	0.135
Biguanide	5 (23.8)	6 (35.3)	0.438
Thiazolidindione	0 (0)	0 (0)	-
α-glucosidase inhibitor	4 (19.1)	8 (47.1)	0.065
Other medications at baseline, *n* (%)			
β-blockers	5 (23.8)	7 (41.2)	0.252
ACE inhibitors/ARBs	9 (42.9)	3 (17.6)	0.096
Statins	7 (33.3)	6 (35.3)	0.899
Other medications after 3 months, *n* (%)			
β-blockers	4 (19.1)	7 (41.2)	0.134
ACE inhibitors/ARBs	11 (52.4)	3 (17.6)	0.027
Statins	7 (33.3)	8 (47.1)	0.389

Data are the means ± S.D. ACE, angiotensin II converting enzyme; ARB, angiotensin II type 1 receptor blocker

Table 2. Effects of exercise training on clinical and metabolic values

	Exercise group ($n=21$)		Control group ($n=17$)	
	Baseline	After 3 months	Baseline	After 3 months
BMI (kg/m^2)	25.7±3.2	25.3±3.4*	24.5±2.9	23.9±2.6
SBP (mmHg)	129.0±21.6	130.5±18.6	126.6±16.8	130.4±16.1
DBP (mmHg)	74.6±11.6	78.5±11.7	73.8±11.8	76.3±13.3
Peak $\dot{V}O_2$/kg (mL/kg/min)	22.4±3.2	24.4±3.8*	22.3±3.7	24.0±4.4
Basal Diameter (mm)	3.90±0.78	3.88±0.75	3.91±0.71	4.19±0.76
FMD (%)	7.3±4.7	10.9±6.2**	6.4±3.6	7.4±5.0
ND (%)	14.5±6.3	12.6±5.1	9.8±5.6	12.3±7.0
FPG (mmol/L)	7.7±2.0	8.1±2.4	8.2±1.6	7.5±1.7
HbA_{1c} (%)	8.5±1.8	7.0±1.3**	7.9±1.1	6.8±0.8**
SSPG (mmol/L)	11.1±5.3	9.7±4.2	14.1±3.4	9.7±4.6**
Total cholesterol (mmol/L)	5.28±0.95	4.84±0.74	5.11±1.45	4.46±0.09*
Triglyceride (mmol/L)	1.67±1.55	1.37±0.70	1.35±0.67	1.34±1.41
HDL cholesterol (mmol/L)	1.17±0.22	1.33±0.36**	1.23±0.26	1.35±0.28*
LDL cholesterol (mmol/L)	3.34±0.64	2.88±0.79**	3.26±1.25	2.50±0.74*
Leptin (pg/mL)	5.3±3.1	6.5±3.5	5.2±5.0	6.6±4.9*
Adiponectin (ng/mL)	6.1±3.3	8.0±4.3**	5.3±2.4	7.1±3.7**
high-sensitivity CRP (ng/mL)	1292.6±1843.4	1178.8±1680.5	841.6±738.0	814.2±1257.0

Data are the means ± S.D. *$p<0.05$, Baseline vs. after 3 months in each group. **$p<0.01$, Baseline vs. after 3 months in each group. BMI, body mass index; SBP, systolic blood pressure; DBP, diastolic blood pressure; FMD, flow-mediated endothelium-dependent vasodilatation; ND, nitroglycerin-induced vasodilatation; FPG, fasting plasma glucose; SSPG, steady state plasma glucose; CRP, C-reactive protein.

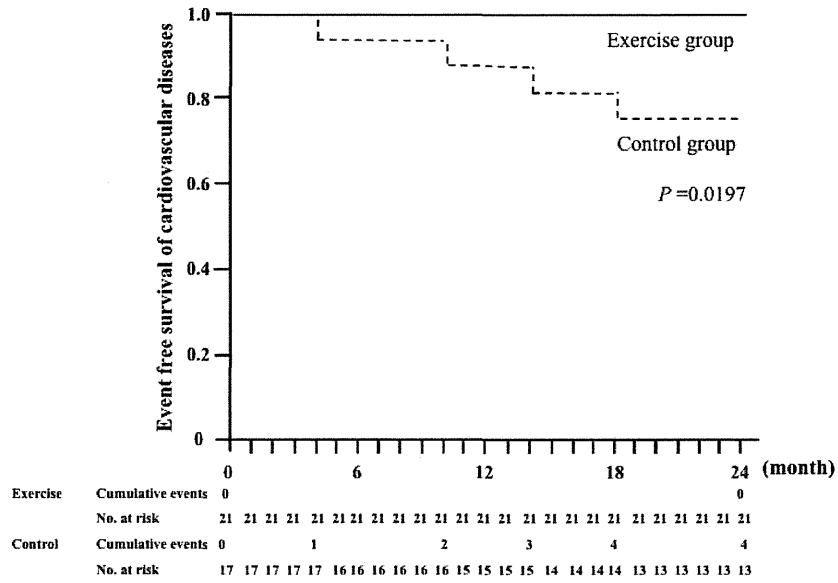

Fig. Kaplan-Meier analysis of the time to a cardiovascular event according to exercise intervention

The 38 patients were followed up until 24 months after randomization. In the control group, 1 patient developed angina pectoris and 3 patients developed cerebral infarction. On the other hand, patients in the exercise group had no cardiovascular events (p=0.0197).

decreased and peak $\dot{V}O_2$ and FMD were significantly increased only in the exercise group. SSPG was significantly decreased only in the control group. Serum leptin levels were increased only in the control group. There were no significant changes in high-sensitivity CRP levels in both groups.

Thirty-two of the 38 patients (exercise group: n=16, control group: n=16) were followed up until 24 months after randomization. We could not follow up 5 patients in the exercise group and 1 patient in the control group, because they went to other clinics after the 3-month intervention period. In the control group, 1 patient developed angina pectoris and 3 patients developed cerebral infarction. On the other hand, patients in the exercise group had no cardiovascular events (**Fig.**).

Discussion

The present study demonstrated that exercise intervention improved FMD, a surrogate marker of endothelial function, in patients with type 2 diabetes. Moreover, the 24-month follow-up study showed that the 3-month exercise intervention prevented new-onset cardiovascular events.

This study was a randomized controlled study of exercise treatment and was analyzed by intention-to-treat. Medications for diabetes, hypertension and dyslipidemia were provided to both groups comparably. Patients using insulin and sulfonylurea usage decreased and those with diet alone increased in the exercise group. These changes in medication might have affected the results of metabolic parameters.

Patients with type 2 diabetes have a greater incidence of cardiovascular diseases than non-diabetic patients[14], and they often have endothelial dysfunction[15, 16]. Vascular endothelium plays an important role in the control of vascular tone, and endothelial dysfunction is considered to be an early manifestation of the atherosclerotic process[17]. Several clinical studies have demonstrated that exercise intervention corrects endothelial dysfunction not only in healthy individuals[18] but also in patients with coronary artery disease[19]. A recent study has shown that exercise training improves the indices of glycemic control and endothelial dysfunction in patients with type 2 diabetes[20]; however, it is unclear whether the amelioration of endothelial dysfunction is independent of glycemic control, because HbA1c is reported to inversely correlate with FMD[21]. In our study, HbA1c was improved in both groups after the 3-month intervention period regardless of exercise training, and SSPG was not significantly improved by exercise intervention. These data suggest that alterations in HbA1c or SSPG levels may

not account for the improvement of FMD, implying that physical exercise has a beneficial impact on endothelial function beyond glycemic control and insulin sensitivity.

Moreover, our 24-month follow-up study showed that the 3-month exercise intervention prevented new-onset cardiovascular events. Few previous studies have investigated the effect of exercise intervention on long-term outcomes in terms of cardiovascular events in a randomized control trial. A previous report suggested that endothelial dysfunction precedes atherosclerosis and future cardiovascular events[22], and our study supports the relevance of short-term exercise intervention in the management of type 2 diabetes, albeit perhaps only for a certain period.

We also investigated the effect of physical exercise on adipocytokines: adiponectin and leptin. Adiponectin plays an important role in inducing insulin resistance and atherosclerosis[23], and several studies concerning the effect of physical exercise on serum adiponectin levels have yielded inconsistent findings[5, 24, 25]. Our study showed that serum adiponectin levels were increased in both groups. This result may imply that serum adiponectin is increased by the improvement of glycemic control, regardless of exercise intervention or weight reduction. An anti-diabetic agents, thiazolidinedione, has been reported to increase plasma adiponectin levels[26, 27], but no patients took thiazolidinediones in our study. Serum leptin levels are positively correlated with total body adiposity[28] and are reported to decrease with weight reduction[29], but it is controversial whether exercise training decreases serum leptin levels without reduction of body fat mass[24, 30]. In our study, serum leptin levels were not changed in the exercise group and increased in the control group, whereas body weight was decreased only in the exercise group. Patients in the control group might have much less lean body mass than those in the exercise group, but further investigation is needed to settle this issue.

Chronic inflammation is thought to present as an early sign of atherosclerosis[31]. Previous studies have demonstrated that regular physical exercise is associated with low serum CRP levels and exercise intervention reduces serum CRP levels[32]. In the present study, serum high-sensitivity CRP levels were not altered in either group. Since serum CRP levels are influenced by various pro-inflammatory and inflammatory factors and the number of participants in our study was limited, it is difficult to conclude whether exercise intervention affects serum CRP levels.

Our study has several limitations. First, since we had no information on physical activity during the follow-up period, we could not exclude the possibility that the extent of physical exercise affects the prevention of cardiovascular events. Second, the persistence of the increased FMD in the exercise group was unclear, and the amelioration of endothelial dysfunction could not be comfirmed as the major mechanism of the prevention of cardiovascular events in this study. Third, the improvement of endothelial function might have been affected by the exercise group having a higher prevalence of taking angiotensin-converting enzyme inhibitors or angiotensin II receptor blockers at baseline and after 3 months.

In conclusion, our study demonstrates that exercise intervention has beneficial effects on endothelial function in patients with type 2 diabetes. Our findings also suggest that exercise training exerts anti-atherosclerotic effects independently of glycemic control and insulin sensitivity. Finally, the favorable effects of a 3-month exercise intervention to reduce cardiovascular events may persist for up to 24 months, although further study is necessary for confirm this.

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Long QT syndrome with compound mutations is associated with a more severe phenotype: A Japanese multicenter study

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BACKGROUND: Long QT syndrome (LQTS) can be caused by mutations in the cardiac ion channels. Compound mutations occur at a frequency of 4% to 11% among genotyped LQTS cases.

OBJECTIVE: The purpose of this study was to determine the clinical characteristics and manner of onset of cardiac events in Japanese patients with LQTS and compound mutations.

METHODS: Six hundred three genotyped LQTS patients (310 probands and 293 family members) were divided into two groups: those with a single mutation (n = 568) and those with two mutations (n = 35). Clinical phenotypes were compared between the two groups.

RESULTS: Of 310 genotyped probands, 26 (8.4%) had two mutations in the same or different LQTS-related genes (compound mutations). Among the 603 LQTS patients, compound mutation carriers had significantly longer QTc interval (510 ± 56 ms vs 478 ± 53 ms, $P = .001$) and younger age at onset of cardiac events (10 ± 8 years vs 18 ± 16 years, $P = .043$) than did single mutation carriers. The incidence rate of cardiac events before age 40 years and use of beta-blocker therapy among compound mutation carriers also were different than in single mutation carriers. Subgroup analysis showed more cardiac events in LQTS type 1 (LQT1) and type 2 (LQT2) compound mutations compared to single LQT1 and LQT2 mutations.

CONCLUSION: Compound mutation carriers are associated with a more severe phenotype than single mutation carriers.

KEYWORDS Compound; Gene; Long QT syndrome; Mutation

ABBREVIATION QTS = long QT syndrome

(Heart Rhythm 2010;7:1411–1418)

Introduction

Congenital long QT syndrome (LQTS) is a heterogeneous disease characterized by prolonged ventricular repolarization and episodes of syncope and/or life-threatening cardiac arrhythmias, particularly polymorphic ventricular tachycardia.[1] Several disease-causing genes have been identified, including genes encoding cardiac ion channel-composing proteins, namely, *KCNQ1* (LQT1), *KCNH2* (LQT2), *SCN5A* (LQT3), *KCNE1* (LQT5), *KCNE2* (LQT6), *KCNJ2* (LQT7), and *CACNA1C* (LQT8), and genes encoding a family of versatile membrane adapters, namely, *ANK2* (LQT4), *CAV3* (LQT9), *SCN4B* (LQT10), *AKAPs* (LQT11), and *SNTA1* (LQT12).[2–5] Two modes of inheritance are involved in this syndrome, which exhibits both an autosomal dominant and an autosomal recessive pattern. The majority of LQTS cases are inherited in an autosomal dominant fashion. This pattern, which has been named as Romano-Ward syndrome,[6,7] can result from a single mutation in one

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of the LQTS candidate genes. On the other hand, Jervell and Lange-Nielsen syndrome, which is inherited in an autosomal recessive fashion, is very rare,[8] affecting less than 1% of LQTS cases. It is caused by homozygous or compound heterozygous mutations of *KCNQ1* or *KCNE1*.[9,10]

Genetic analysis sometimes reveals two or more mutations in LQTS patients with clinical phenotypes of Romano-Ward syndrome. These compound mutations were shown to be associated with an increased arrhythmic risk.[11,12] However, most previous studies were conducted in Caucasian patients, and few systematic studies have involved Asian cohorts. In the present study, we analyzed the clinical characteristics of LQTS patients who were registered in a Japanese multicenter study. Analysis of the more 600 genotyped patients revealed that LQTS patients with compound mutations not only were common in Japan (8.4% among probands) but were associated with longer QTc and earlier onset of cardiac events. In patients who initially are diagnosed as LQT1 or LQT2, additional mutations may be present if patients have a more severe phenotype than expected; therefore, conducting a survey for major LQTS-related genes is critically important.

Methods

Patients and data collection

Major candidate genes were analyzed in 612 consecutive and unrelated probands with a suspected clinical diagnosis of congenital LQTS, who were referred to four centers in Japan (Shiga University of Medical Science, Otsu; Kyoto University Graduate School of Medicine, Kyoto; Kanazawa University Graduate School of Medical Science, Kanazawa; and National Cardiovascular Center, Suita) between June 1996 and January 2009. If gene mutations in LQTS-related genes were identified, further genetic analysis was conducted among family members as extensively as possible. All patients in the cohort were Japanese.

Genetic analysis

Informed consent was obtained from all individuals or their guardians according to standards established by the local institutional review boards. Genotypic and DNA sequence analyses of *KCNQ1, KCNH2, SCN5A, KCNE1,* and *KCNE2* were performed as described previously.[13] In addition, *KCNJ2* (Andersen syndrome [LQT7][14,15]) was analyzed in patients who had not only QT prolongation but also the clinical phenotype of Andersen syndrome, for example, periodic paralysis or dysmorphic features. Other candidate genes (e.g., ankyrin-B [LQT4], *CACNA1C* [Timothy syndrome, LQT8]) were not analyzed because mutations in these genes are extremely rare. Denaturing high-performance liquid chromatography was performed as described previously.[16] Abnormal conformers were amplified by polymerase chain reaction and sequenced using an ABI PRISM310 DNA sequencer (Perkin-Elmer Applied Biosystems, Wellesley, MA, USA). "Splicing error" mutations were defined as those that occurred within three bases of the splicing sites. When mutations were detected, 200 Japanese control subjects were checked and single nucleotide polymorphisms were excluded from the study. If mutations of these genes were detected in the probands, their family members were also analyzed and genotype–phenotype correlations confirmed. Mutation-negative controls were defined as family members without mutations detected in each proband. Nonsynonymous as well as synonymous single nucleotide polymorphisms were excluded with the assistance of data from previous reports[17–19] and from the National Center for Biotechnology Information database.

Clinical characterization

Baseline clinical data were recorded for each patient and included the following: age at diagnosis, age at first cardiac event, sex, cardiac events, family history of sudden cardiac death or LQTS members, ECG measurements, and therapeutic regimens administered. Schwartz scores also were calculated.[20,21] In the analysis of triggers of arrhythmic events, triggers were divided into four categories: exercise/swimming, emotional stress/arousal stress, sleep/rest, and other conditions.

ECG parameters measured at baseline included RR, QT_{end}, QT_{peak}, and $T_{peak\text{-}end}$ ($QT_{end\text{-}peak}$) intervals. The latter is thought to reflect transmural dispersion of ventricular repolarization.[22] Measurements were the mean of at least three beats measured in lead V_5 from the 12-lead ECG during stable sinus rhythm and corrected by the Bazett formula.[23] QT_{end} was manually measured as the time interval between QRS onset (Q) and the point at which the isoelectric line intersected a tangential line drawn at the maximal downslope of the positive T wave or the maximal

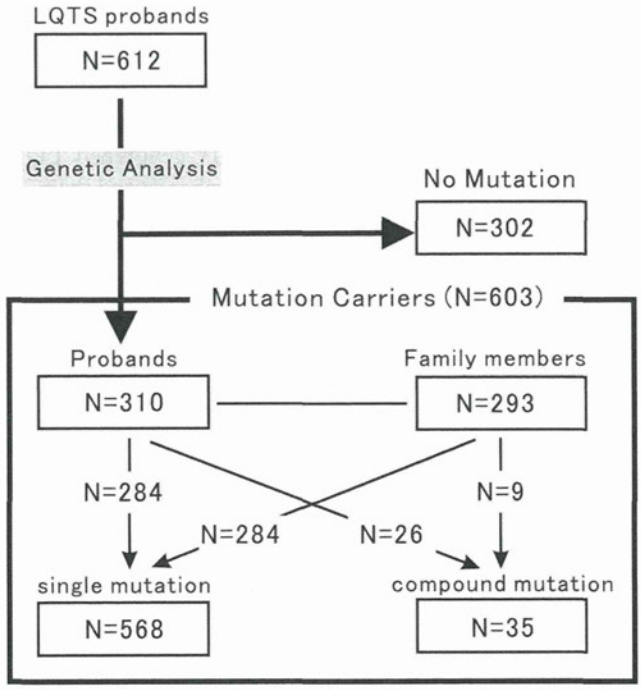

Figure 1 Schematic representation of the positive-mutation carriers in this study. LQTS = long QT syndrome.

Table 1 Overall data of patients with compound mutations

Research groups	Schwartz et al.	Westenkow et al.	Tester et al.	This study
Reported years	2003	2004	2005	2010
The corresponding number in the reference list	25	11	12	
Percentage of probands with compound mutations (probands with compound mutations/total probands) subtypes	4.6% (6/130)	5.2% (9/172*)	10.8% (29/269)	8.4% (26/310)
LQT1	7 (58%)	14 (35%)	30 (52%)	18 (35%)
LQT2	2 (17%)	10 (25%)	15 (26%)	17 (33%)
LQT3	3 (25%)	2 (5%)	13 (22%)	14 (27%)
LQT5-D85N	0 (0%)	10 (25%)	0 (0%)	0 (0%)
vs. single mutation carriers				
QTc interval	NA	prolonged	not significant	prolonged
Cardiac events	NA	frequent	not significant	not significant
Age of onset	NA	NA	younger onset	younger onset

*This table excluded probands with single nucleotide polymorphisms (SNP), NA = not available.

upslope of the negative T wave (QT_{end}). $QT_{end-peak}$ then was obtained by calculating as QT_{end} minus QT_{peak}.

Statistical analysis

All analyses were performed using the SPSS 16.0 statistical package (SPSS, Inc., Chicago, IL. USA). Data are expressed as mean ± SD. $P < 0.05$ was considered significant. Univariate comparison of parameters between groups was performed by an unpaired t-test. Differences in incidence between groups were analyzed by Chi-square test or Fisher exact probability test. The cumulative probability of a first cardiac event (syncope, torsades de pointes, ventricular fibrillation, cardiac arrest, or sudden death) occurring before age 40 years and before beta-blocker therapy or after beta-blocker therapy was determined by means of the life-table method of Kaplan-Meier, and results were compared using log rank test.[24]

Results

Genetic characteristics of mutations associated with single and compound mutations

Genetic analysis revealed gene mutations in 310 (51%) of 612 probands. The study enrolled 603 genotyped LQTS patients consisting of 310 genotyped probands and their 293 genotyped family members. A flowchart of the genetic diagnosis of the study population is shown in Figure 1.

Of the 310 genotyped probands, 26 (8.4%) had compound mutations. This rate is comparable to the rates in previous reports of Caucasian patients (Table 1). The 26 probands all had two mutations in the LQTS-related genes we examined. These 52 mutations in 26 probands consisted of 45 missense mutations, 4 frameshift mutations, 2 splice-site mutations, and 1 nonsense mutation (see Online Supplemental Data 1). The mutation types of the 284 single mutation carriers were 210 missense mutations, 34 frameshift mutations, 18 splicesite mutations, 12 deletions, 9 nonsense mutations, and 1 insertion mutation (see Online Supplemental Data 2). Therefore, the mutation types were similar between the two groups (Figure 2).

Among the 293 genotyped family members, there were 284 single mutation carriers and 9 compound mutation carriers. In total, 568 patients with a single mutation (284 probands and 284 family members) consisted of 256 with LQT1, 248 with LQT2, 62 with LQT3, and 2 with LQT5. Thirty-five compound mutation carriers (26 probands and 9 family members) consisted of 9 with LQT2 and LQT3, 7 with LQT1 and LQT2, 6 with LQT1 and LQT3, 4 with double LQT1, 3 with double LQT2 mutations, 2 with LQT1 and LQT7, 2 with LQT2 and LQT7, 1 with double LQT3, and 1 with LQT1 and LQT6.

Families associated with compound mutations

In the analysis of family members associated with compound mutations, 28 single heterozygous mutation carriers and 4 obligate single mutation carriers were identified from 9 families, and single mutation carriers had milder clinical phenotypes than compound mutation carriers (Figure 3). Only 2 (6%) of the 32 single mutation carriers had syncope but no torsades de pointes, an incidence lower than that in compound mutation carriers (54% [19/35] patients, $P < .001$). For single heterozygous mutation carriers in compound mutation families, average QTc interval was 442 ± 30 ms, which was longer than that of the 15 mutation-negative controls (408 ± 28 ms, $P = .001$) but significantly shorter than that of compound mutation carriers (510 ± 56 ms, $P < .001$).

Early onset of cardiac events and more severe QT prolongation was observed in patients with compound mutations

Table 2 compares the clinical characteristics of 35 LQTS patients with compound mutation and 568 LQTS patients with a single mutation. The female-to-male ratio was similar between the two groups. However, the incidence of family members associated with double-hit patients was significantly smaller than that with a single mutation (26% vs 50%, $P = .005$). In the ECG analysis of 496 patients with available information, corrected QT interval was significantly longer in compound mutation carriers than in single mutation carriers (510 ± 56 ms vs 478 ± 53 ms, respectively, $P = .001$), whereas other ECG findings, R-R interval, corrected QT_{peak}, corrected $QT_{peak-end}$, and rates of

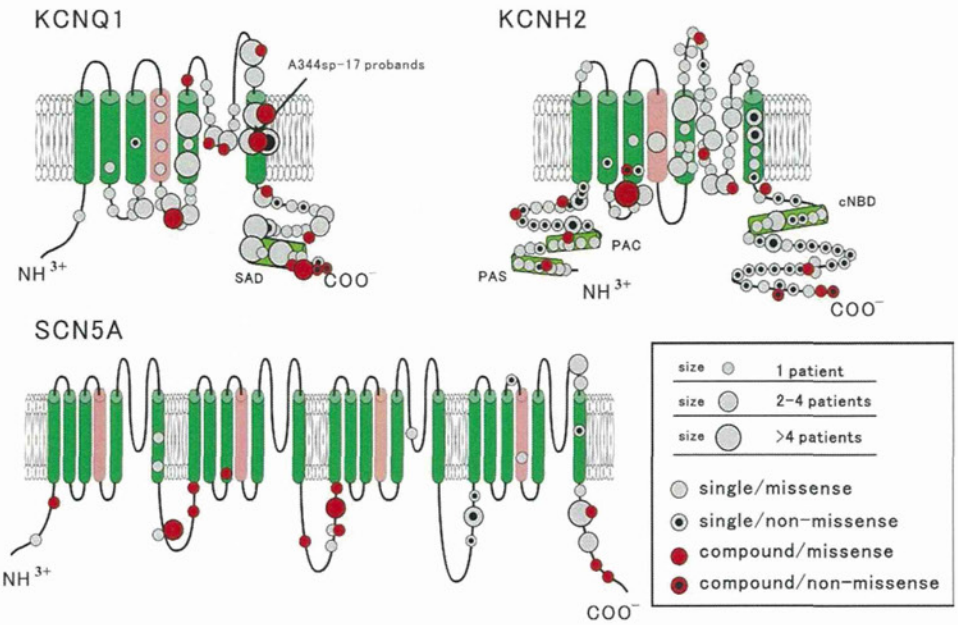

Figure 2 Conventional transmembrane topology of all mutations in the probands.

notched T wave and T-wave alternans were not different between the two groups. The frequency of patients with a normal QTc interval <440 ms was similar between the two groups, whereas the frequency of double-hit patients with QTc intervals >500 ms was significantly higher than in those with a single mutation (66% vs 26%, $P < .001$). Schwartz scores in the compound mutation group and the rate of patients with a score ≥4 were higher than those in the single mutation group (Schwartz score: 4.3 ± 2.1 vs 3.4 ± 1.9 points, $P = .017$; rates of Schwartz score ≥4 points: 70% vs 47%, $P = .026$). A significantly higher number of patients with compound mutations received beta-blocker therapy than did those with a single mutation (56% vs 33%, $P = .006$).

In the analysis of "all age groups," the frequency of cardiac events was similar between compound and single mutation groups, whereas age at first cardiac event was significantly lower in the compound mutation group (10 ± 8 years vs 18 ± 16 years, $P = .043$). For the occurrence of syncope or torsades de pointes before age 40 years, compound mutation carriers had significantly more events than did single mutation carriers (54% vs 37%, $P = .043$). The occurrence of cardiac arrest or ventricular fibrillation was similar between the two groups for patients before age 40 years. In 561 patients with available information on age at first cardiac events, Kaplan-Meier analysis showed that the cumulative rate of survival without a cardiac event before age 40 years and use of beta-blocker therapy differed significantly between compound and single mutation carriers ($P = .004$ by log rank test; Figure 4A) and between compound mutation carriers and each subgroup of single mutation carriers ($P = .004$ vs LQT1, $P = .018$ vs LQT2, $P = .001$ vs LQT3, by log rank test; Figure 4B). In the analysis of matched subtypes between single and compound mutation carriers, patients with additional mutations in an LQTS subtype had a significantly poorer prognosis than LQT1 alone ($P = .001$; Figure 5) and LQT2 alone ($P = .035$) but not LQT3 alone ($P = .06$).

Discussion

In this multicenter study, the major findings were as follows. (1) LQTS-associated compound mutations in the Japanese population were as common as previously reported in studies of Caucasian patient cohorts. (2) Patients with compound mutations displayed longer QTc and earlier onset of cardiac events. (3) Patients with compound mutations had more cardiac events before age 40 years and more beta-blocker therapy. (4) Subgroup analysis showed more cardiac events in LQT1 and LQT2 compound mutations compared to single LQT1 and LQT2 mutations.

Twenty-six probands (8.4% of genotyped LQTS) were found to have two variants in genes encoding ion channels *(KCNQ1, KCNH2, SCN5A, KCNE1, KCNE2,* or *KCNJ2)*. This incidence rate is in general agreement with other studies that reported a prevalence of compound or multiple mutations of 5% to 11% of genotyped LQTS (Table 1).[11,18,25]

Table 1 summarizes the genetic and clinical characteristics of patients enrolled in previous studies and compares them with the characteristics of patients enrolled in the present study. Sanguinetti and colleagues reported that patients with compound mutations not only had longer QT intervals than single mutation carriers but also had more frequent cardiac events.[11] However, Ackerman and colleagues demonstrated that, although compound mutation carriers were diagnosed at a younger age than single mutation carriers, they did not have significantly longer QT intervals.[12] The difference between these results might be explained by half of the 20 compound probands in the cohort of Sanguinetti et al possessing the common *KCNE1-*

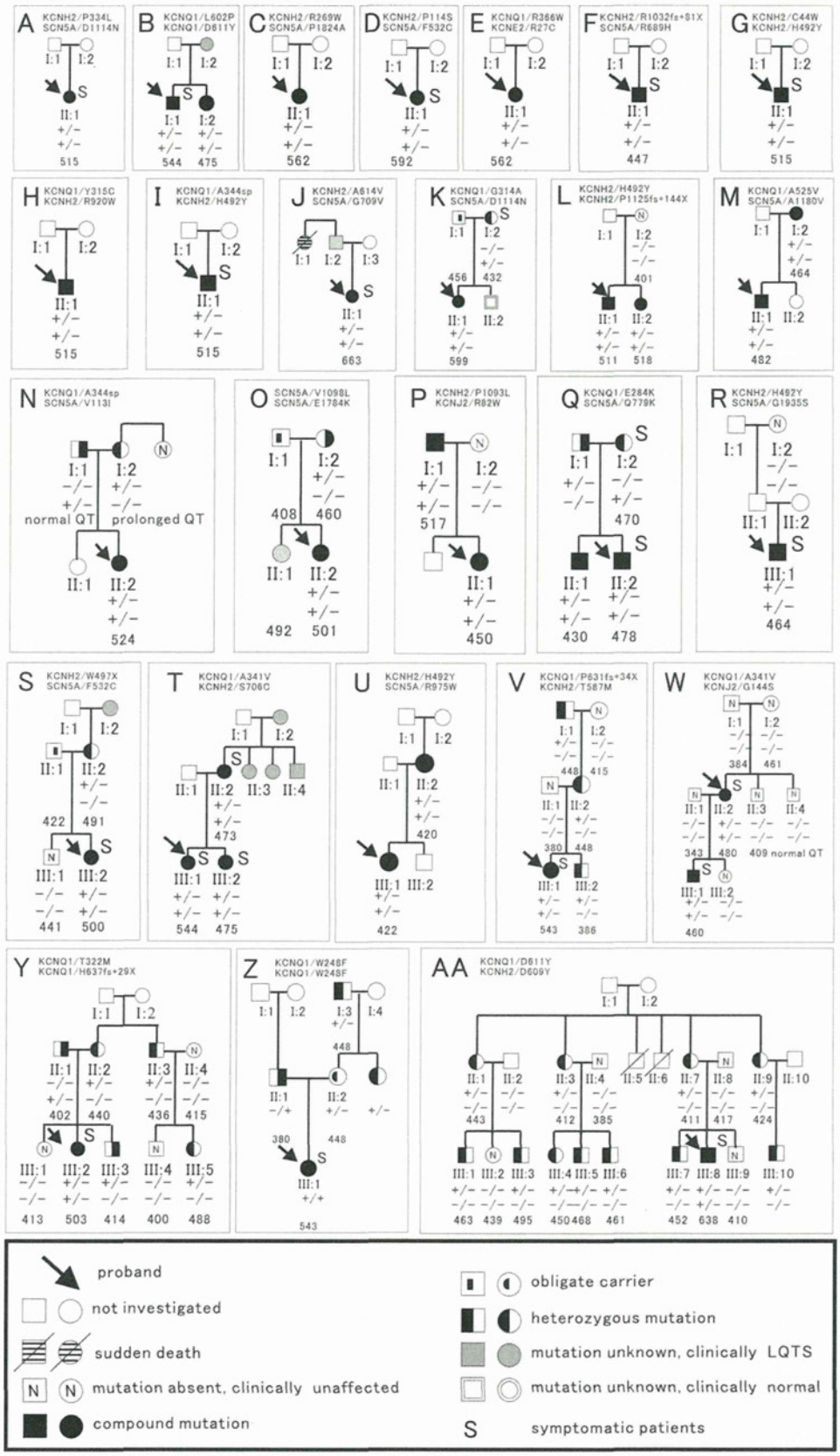

Figure 3 Pedigrees of the families associated with compound mutation probands.

Table 2 Clinical characteristics of LQTS patients with gene mutations

	Compound mutations (N=35)	Single mutations (N=568)	p value
Demographic			
Age at diagnosis (yrs)	19 ± 14 [15, 9–27]	28 ± 19 [22, 12–42]	0.001
Female gender	23 (66%)	330 (58%)	0.394
Proband	26 (74%)	284 (50%)	0.005
Family members	9 (26%)	284 (50%)	0.005
Cardiac events			
cardiac events in all age groups			
Age at first cardiac event (yrs)	10 ± 8 [11, 3.5–13.5]	18 ± 16 [12, 7–19]	0.043
syncope	19 (54%)	235 (41%)	0.161
TdP	10 (29%)	102 (18%)	0.136
cardiac arrest or VF	3 (9%)	44 (8%)	0.748
sudden death	0 (0%)	4 (1%)	1.000
cardiac events before 40 yrs			
syncope or TdP	19 (54%)	205 (37%)	0.043
cardiac arrest or VF	3 (9%)	37 (7%)	0.500
ECG measurements			
RR interval (ms)	866 ± 210	914 ± 174	0.252
corrected QT (ms)	510 ± 56	478 ± 53	0.001
corrected QT >500 ms (%)	23 (66%)	122 (26%)	<0.001
corrected QT <440 ms (%)	3 (9%)	91 (20%)	0.351
corrected QT peak (ms)	385 ± 70	384 ± 50	0.906
corrected QT peak-end (ms)	121 ± 73	95 ± 41	0.081
notched T wave	11 (31%)	200 (37%)	0.540
T-wave alternans	0 (0%)	30 (5%)	0.246
Diagnosis			
Schwartz score	4.2 ± 2.1	3.4 ± 1.9	0.017
Schwartz score ≧4	21 (70%)	219 (47%)	0.026
Therapy			
β-blocker	10 (56%)	175 (33%)	0.006
class Ib antiarrhythmic drugs	3 (9%)	53 (10%)	1.000
pacemaker	1 (3%)	15 (3%)	1.000
sympathectomy	1 (3%)	3 (1%)	0.218
defibrillator	1 (3%)	32 (6%)	0.712

TdP = torsades de pointes, VF = ventricular fibrillation, NS = not significant, corrected QT = QT interval corrected for heart rate with Bazett formula [A, B], A = median, B–C = first interquartile range–third interquartile range.

D85N polymorphism as the "second hit" (Table 1).[11,26] In all age groups of this study, the incidence of cardiac events, such as torsades de pointes or syncope, was similar between single and compound mutation carriers; however, the clinical phenotypes of those with compound mutations before 40 years of age were more serious than in those with a single mutation (Table 2). Thus, phenotypes with compound mutations appear to be more serious than single mutation carriers, regardless of race.

Beta-blocker therapy is first-line treatment for the prevention of cardiac events in LQTS. Beta-blockers have been shown to significantly reduce cardiac events in LQTS patients, especially LQT1 type.[27–29] However, patients with LQT2 or LQT3 have been reported to be less responsive to beta-blocker therapy[27,30] and may require additional therapy, such as pacemaker implantation for LQT2 or a Class Ib antiarrhythmic drug for LQT3. It may be recommended that patients with compound mutations receive additional individual therapy based on their LQTS subtype, for example, the combination of beta-blocker and Class Ib antiarrhythmic drugs for patients with LQT1 and LQT3. In patients who were first diagnosed as LQT1, Kobori et al[31] reported that additional mutations in different LQTS-related genes influenced phenotype severity and reduced beta-blocker effectiveness. Previous reports showed that approximately 20% of LQT1 patients were resistant to beta-blocker therapy. Additional or "latent" mutations may be present in these patients, and conducting a survey for major all LQTS-related genes, even after a possible mutation is identified, is critically important.

Family study analyses are of enormous importance because single mutation carriers in this study tended to have mild phenotypes. Most of the single mutation carriers in families of compound probands remained asymptomatic. However, double hits of these "latent" gene carriers could cause more serious phenotypes.[32,33] Jervell and Lange-Nielsen syndrome is a well-documented LQTS phenotype with an autosomal recessive pattern. The loss of function of I_{Ks} on both alleles generally causes not only more severe clinical phenotypes but also deafness.[9,10] In our study, two of three probands with double *KCNQ1* mutations had no deafness. We speculate that these mutations would functionally cause mild changes without complete loss of I_{Ks}. Westenskow et al[11] reported the molecular mechanism of

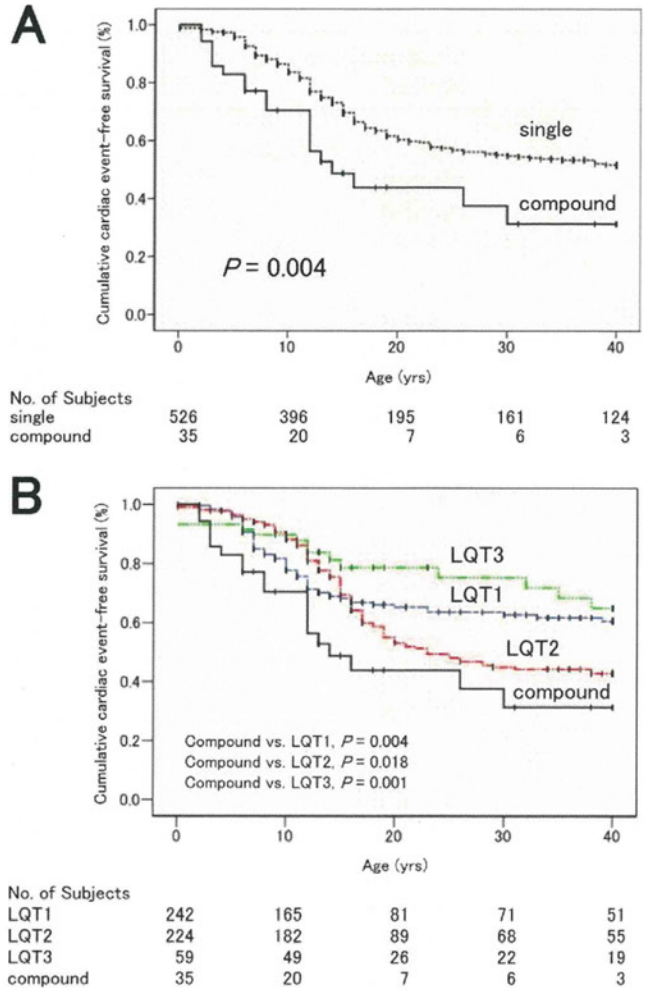

Figure 4 Kaplan-Meier cumulative probability of cardiac event-free survival from birth to age 40 years and before therapy. **A:** Comparison between patients with a single mutation and compound mutations. **B:** Comparison among patients with long QT syndrome type 1 (LQT1), type 2 (LQT2), type 3 (LQT3), and compound mutations.

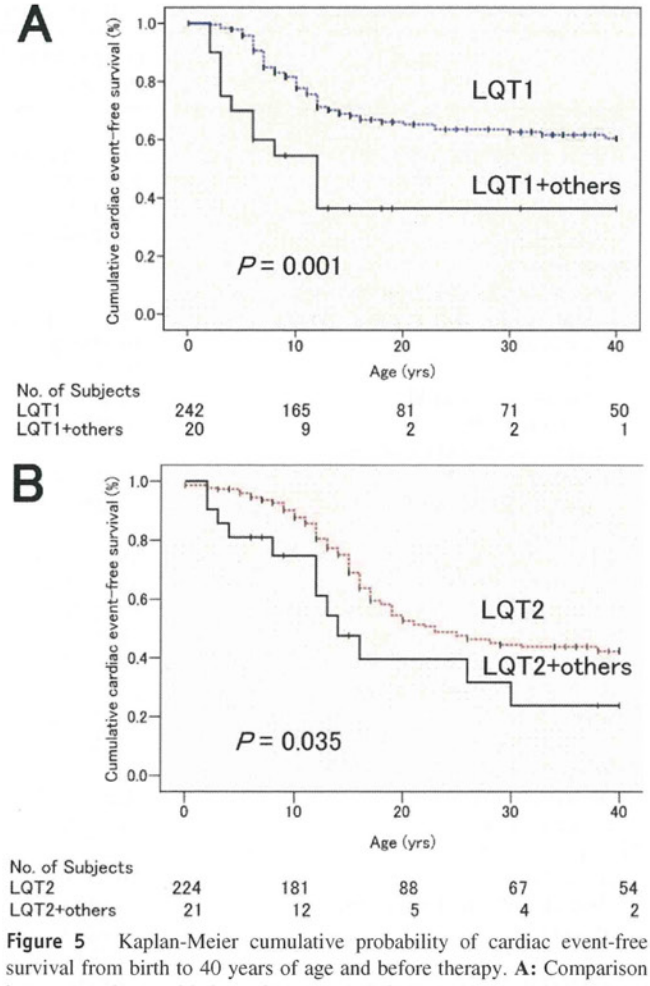

Figure 5 Kaplan-Meier cumulative probability of cardiac event-free survival from birth to 40 years of age and before therapy. **A:** Comparison between patients with long QT type 1 (LQT1_ subtype and compound mutation carriers with LQT1 plus other mutations. **B:** Comparison between patients with long QT syndrome type 2 (LQT2) and those with LQT2 plus other mutations.

increased risk through compound mutations using heterologous expressions in *Xenopus* oocytes. When wild-type and variant subunits were coexpressed in appropriate ratios to mimic the genotype of the probands with mutations, the reduction in current density was equivalent to the additive effects of the single mutations. Coexpression of two mutant subunits caused a significant but incomplete reduction. Thus, either compound mutation seems to be associated with mild functional damage. It is necessary to have "double hits" of these mild mutations in order to produce symptoms.

Study limitations

This study has several limitations. First, six major LQTS candidate genes were examined, but not for minor genes encoding a family of versatile membrane adapters. However, excluding these minor genes from our investigations would not have affected the overall study results, largely because the incidence of these minor gene mutations reportedly is $\leq 1\%$. Second, analysis of single mutation carriers in compound mutation families is dominated by their presence in only 35% (9/26) of families. Therefore, there might be a statistical bias due to a mutation-specific effect. Third, Kapa et al[19] reported the need for further studies on whether regions such as the interdomain linker of *SCN5A* could affect the clinical phenotypes of LQTS. In this study, we were able to distinguish mutations from these "genetic noises," especially in the *SCN5A* gene.

Acknowledgment

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Appendix

Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.hrthm.2010.06.013.

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KCNE2 modulation of Kv4.3 current and its potential role in fatal rhythm disorders

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BACKGROUND The transient outward current I_{to} is of critical importance in regulating myocardial electrical properties during the very early phase of the action potential. The auxiliary β subunit *KCNE2* recently was shown to modulate I_{to}.

OBJECTIVE The purpose of this study was to examine the contributions of *KCNE2* and its two published variants (M54T, I57T) to I_{to}.

METHODS The functional interaction between Kv4.3 (α subunit of human I_{to}) and wild-type (WT), M54T, and I57T *KCNE2*, expressed in a heterologous cell line, was studied using patch-clamp techniques.

RESULTS Compared to expression of Kv4.3 alone, co-expression of WT *KCNE2* significantly reduced peak current density, slowed the rate of inactivation, and caused a positive shift of voltage dependence of steady-state inactivation curve. These modifications rendered Kv4.3 channels more similar to native cardiac I_{to}. Both M54T and I57T variants significantly increased I_{to} current density and slowed the inactivation rate compared with WT *KCNE2*. Moreover, both variants accelerated the recovery from inactivation.

CONCLUSION The study results suggest that *KCNE2* plays a critical role in the normal function of the native I_{to} channel complex in human heart and that M54T and I57T variants lead to a gain of function of I_{to}, which may contribute to generating potential arrhythmogeneity and pathogenesis for inherited fatal rhythm disorders.

KEYWORDS Cardiac arrhythmia; M54T variation; I57T variation; *KCNE2*; Kv4.3; Sudden cardiac death

ABBREVIATIONS CHO = Chinese hamster ovary; **HERG** = human ether-a-go-go related gene; **WT** = wild type

(Heart Rhythm 2010;7:199–205)

Introduction

Classic voltage-gated K^+ channels consist of four pore-forming (α) subunits that contain the voltage sensor and ion selectivity filter[1,2] and accessory regulating (β) subunits.[3] *KCNE* family genes encode several kinds of β subunits consisting of single transmembrane-domain peptides that co-assemble with α subunits to modulate ion selectivity, gating kinetics, second messenger regulation, and the pharmacology of K^+ channels. Association of the *KCNE1* product minK with the α subunit Kv7.1 encoding *KCNQ1* forms the slowly activating delayed rectifier K^+ current I_{Ks} in the heart.[4,5] In contrast, association of the *KCNE2* product MiRP1 with the human ether-a-go-go related gene (HERG) forms the cardiac rapid delayed rectifier K^+ current I_{Kr}.[6]

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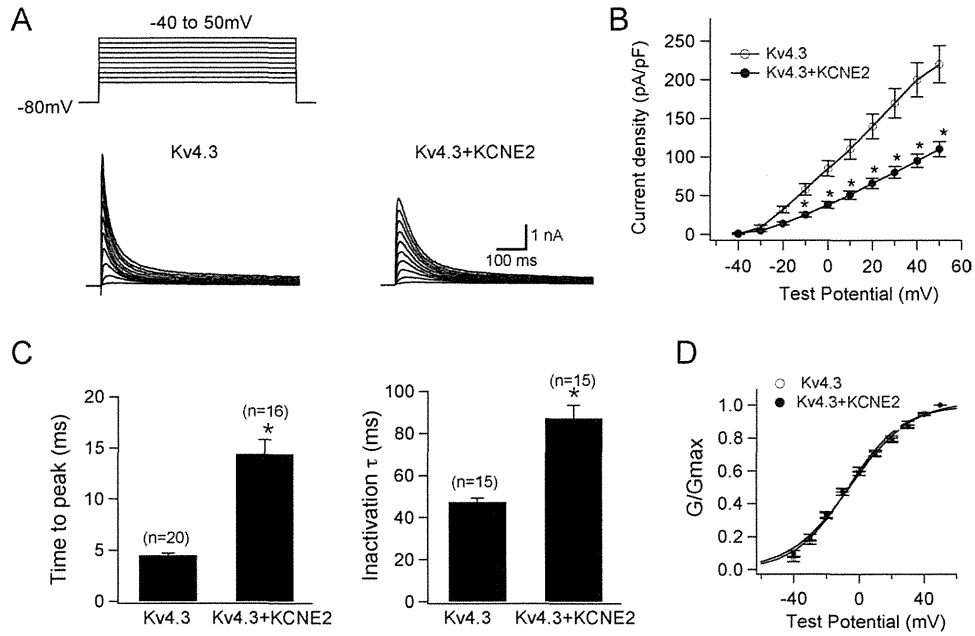

Figure 1 *KCNE2* co-expression with Kv4.3 produces smaller I_{to}-like currents with slower activation/inactivation kinetics. **A:** Representative current traces recorded from Chinese hamster ovary (CHO) cells expressing Kv4.3 **(left)** and Kv4.3 + *KCNE2* **(right).** As shown in the **inset** in panel A, depolarizing step pulses of 1-second duration were introduced from a holding potential of −80 mV to potentials ranging from −40 to +50 mV in 10-mV increments. **B:** Current–voltage relationship curve showing peak current densities in the absence and presence of co-transfected *KCNE2* (*P <.05 vs Kv4.3). **C:** Bar graphs showing the kinetic properties of reconstituted channel currents: time to peak of activation course **(left)** and inactivation time constants **(right)** measured using test potential to +20 mV (*P <.05 vs Kv4.3). Numbers in parentheses indicate numbers of experiments. **D:** Normalized conductance–voltage relationship for peak outward current of Kv4.3 and Kv4.3 + *KCNE2* channels.

Abbott et al reported that three *KCNE2* variants (Q9E, M54T, I57T) caused a loss of function in I_{Kr} and thereby were associated with the congenital or drug-induced long QT syndrome.[6,7] However, the reported QTc values in two index patients with M54T and I57T variants, both located in the transmembrane segment of MiRP1, were only mildly prolonged (390–500 ms and 470 ms).[6] We recently identified the same missense *KCNE2* variant, I57T, in which isoleucine was replaced by threonine at codon 57, in three unrelated probands showing a Brugada type 1 ECG. These findings are difficult to explain on the basis of a loss of function in I_{Kr}, thus leading us to explore other mechanisms.

Recent studies have demonstrated that interaction between α and β subunits (*KCNE*s) of voltage-gated K^+ channel is more promiscuous; for example, MiRP1 has been shown to interact with Kv7.1,[8–10] HCN1,[11] Kv2.1,[12] and Kv4.2.[13] These studies suggest that MiRP1 may also co-associate with Kv4.3 and contribute to the function of transient outward current (I_{to}) channels.[14] Indeed, a recent study reported that I_{to} is diminished in *kcne2* (–/–) mice.[15]

In the human heart, I_{to} currents are of critical importance in regulating myocardial electrical properties during the very early phase of the action potential and are thought to be central to the pathogenesis of Brugada-type ECG manifestations.[16] Antzelevitch et al demonstrated that a gain of function in I_{to} secondary to a mutation in *KCNE3* contributes to a Brugada phenotype by interacting with Kv4.3 and thereby promoting arrhythmogenicity.[14]

We hypothesized that mutations in *KCNE2* may have similar actions and characterize the functional consequences of interaction of wild-type (WT) and two mutant (I57T, M54T) MiRP1 with Kv4.3[17,18] using heterologous co-expression of these α and β subunits in Chinese hamster ovary (CHO) cells.

Methods

Heterologous expression of hKv4.3 and β subunits in CHO cells

Full-length cDNA fragment of *KCNE2* in pCR3.1 vector[10] was subcloned into pIRES-CD8 vector. This expression vector is useful in cell selection for later electrophysiologic study (see below). Two *KCNE2* mutants (M54T, I57T) were constructed using a Quick Change II XL site-directed mutagenesis kit according to the manufacturer's instructions (Stratagene, La Jolla, CA, USA) and subcloned to the same vector. Two *KCNE2* mutants were fully sequenced (ABI3100x, Applied Biosystems, Foster City, CA, USA) to ensure fidelity. Full-length cDNA encoding the short isoform of human Kv4.3 subcloned into the pIRES-GFP (Clontech, Palo Alto, CA, USA) expression vector was kindly provided by Dr. G.F. Tomaselli (Johns Hopkins University). Full-length cDNA encoding Kv channel-interacting protein (*KCNIP2*) subcloned into the PCMV-IRS expression vector was a kind gift from Dr. G.-N. Tseng (Virginia Commonwealth University). *KCND3* was transiently transfected into CHO cells together with *KCNE2* (or M54T or I57T) cDNA at equimolar ratio (*KCND3* 1.5 μg,

Table 1 Effects of *KCNE2* on Kv4.3 and Kv4.3 + KChIP2b

Parameter	Kv4.3	Kv4.3 *KCNE2*	Kv4.3 KChIP2b	Kv4.3 KChIP2b *KCNE2*
Current density at +20 mV (pA/pF)	142.0 ± 16.0 (n = 12)	66.0 ± 6.6* (n = 12)	191.5 ± 33.8 (n = 15)	77.8 ± 5.9† (n = 20)
Steady-state activation ($V_{0.5}$ in mV)	−6.5 ± 2.1 (n = 9)	−5.5 ± 1.7 (n = 11)	−7.5 ± 1.7 (n = 8)	−7.4 ± 1.4 (n = 8)
Steady-state inactivation ($V_{0.5}$ in mV)	−46.0 ± 1.3 (n = 10)	−40.8 ± 1.7* (n = 8)	−49.8 ± 1.4 (n = 7)	−44.5 ± 1.9† (n = 7)
τ of inactivation at +20 mV (τ_{inact} in ms)	47.3 ± 2.0 (n = 15)	87.2 ± 6.2* (n = 15)	47.5 ± 2.2 (n = 15)	66.6 ± 3.5† (n = 15)
Time to peak at +50 mV (TtP in ms)	4.5 ± 0.2 (n = 20)	14.4 ± 1.4* (n = 16)	4.1 ± 0.2 (n = 15)	6.1 ± 0.5† (n = 21)
τ of recovery from inactivation (ms)	419.6 ± 18.8 (n = 6)	485.6 ± 74.8 (n = 6)	89.2 ± 5.3 (n = 6)	60.2 ± 6.9† (n = 6)

*Significantly different from Kv4.3.
†Significantly different from Kv4.3 + KChIP2b.

KCNE2 1.5 μg) using Lipofectamine (Invitrogen Life Technologies, Carlsbad, CA, USA) according to the manufacturer's instructions. In one set of experiments, we also co-transfected equimolar levels of KChIP2b (*KCND3* 1.5 μg, *KCNE2* 1.5 μg, *KCNIP2* 1.5 μg). The transfected cells were then cultured in Ham's F-12 medium (Nakalai Tesque, Inc., Kyoto, Japan) supplemented with 10% fetal bovine serum (JRH Biosciences, Inc., Lenexa, KS, USA) and antibiotics (100 international units per milliliter penicillin and 100 μg/mL streptomycin) in a humidified incubator gassed with 5% CO_2 and 95% air at 37°C. The cultures were passaged every 4 to 5 days using a brief trypsin-EDTA treatment. The trypsin-EDTA treated cells were seeded onto glass coverslips in a Petri dish for later patch-clamp experiments.

Electrophysiologic recordings and data analysis

After 48 hours of transfection, a coverslip with cells was transferred to a 0.5-mL bath chamber at 25°C on an inverted microscope stage and perfused at 1 to 2 mL/min with extracellular solution containing the following (in mM): 140 NaCl, 5.4 KCl, 1.8 $CaCl_2$, 0.5 $MgCl_2$, 0.33 NaH_2PO_4, 5.5 glucose, and 5.0 HEPES; pH 7.4 with NaOH. Cells that emitted green fluorescence were chosen for patch-clamp experiments. If co-expressed with *KCNE2* (or its mutants), the cells were incubated with polystyrene microbeads precoated with anti-CD8 antibody (Dynabeads M450, Dynal, Norway) for 15 minutes. In these cases, cells that emitted green fluorescence and had attached beads were chosen for electrophysiologic recording. Whole-cell membrane currents were recorded with an EPC-8 patch-clamp amplifier (HEKA, Lambrecht, Germany), and data were low-pass filtered at 1 kHz, acquired at 5 kHz through an LIH-1600 analog-to-digital converter (HEKA), and stored on hard disk using PulseFit software (HEKA). Patch pipettes were fabricated from borosilicate glass capillaries (Narishige, Tokyo, Japan) using a horizontal microelectrode puller (P-97, Sutter Instruments, Novato, CA, USA) and the pipette tips fire-polished using a microforge. Patch pipettes had a resistance of 2.5 to 5.0 MΩ when filled with the following pipette solution (in mM): 70 potassium aspartate, 50 KCl, 10 KH_2PO_4, 1 $MgSO_4$, 3 Na_2-ATP (Sigma, Japan, Tokyo), 0.1 Li_2-GTP (Roche Diagnostics GmbH, Mannheim, Germany), 5 EGTA, and 5 HEPES (pH 7.2).

Cell membrane capacitance (C_m) was calculated from 5 mV-hyperpolarizing and depolarizing steps (20 ms) applied from a holding potential of −80 mV according to Equation 1[19]:

$$C_m = \tau_c I_0 / \Delta V_m (1 - I_\infty / I_0), \quad (1)$$

where τ_c = time constant of capacitance current relaxation, I_0 = initial peak current amplitude, ΔV_m = amplitude of voltage step, and I_∞ = steady-state current value. Whole-cell currents were elicited by a family of depolarizing voltage steps from a holding potential of −80 mV. The difference between the peak current amplitude and the current at the end of a test pulse (1-second duration) was referred to as the transient outward current. To control for cell size variability, currents were expressed as densities (pA/pF).

Steady-state activation curves were obtained by plotting the normalized conductance as a function of peak outward potentials. Steady-state inactivation curves were generated by a standard two-pulse protocol with a conditioning pulse of 500-ms duration and obtained by plotting the normalized current as a function of the test potential. Steady-state inactivation/activation kinetics were fitted to the following Boltzmann equation (Eq. 2):

$$Y(V) = 1/(1 + \exp[(V_{1/2} - V)/k]), \quad (2)$$

where Y = normalized conductance or current, $V_{1/2}$ = potential for half-maximal inactivation or activation, respectively, and k = slope factor.

Data relative to inactivation time constants, time to peak, and mean current levels were obtained by using current data recorded at +50 mV or +20 mV. Recovery from inactivation was assessed by a standard paired-pulse protocol: a 400-ms test pulse to +50 mV (P1) followed by a variable

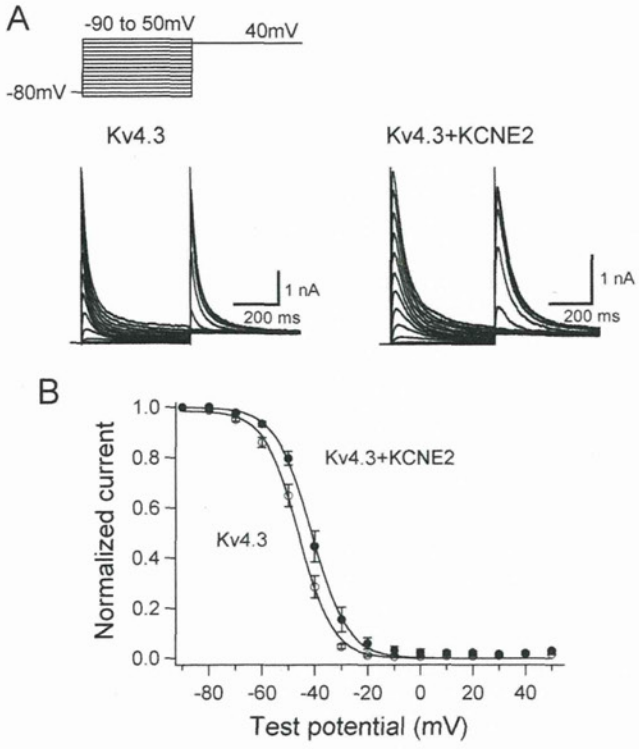

Figure 2 *KCNE2* co-expression with Kv4.3 causes a positive shift of voltage dependence of steady-state inactivation. **A:** Representative Kv4.3 and Kv4.3 + *KCNE2* current traces induced by 500-ms pulses (P1) from −90 to +50 mV applied from the holding potential −80 mV in 10-mV steps followed by a second pulse (P2) to +40 mV. **B:** Steady-state inactivation curves for Kv4.3 *(open circles)* and Kv4.3 + *KCNE2 (closed circles)* channels.

recovery interval at −80 mV and then a second test pulse to +50 mV (P2). Both the inactivation time constants and the time constant for recovery from inactivation were determined by fitting the data to a single exponential (Eq. 3):

$$I(t) \text{ (or P2/P1)} = A + B_{exp}(-t/\tau), \quad (3)$$

where I(t) = current amplitude at time t, A and B = constants, and τ = inactivation time constant or time constant for recovery from inactivation. For measurement of recovery from inactivation, the plot of P2/P1 instead of I(t) was used.

All data were given as mean ± SEM. Statistical comparisons between two groups were analyzed using Student's unpaired t-test. Comparisons among multiple groups were analyzed using analysis of variance followed by Dunnett test. $P < .05$ was considered significant.

Results

Effects of *KCNE2* on Kv4.3 currents and its gating kinetics

WT *KCNE2* initially was co-expressed with *KCND3*, the gene encoding Kv4.3, the α subunit of the I_{to} channel,[17,18] in CHO cells. Figure 1A shows representative whole-cell current traces recorded from cells transfected with *KCND3* and co-transfected with (right) or without (left) *KCNE2*. Cells expressing Kv4.3 channels alone showed rapidly activating and inactivating currents. Co-expression of *KCNE2* significantly reduced peak current densities as summarized in the current–voltage relationship curve shown in Figure 1B and slowed both activation and inactivation kinetics (Table 1). Figure 1C (left) shows mean time intervals from the onset of the pulse to maximum current (time to peak), whereas the right panel shows time constants of inactivation (at +20 mV) obtained using Equation 3. Thus, co-transfection of *KCNE2* significantly increased both the time to peak and the time constant.

In contrast, *KCNE2* did not affect the voltage dependence of steady-state activation as assessed by plotting the normalized conductance as a function of test potential (Figure 1D). Fitting to the Boltzmann equation (Eq. 2) yielded half-maximal activation potentials of −6.5 ± 2.1 mV for Kv4.3 alone (open circles) and −5.5 ± 1.7 mV for Kv4.3 + *KCNE2* channels (filled circles, P = NS; Table 1). These findings are consistent with those previously reported for studies using *Xenopus* oocytes, CHO cells, and HEK293 cells.[20,21]

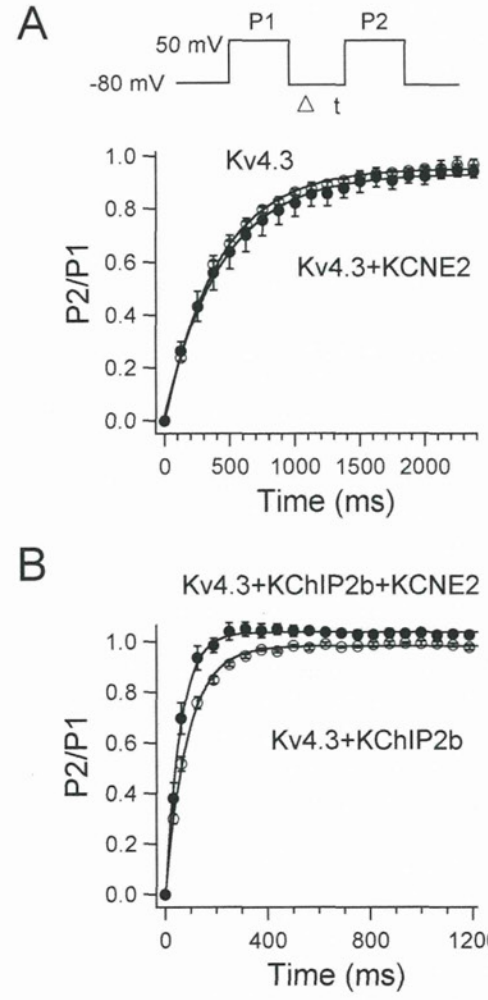

Figure 3 Effects of *KCNE2* co-expression on recovery from inactivation of Kv4.3 **(A)** and Kv4.3 + KChIP2b **(B)** currents. Recovery from inactivation was assessed by a two-pulse protocol **(A, inset):** a 400-ms test pulse to +50 mV (P1) followed by a variable interval at −80 mV, then by a second test pulse to +50 mV (P2). Data were fit to a single exponential.

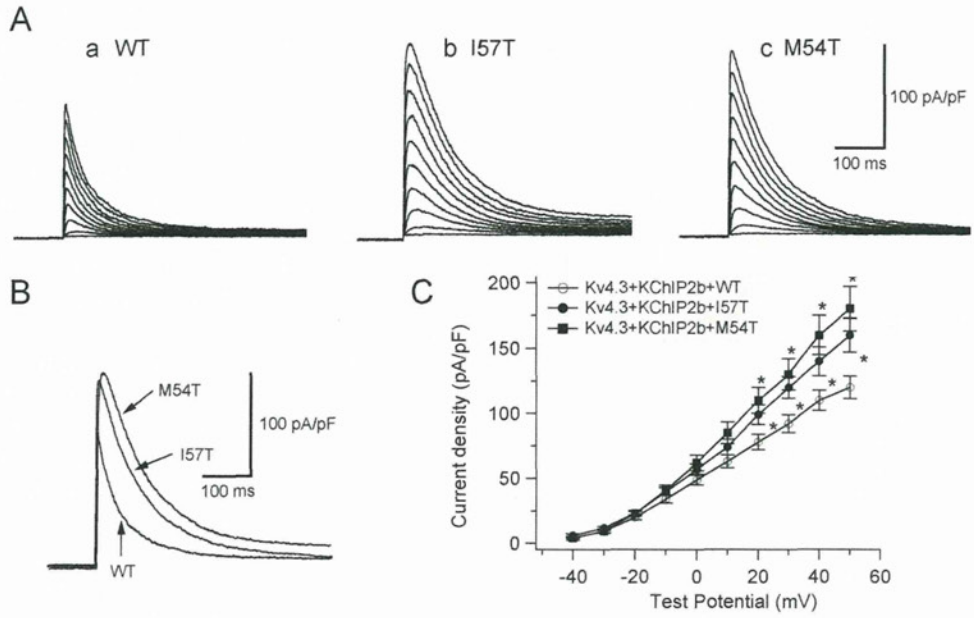

Figure 4 Two *KCNE2* transmembrane variants, I57T and M54T, increase the reconstituted Kv4.3 + KChIP2b channel current and slow its inactivation. **A:** Three sets of current traces elicited by depolarizing pulses for 500 ms from a holding potential of −80 mV to potentials ranging between −40 and +50 mV in 10-mV increments (same protocol as in experiments of Figure 1A). **B:** Superimposition of three original current traces recorded upon depolarization showing variant-related increase in peak outward current density. **C:** Current–voltage relationship curve showing average peak outward current densities (*P <.05 vs Kv4.3 + KChIP2b + WT). WT = wild type.

KCNE2 co-expression also caused a positive shift (approximately +5 mV) of voltage dependence of steady-state inactivation. Steady-state inactivation was assessed using a double-step pulse method (Figure 2A, inset). Peak outward currents recorded at various levels of prepulse (Figure 2A) were normalized by that measured after a 500-ms prepulse at –90 mV and are plotted as a function of prepulse test potentials (Figure 2B). Half-inactivation potentials of steady-state inactivation, determined by fitting data to the Boltzmann equation (Eq. 2), were −46.0 ± 1.3 mV for Kv4.3 (open circles) and −40.8 ± 1.7 mV for Kv4.3 + *KCNE2* (filled circles, P <.01), consistent with the observation of Tseng's group.[13]

A double-pulse protocol (Figure 3A, inset) was used to test the effect of *KCNE2* co-expression on the time course for recovery from inactivation. Figure 3A shows the time course of recovery of Kv4.3 alone (open circles) and Kv4.3 + *KCNE2* (filled circles). Mean time constants for recovery from inactivation were not significantly different, indicating that co-transfection of *KCNE2* did not affect the time course of recovery from inactivation.

Effects of *KCNE2* on Kv4.3 + KChIP2b current and its gating kinetics

For human native cardiac I_{to}, KChIP2 has been shown to serve as a principal β subunit.[22–25] Accordingly, in another series of experiments, we examined the effect of WT and mutant *KCNE2* on Kv4.3 + KChIP2b current. Consistent with previous reports, in the presence of KChIP2, Kv4.3 currents showed a significantly faster recovery from inactivation (Figure 3B and Table 1).[26,27] Co-expression of WT *KCNE2* produced similar changes on Kv4.3 + KChIP2b current as on Kv4.3 current (Table 1). Kv4.3 + KChIP2b current recovery from inactivation was further accelerated: average time constant was 89.2 ± 6.5 ms for Kv4.3 + KChIP2b alone (open circles) and 60.2 ± 8.4 ms for Kv4.3 + KChIP2b + *KCNE2* (filled circles, P <.05). In 16 of 21 cells transfected with *KCNE2*, we observed an "overshoot" phenomenon, which is commonly seen during recording of native I_{to} in human ventricular myocytes.[28]

KCNE2 variants increase Kv4.3 + KChIP2b current and alter its gating kinetics

The I57T variant was first identified in an asymptomatic middle-aged woman with very mild QT prolongation.[6] In addition to this variant, the authors reported another *KCNE2* variant of the transmembrane segment (M54T) that was associated with ventricular fibrillation during exercise in a middle-aged woman. This patient appeared to show a wide range of QTc interval (390–500 ms). Therefore, we tested the functional effects of these two transmembrane *KCNE2* variants on Kv4.3 + KChIP2b currents.

The three panels of Figure 4A show three sets of current traces elicited by depolarizing pulses from a holding potential of −80 mV in cells co-transfected with WT (a), I57T (b), or M54T (c) *KCNE2*. Neither variant caused a significant shift of half-maximal activation voltage: –7.4 ± 1.4 mV (n = 8) for co-expression of WT *KCNE2*, −6.1 ± 1.5 mV (n = 8) for I57T, and −6.6 ± 1.6 mV (n = 8) for M54T. Both variants significantly increased I_{to} density: 125.0 ± 10.6 pA/pF in WT *KCNE2* (n = 21), 178.1 ± 12.1 pA/pF with I57T (n = 9), and 184.3 ± 27.9 pA/pF with M54T (n = 9, Figure 4C).

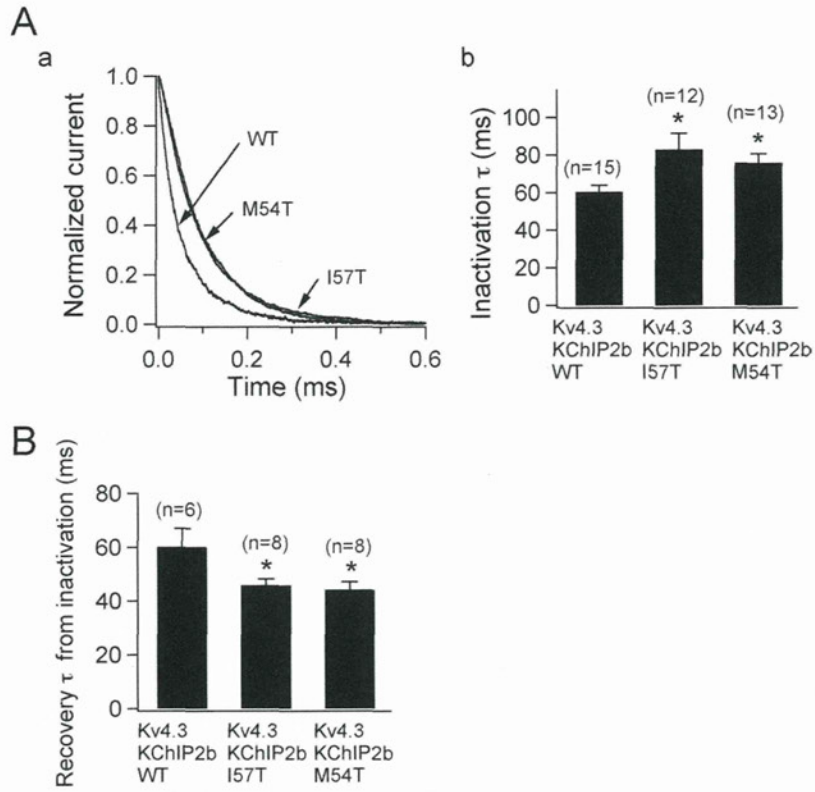

Figure 5 Two *KCNE2* variants slow inactivation kinetics and accelerate recovery from inactivation. **A, a:** Three current traces obtained from Chinese hamster ovary (CHO) cells transfected with wild-type (WT), I57T, and M54T *KCNE2* variant co-expressed with Kv4.3 and KChIP2b. Traces, which are normalized and superimposed, show that the variants slow inactivation. **A, b:** Time constants of decay at +20 mV for WT and variant *KCNE2* (*$P < .05$ vs Kv4.3 + KChIP2b + WT). Numbers in parentheses indicate numbers of observations. **B:** Time constants of recovery from inactivation recorded using a double-pulse protocol (*$P < .05$ vs Kv4.3 + KChIP2b + WT). Numbers in parentheses indicate numbers of observations.

Figure 5A shows the three traces depicted in Figure 4B normalized to their peak current level. This representation shows that the time course of inactivation of the two variant currents is slowed. The current decay was fitted by Equation 3 and the time constants (at +20 mV) summarized in Figure 5A, panel b. Finally, Figure 5B shows that the time constants of recovery of the two mutant channels from inactivation were significantly reduced. Thus, compared to WT *KCNE2*, recovery of reconstituted Kv4.3 + KChIP2b channels from inactivation was significantly accelerated with both I57T and M54T mutants.

Discussion

Kv4.3/KChIP2/MiRP1 complex can recapitulate the native I_{to}

In the present study, co-expression of WT *KCNE2* produced changes in kinetic properties (Figures 1–3 and Table 1) that led to close recapitulation of native cardiac I_{to}.[28,29] Notably, in addition to causing a positive shift of steady-state inactivation (Figure 2), *KCNE2* co-expression hastened the recovery of Kv4.3 + KChIP2b channels from inactivation (Figure 3). These modifications rendered Kv4.3 + KChIP2b channels more similar to native cardiac I_{to}, suggesting that *KCNE2* may be an important component of the native I_{to} channel complex. In contrast to a previous observation in HEK293 cells,[21] *KCNE2* co-expression decreased the current density of Kv4.3 and Kv4.3 + KChIP2b channel current in the present study, which seems to be a more reasonable result as the native I_{to} density reportedly was smaller in isolated human heart.[28] *KCNE2* co-expression has also been shown to reduce the density of Kv7.1[8,9] and HERG[6,7] channels.

Similar to the result of Deschenes and Tomaselli,[21] we failed to observe an overshoot during recovery from inactivation when *KCNE2* was co-expressed with Kv4.3 (Figure 3A), which is in contrast to the report of another group.[13] However, co-expression of *KCNE2* with Kv4.3 + KChIP2 channels produced an overshoot (Figure 3B), consistent with the report of Wettwer's group.[25] Wettwer et al also found that other *KCNE* subunits either were ineffective or induced only a small overshoot in CHO cells. Therefore, both MiRP1 and KChIP2 subunits are sufficient and necessary to recapitulate native I_{to} in the heart. Considering that the overshoot phenomenon has been described only in human ventricular I_{to} channels of the epicardial but not endocardial region,[28] these results may further implicate participation of MiRP1 and KChIP2 in the I_{to} channel complex in epicardium.

KCNE2 variants may alter the arrhythmogenic substrate by modulating I_{to}

Heterologous expression in CHO cells was conducted to examine the functional effects of I57T and M54T variants on Kv4.3 + KChIP2 channels. Both I57T and M54T

KCNE2 variants significantly (1) increased peak transient outward current density (Figure 4), (2) slowed the decay of the reconstituted I_{to} (Figure 5A), and (3) accelerated its recovery from inactivation (Figure 5B). Both variants thus caused an important gain of function in human I_{to}. These sequence changes may play a role in modulating I_{to} and thereby predispose to some inherited fatal rhythm disorders.

Functional effects on I_{to} induced by I57T and M54T resemble each other, increasing I_{to} density and accelerating its recovery from inactivation. The gain of function in I_{to} opposes the fast inward Na^+ currents during phase 0 of the action potential, leading to all or none repolarization at the end of phase 1 and loss of the epicardial action potential dome, thus promoting phase 2 reentry and fatal ventricular arrhythmias.[30]

Another *KCNE2* variant (M54T) associated with fatal arrhythmias was first identified in a woman who had a history of ventricular fibrillation and varied QT intervals.[6] It is possible that her arrhythmia was also related to a gain of function in I_{to} secondary to this variation in *KCNE2*. Interestingly, the I57T variant has been reported to produce a loss of function of HERG or Kv7.1 channels, thereby predisposing to long QT syndrome,[6,8] indicating that the same *KCNE2* variant could cause two different cardiac rhythm disorders, similar to long QT syndrome and Brugada syndrome caused by *SCN5A* mutations.[31,32]

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CLINICAL RESEARCH

Heart rate-dependent variability of cardiac events in type 2 congenital long-QT syndrome

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Aims We aimed to examine the validity of heart rate (HR) at rest before β-blocker therapy as a risk factor influencing cardiac events (ventricular fibrillation, torsades de pointes, or syncope) in long QT type 2 (LQT2) patients.

Methods and results In 110 genetically confirmed LQT2 patients (45 probands), we examined the significance of variables [HR at rest, corrected QT (QTc), female gender, age of the first cardiac event, mutation site] as a risk factor for cardiac events. We also evaluated frequency of cardiac events in four groups classified by the combination of basal HR and QTc with cutoff values of 60 b.p.m. and 500 ms to estimate if these two electrocardiographic parameters in combination could be a good predictor of outcome (mean follow-up period: 50 ± 39 months). Logistic regression analysis revealed three predictors: HR <60 b.p.m., QTc ≥500 ms, and female gender. When the study population was divided into four groups using the cutoff values of 60 b.p.m. for HR and 500 ms for QTc, the cumulative event-free survival by the Kaplan–Meier method was significantly higher in the group with HR ≥60 b.p.m. and QTc <500 ms than in the group with HR <60 b.p.m. and QTc <500 ms or that with HR <60 b.p.m. and QTc ≥500 m ($P < 0.05$). Irrespective of QTc interval, LQT2 patients with basal HR <60 b.p.m. were at significantly higher risk.

Conclusion The basal HR of <60 b.p.m. is a notable risk factor for the prediction of life-threatening arrhythmias in LQT2 patients.

Keywords Long QT syndrome • Arrhythmia • Genetics • Heart rate • Torsades de pointes

Introduction

Long QT syndrome (LQTS) is a primary electrical disease characterized by an abnormality in myocardial repolarization that leads to the prolongation of QT interval, morphological changes in T waves, and torsades de pointes (TdP) type of ventricular tachyarrhythmias on surface electrocardiogram (ECG).[1] Studies on genotype–phenotype correlation identified the clinical characteristics in each genetic subgroup, which made it possible to diagnose and introduce β-blocker therapy (BBT) appropriately in LQTS patients.[2–4] In patients with LQTS type 1 (LQT1), β-blockers are quite effective, whereas they are less effective in suppressing arrhythmic events in LQT2 and 3.[2]

Previous studies have demonstrated the importance of evaluating patients by clinical symptoms, gender, causative mutations, the type or biophysical function of mutations, and corrected QT (QTc) interval to stratify the arrhythmic risk in LQTS.[3,5–14] Heart rate (HR) has been recognized since the establishment of LQTS as a clinical entity, and a low HR for age was included in the diagnostic criteria.[15] A recent study by Schwartz *et al.*[16] demonstrated that a lower resting HR and a relatively low baroreflex sensitivity in *KCNQ1* A341V carriers are protective factors,

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