Risk of Syncope in Family Members Who Are Genotype Negative for a Family-Associated Long QT Syndrome Mutation

Running title: Barsheshet et al.; Genotype negative family members of LQTS patients

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Abstract:

**Background** - Current clinical diagnosis of long-QT syndrome (LQTS) includes genetic testing of family members of mutation positive patients. The present study was designed to assess the clinical course of individuals who are found negative for the LQTS-causing mutation in their families.

**Methods and Results** - Multivariate Cox proportional hazards model was used to assess the risk for cardiac events (comprising syncope, aborted cardiac arrest [ACA], or sudden cardiac death [SCD]) from birth through age 40 years among 1828 subjects from the LQTS Registry who were found negative for their family LQTS-causing mutation. The median QTc of study subjects was 423 msec (interquartile-range: 402-442 msec). The cumulative probability of a first syncope through age 40 years was 15%. However, only 2 patients (0.1%) experienced ACA and none died suddenly during follow-up. Independent risk factors for syncope in genotype negative subjects included female gender (HR 1.60, p=0.002), prolonged QTc (HR=1.63 per 100 msec increment, p=0.02), family history of ACA or SCD (HR=1.89, p=0.002), and LQT2 vs. LQT1 family mutation (HR =1.41, p=0.03). Subgroup analysis showed that the presence of the K897T polymorphism in the LQT2 gene in an affected family was associated with an 11-fold (p=0.001) increase in the risk of recurrent syncope in genotype negative subjects.

**Conclusions** - Our findings suggest that cardiac events among genotype-negative family members of LQTS patients are dominated by nonfatal syncopal episodes without occurrence of sudden cardiac death. The risk for nonfatal events in this population may be mediated by the presence of common polymorphisms in LQTS genes.

**Key words:** gene mutation, genetic polymorphisms, long-QT syndrome, sudden cardiac death arrhythmia, syncope.
Congenital long QT syndrome (LQTS) is an inherited channelopathy associated with variable penetrance, prolongation of the heart-rate corrected QT interval (QTc), and an increased risk for syncope and sudden cardiac death (SCD) due to ventricular tachyarrhythmias. Genetic testing provides important information for diagnosis, risk stratification, and management of patients with LQTS. To date, more than 600 mutations have been identified in 13 LQTS genes, with the LQT1, LQT2 and LQT3 genotypes comprising more than 95% of genotype positive LQTS and approximately 75% of all patients with LQTS.

The current clinical diagnosis of congenital LQTS includes genetic testing of family members of identified LQTS probands. However, the clinical course of individuals who are found negative for the LQTS-causing family mutation is unknown. Specifically, data regarding the risk for syncope and life-threatening events in this population are limited. Accordingly, the present study was carried out in a large cohort of genotype-negative family members from genotype-positive families enrolled in the International LQTS Registry. We investigated the risk for, and the factors associated with, cardiac events in this mutation-negative group of patients.

**Methods**

**Study Population**

Patients were included in the study if they were genetically tested and found negative for the family’s LQTS causing mutation (KCNQ1, KCNH2, or SCN5A). Subjects related to family probands who had multiple gene mutations were excluded from the study. The current study included patients from the US and Israeli portions of the international LQTS Registry since only patients from these centers met the inclusion criteria of genetic testing among family members of LQTS mutation positive patients. The final study sample comprised 1828 subjects who were
genotype negative for a known family mutation. All subjects or their guardians provided informed consent for the genetic and clinical studies.

**Genotype characterization**

The *KCNQ1*, *KCNH2*, and *SCN5A* mutations were identified with the use of standard genetic tests performed in academic molecular-genetic laboratories (including the Functional Genomics Center, University of Rochester Medical Center, Rochester, NY; Baylor College of Medicine, Houston, TX; Mayo Clinic College of Medicine, Rochester, MN; and Boston Children’s Hospital, Boston, MA) and by commercial genetic laboratories (including GeneDx, Gaithersburg, MD; and PGx Health [FAMILION], New Haven, CT).

Data regarding the co-existence of LQTS-related gene polymorphisms, in addition to the LQTS-causing mutation, were collected for first degree family members of 218 study subjects. LQTS-gene polymorphisms were evaluated in the 5 most common LQTS genes: *KCNQ1*, *KCNH2*, *SCN5A*, *KCNE1*, and *KCNE2*. The frequency of the specific polymorphism in the families of the 218 study subjects, by family LQTS mutation, is presented in the supplementary appendix (Table 1S).

**Phenotype characterization**

Routine clinical and electrocardiographic parameters were acquired at the time of enrollment. Follow-up was censored at age 41 years to minimize the influence of coronary and acquired heart disease on cardiac events. Measured parameters on the first recorded ECG included QT and R-R intervals in milliseconds, with QT corrected for heart rate by Bazett’s formula. Clinical data were collected on prospectively designed forms with information on demographic characteristics, personal and family medical history, electrocardiographic findings, therapy, and the occurrence of cardiac events. Information on end-point events was determined from the
clinical history ascertained by routine follow-up contact with the patient, family members, attending physician, or the medical records. No implantable cardioverter defibrillator (ICD) events were recorded in this population.

**End points**

The primary end point of the present study was pre-specified as the occurrence of a first cardiac event, comprising syncope (defined as transient loss of consciousness being abrupt in onset and offset), aborted cardiac arrest ([ACA] requiring external defibrillation as part of the resuscitation), or LQTS-related sudden cardiac death ([SCD] abrupt in onset without evident cause, if witnessed, or death that was not explained by any other cause if it occurred in a non-witnessed setting). Since only 2 study subjects experienced ACA and none experienced SCD during follow-up, syncope is reported as the primary end point, and the risk for recurrent syncope was assessed as a secondary end point. The circumstances of the syncopeal events (including data on onset, prodromal symptoms, and seizures) were corroborated by the study coordinators through the patient’s medical files and interviews with individuals about themselves or about family members, and categorized by the study specialists using pre-specified codes.

**Statistical analysis**

Characteristics of the 3 subgroups of patients categorized by family proband’s LQTS causing mutation (LQT1, LQT2, and LQT3) were compared with the chi-square test and the Fisher’s exact test for categorical variables, and ANOVA test or the Kruskal–Wallis one-way analysis of variance for continuous variables.

The overall incidence rate of syncope and the incidence rates for syncope with specific age and gender subgroups were calculated by dividing the number of subjects with syncope by the total number of person-years of follow-up in each subgroup. The probability of a first
syncope was graphically displayed by QTc, gender and family mutation according to the method of Kaplan and Meier, with comparison of cumulative probability of events by the log-rank test. A Mantel-Byar graph \(^{13}\) was used for displaying cumulative risk for the time-dependent covariate of the occurrence of a life-threatening cardiac event in a first degree family member. This analysis accrues patients over time, in whom a life-threatening cardiac event occurs in a first degree family member during follow-up, and accounts for time-varying entry into this group. The Cox proportional-hazards survivorship model was used to evaluate the independent contribution of clinical and genetic factors to the first occurrence of syncope from birth through age 40 years. Pre-specified covariates in the multivariate model included: gender, baseline QTc (dichotomized at the upper quartile value \([\geq 440\text{ msec}]\) and assessed also as continuous measure \([\text{per 100 msec increment}]\)), the family gene mutation, a family history of life threatening cardiac event in a first degree relative, and treatment with \(\beta\)-blockers. Family history of life threatening cardiac event and the administration of \(\beta\)-blocker therapy from birth to age 40 years in a study individual were evaluated as time-dependent covariates. In a secondary analysis, among the 218 genotype-negative patients on whom polymorphism data were available, we used the conditional model proposed by Prentice, Williams, and Peterson (PWP), to evaluate the risk for recurrent syncope events. This model assumes a subject cannot be at risk for event 2 until event 1 occurs. It simultaneously models the distribution of the time to first syncope and the gap times between subsequent syncopal events as functions of risk factors of interest \(^{14}\). Pre-specified covariates that were included as potential predictors of recurrent syncope were gender, QTc at baseline, family history of life threatening cardiac event in a first degree relative, treatment with \(\beta\)-blockers, the presence of a polymorphism and the specific type of polymorphism in a first degree affected family member. All models were stratified by the decade in which study patients were born to
account for changes in the baseline hazard function for different calendar time periods. The
effect of lack of independence between subjects was evaluated in the Cox model with grouped
jackknife estimates for family membership. All grouped jackknife standard errors for the
covariate risk factors fell within 3% of those obtained from the unadjusted Cox model, and
therefore only the Cox model findings are reported. The statistical software used for the analyses
was SAS version 9.20 (SAS Institute Inc, Cary, NC). A 2-sided 0.05 significance level was used
for hypothesis testing.

Results

Study population

Of the total 1828 subjects (239 families) who were genetically tested and found negative for the
family’s LQTS-causing mutation, there were 696 subjects from 109 families with LQT1
mutations, 816 subjects from 108 families with LQT2 mutations, and 316 subjects from 22
families with LQT3 mutations. The median (interquartile range) number of members of a family
was 4 (2-9) (including genotype positive and genotype negative patients). The current study
population comprised up to 4th degree genotype-negative relatives of probands (22% of subjects
were 1st degree relatives of the proband, 25% 2nd degree, 32% 3rd degree, and 20% 4th degree).

The clinical characteristics of all study subjects and of the subgroups categorized by their
family’s LQTS-causing mutation are presented in Table 1. The median QTc (interquartile range)
of the study cohort was 423 msec (402-442 msec); there were no significant differences among
the 3 subgroups with regard to gender, QTc at baseline, or the proportion of subjects with a
family history of life threatening cardiac event. However, during follow-up medical treatment
with beta-blockers and the frequency of cardiac events were highest among study subjects with a
family LQT2 mutation (Table 1).
The baseline clinical and ECG characteristic of study subjects with and without collected data regarding the co-existence of family polymorphisms were similar (not shown). Among the 218 study subjects for whom data regarding the co-existence of family polymorphisms were collected, the highest frequency of family polymorphisms (and specifically the K897T polymorphism in the KCNH2 gene) was observed among subjects from LQT2 families (Table 1).

Risk of syncope in genotype-negative family members

Almost all cardiac events were nonfatal syncope; only 2 study subjects (0.1%) experienced ACA or SCD during follow-up. The cumulative probability of a first syncope at age 40 years among the 1828 genotype-negative study subjects was 15%. The overall incidence rate of a first syncope event was 4.2 per 1000 person-years. The incidence rate increased after the age of 10 and was higher in women than in men (Fig. 1). One hundred and one subjects (5.5%) experienced one or more recurrences of syncope. The overall incidence rate of recurrent syncope events was 8.6 per 1000 person-years.

Consistent with the incidence rates, the cumulative probability of a first syncope by age 40 years was higher among women as compared with men (18% vs. 11%, respectively; p log-rank =0.001 [Fig. 2A]). In addition, the rate of syncope events was higher among subjects with an LQT2 family mutation (20%) as compared with those with an LQT1 or LQT3 family mutation (12% and 10%, respectively; p log-rank =0.003 for the comparison among the 3 groups [Fig. 2B]), and among subjects with QTc ≥ 440 msec as compared with lower QTc values (19% vs. 14%, respectively; p log-rank =0.01 [Fig. 2C]). Mantel-Byar survival analysis showed that the occurrence of a life-threatening event in a genotype-positive sibling was associated with a significant increase in the risk of a subsequent syncope in genotype-negative family members (Fig. 3).
Multivariate analysis in the total study population (Table 2) showed consistent results regarding the high-risk factors that were identified in the univariate analyses. Thus, women experienced a significant 1.6-fold increased risk as compared with men (p=0.002); subjects with family-associated LQT2 mutations had a 1.4-fold increased risk for a first syncope as compared with family-associated LQT1 mutations (p=0.03); and those with a family history of life-threatening cardiac event had nearly a 2-fold increased risk (p=0.002) for a first syncope as compared with patients without a family history for life-threatening cardiac events (Table 2).

Subgroup analysis, among the 218 study subjects for whom data regarding the co-existence of LQTS-gene polymorphisms in affected first degree family members were collected, showed that the cumulative probability of a first syncope at age 40 years was significantly higher among genotype negative subjects with a family LQTS-gene polymorphism (25%) as compared with those in whom a family polymorphism was not present (5%; p=0.004, Figure 4). Consistently, a secondary analysis that assessed the risk for recurrent syncope in the same subgroup (Table 3), showed that the presence of an LQTS-gene polymorphisms in an affected first degree relative was associated with an 8-fold (p<0.001) increase in the adjusted risk for recurrent syncope in a genotype negative study subject. Specifically, the co-existence of the K897T polymorphism in the LQT2 gene in affected family members was associated with the highest risk (HR=11.1; p<0.001) for recurrent syncope in genotype negative study subjects (Table 3).

Medical therapy with beta-blockers was not associated with a statistically significant reduction in the risk of a first syncope in the total study population (HR=0.42; p=0.23 [Table 2]), but was associated with a significant 71% (p=0.02) risk reduction in the model that evaluated the
risk of recurrent syncope (Table 3), suggesting that this therapeutic modality may be effective in symptomatic family members of LQTS patients.

There was no statistical significant difference in the effect of beta-blockers among the different family genotypes, or in the effect of beta-blockers among women during pregnancy and post partum period. Additional secondary analyses stratifying country of origin (US and Israeli centers) showed similar results for all analyses.

The risk for life threatening cardiac events

Only 2 subjects, comprising 0.1% of this study cohort, experienced aborted cardiac arrest during follow-up and none died due to SCD during follow-up. The characteristics of the 2 patients are shown in Table 4. Both patients were female who had an LQT2-causing family mutation and the K897T polymorphism in the LQT2 gene. One patient experienced an ACA at the age of 14 years during a volleyball game, which was her first cardiac event. The other patient had syncope at the age of 6 years during vigorous physical activity while traveling down a snowy hill with a sled and had an aborted cardiac arrest at the age of 24 during delivery of her first child. Both patients were not treated with beta-blockers at the time of the event (Table 4).

Discussion

In the present study we assessed the clinical course and risk factors for cardiac events among subjects who were genetically tested and found negative for the family proband’s LQTS-causing mutation. Our findings suggest that 1) genotype-negative family members of LQTS patients experience a 15% rate of nonfatal syncope events, but a near zero (0.1%) of life-threatening events; and 2) specific clinical and genetic factors identify increased risk for syncope in this population. These findings can be used to guide risk assessment and management of family members of LQTS patients.
The availability of genetic testing and advancements in the understanding of the genetics of LQTS have demonstrated the importance of this information in the diagnosis of LQTS\(^{16-17}\), understanding the clinical differences between individual genetic disorders, and improved risk stratification and management strategies\(^4,6,18\). Screening for the patient’s genotype, usually for the common genes (i.e. \(KCNQ1, KCNH2, SCN5A, KCNE1, and KCNE2\)), can be completed in several weeks. If a mutation is found, the cost of genotype testing can be reduced substantially by checking only for the mutation found in the proband\(^19\). Thus, carrying out genetic testing for the mutation identified in a family member has become a common practice for the diagnosis of LQTS. Patients identified as positive for the family-causing mutation are managed on the basis of their molecular diagnosis and clinical symptoms. In contrast, currently there are no data regarding the clinical course of asymptomatic and symptomatic genotype-negative family members of LQTS patients.

In the present study we evaluated the risk for syncope and life-threatening cardiac events in 1828 subjects from the International LQTS Registry who were genetically tested and found negative for the family proband’s LQTS-causing mutation. Genotype-negative family members of LQTS patients were shown to experience a 15% cumulative rate of cardiac events up to the age of 40. However, virtually all cardiac events in this patient subset comprised nonfatal syncopal events. Furthermore, none of the patients experienced SCD during follow-up. Thus, children and young adults who undergo genetic testing and are identified as negative for a mutation in a family member can be reassured of a favorable long-term outcome even if nonfatal symptoms occur during follow-up.

Independent risk factors associated with increased risk for nonfatal cardiac events in study patients included female gender, prolonged QTc, family history of life threatening cardiac
event, and LQT2 family mutation. The latter association between LQT2 family mutation and increased risk for syncope events may be related to a higher prevalence of LQTS gene polymorphism among individuals with a LQT2 family mutation, and particularly a greater prevalence of the common single nucleotide polymorphism K897T present in the KCNH2 gene. Indeed, several studies demonstrated that LQTS gene polymorphisms lead to KCNQ1 or KCNH2 channel loss of function 20-21, increased risk for cardiac events in congenital LQTS patients 20-23 and increased risk for developing drug-associated torsade de pointes 24. It was also suggested that K897T polymorphism may increase the risk for torsade de pointes and ventricular fibrillation following acute myocardial infarction 25-26. However, it should be noted that the role of K897T polymorphism in LQTS is controversial with several large-scale population studies showing that K897T polymorphism is associated with either shortening or prolongation of the QTc interval 27-30. Herein we found in a subgroup of genotype-negative subjects, for whom data regarding the presence of LQTS gene polymorphism in a first degree relative were available, that LQTS gene polymorphisms in general, and the K897T polymorphism specifically, were the most powerful predictors of recurrent syncope in this population. Thus, genotype negative subjects with a family polymorphism in an LQTS gene experienced an 8-fold increase in the risk of recurrent syncope, and genotype-negative subjects with the K897T polymorphism had a pronounced 11-fold increase in the risk of this end point. In addition, K897T polymorphism in affected first degree family members was associated with increased risk for syncope without evidence of a significant QTc prolongation or with a mildly prolonged QTc. These findings suggest the possibility that mild abnormalities in ion channel current associated with a single nucleotide polymorphism may increase the risk of nonfatal self-limited ventricular tachyarrhythmias in
genotype-negative family members of LQTS patients with a normal-range or a mildly prolonged QTc.

Chronic treatment with estradiol was shown to be associated with QT prolongation secondary to drug therapy \(^{31-32}\). Consistent with this mechanism, female gender was associated with a significant increase in the risk for syncope in the study population. Furthermore, the 2 genotype-negative patients who experienced ACA during follow-up were women, who experienced the event after the onset of adolescence period in women from families with the \(K897T\) polymorphism during higher risk conditions such as exercise or the post-partum period. Thus, a combination of environmental, physiological, and genetic factors may predispose to the occurrence of arrhythmic events in genotype-negative family members of LQTS patients.

Most recently, it was shown that the risk for a first cardiac event of any type (comprising mainly non-life-threatening syncopal episodes) and the risk of a first life-threatening cardiac event (comprising ACA/SCD) were highest among genotype positive patients with QTc>440msec, intermediate among genotype positive patients with QTc≤440msec and lowest among genotype negative patients \(^{33}\). Data on the incidence rate of syncope in the general population are limited and conflicting. Thus, it is difficult to compare the incidence of first syncope in the present study population with the incidence in the general population. The Framingham Heart Study, evaluating 7814 participants (age range 20-96) over an average follow-up of 17 years, reported an incidence rate of 3-4 events (first syncope) per 1000 person-years during the 3\(^{rd}\) and 4\(^{th}\) decades of life \(^{34}\). The present study showed a higher incidence rate, with 6.1 and 4.3 events per 1000 person-years during the 3\(^{rd}\) and 4\(^{th}\) decades of life respectively (with the incidence rate more than doubled among women), suggesting increased frequency of nonfatal syncopal episodes in family members of LQTS patients. The reported ACA/SCD event
rate among children and adolescents from the general population ranges from 2 to 20 per
100,000 person-years \(^{35-40}\); the present study showed an ACA/SCD event rate of 4 per 100,000
person years.

**Limitations**

Since study subjects were tested only for the mutation that was identified in an affected family
member, we cannot rule out that patients who experienced syncope had other LQTS-causing
mutations or other genetic syndromes associated with ventricular tacharrhythmias.

Genetic testing for the presence of LQTS-gene polymorphisms was carried out among
family members of only 218 study subjects. However, despite the smaller sample size, the results
in this subgroup showed an independent and a powerful association between the presence of
LQTS-gene polymorphisms in general (and the K\textsuperscript{897}T polymorphism in the \textit{KCNH2} gene,
specifically) and the risk for recurrent syncope events, suggesting that this genetic factor may
contribute to increased risk for nonfatal events in genotype-negative subjects. It should also be
noted that only affected first degree relatives were tested for LQTS-gene polymorphisms.

However, it is conceivable that genotype negative subjects also had increased frequency of
polymorphisms that were identified in their first degree family members.

We did not identify a statistical significant difference in the effect of beta-blockers among the
different family genotypes, or in the effect of beta-blockers among women during pregnancy and
post partum period. We did not identify a polymorphism that has a protective effect in LQTS.

However, the current study may be underpowered to detect these effects.

**Summary, implications, and future research**

Human genetic variation is facilitating an understanding of why susceptibility to diseases varies
among individuals. The present study among 1828 subjects from the large LQTS Registry
suggests that the presence of a latent genetic background may affect the risk for nonfatal cardiac events even among subjects who were genetically tested and found negative for the family proband’s LQTS-causing mutation. These subjects were shown to have similar rate of life threatening cardiac events as the general population. Thus, based on these findings subjects who are tested negative for their family members LQTS-causing mutation could be reassured of a benign course regardless of the occurrence of symptoms or the presence of risk factors. Our findings also suggest that beta-blocker therapy can be used to reduce the risk of syncope among symptomatic genotype-negative subjects, especially those with high risk factors (including women, subjects with mildly prolonged QTc, those with family history of life-threatening cardiac events, and those with family members with a KCNH2 gene mutation or polymorphism).

Further research is needed to determine the effect of LQTS-gene polymorphisms on the clinical course of patients with congenital LQTS and their family members and how these effects relate to the risk for nonfatal arrhythmic events in the general population or in those who experience drug-induced LQTS.

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References:


Table 1. Patient Characteristics of Genotype-negative Subjects from LQTS Families

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<thead>
<tr>
<th>Parameter</th>
<th>All patients</th>
<th>Family mutation</th>
<th>P value*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>LQT1</td>
<td>LQT2</td>
</tr>
<tr>
<td>Number of pts</td>
<td>1828</td>
<td>696</td>
<td>816</td>
</tr>
<tr>
<td>Female, %</td>
<td>54</td>
<td>52</td>
<td>55</td>
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<tr>
<td>QTc at enrollment, msec (median, IQR)</td>
<td>423 (402-442)</td>
<td>424  (402-439)</td>
<td>423 (402-442)</td>
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<tr>
<td>QTc at enrollment ≥ 440 msec, %</td>
<td>26</td>
<td>25</td>
<td>27</td>
</tr>
<tr>
<td>Family history (1st degree relative) of ACA/SCD, %</td>
<td>12</td>
<td>11</td>
<td>14</td>
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<tr>
<td>Any LQTS family polymorphism†, %</td>
<td>71</td>
<td>57</td>
<td>84</td>
</tr>
<tr>
<td>Family K897T polymorphism†, %</td>
<td>35</td>
<td>32</td>
<td>50</td>
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**Therapy during follow-up**

<table>
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<th>Family mutation</th>
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<tr>
<td></td>
<td></td>
<td>LQT1</td>
<td>LQT2</td>
</tr>
<tr>
<td>Beta-blockers, %</td>
<td>7.4</td>
<td>6.5</td>
<td>9.1</td>
</tr>
<tr>
<td>Pacemaker, %</td>
<td>0.2</td>
<td>0.1</td>
<td>0.2</td>
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<td>Defibrillator, %</td>
<td>0.3</td>
<td>0.3</td>
<td>0.4</td>
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**Cardiac event during follow-up**

<table>
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<tr>
<th></th>
<th>All patients</th>
<th>Family mutation</th>
<th>P value*</th>
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<tbody>
<tr>
<td></td>
<td></td>
<td>LQT1</td>
<td>LQT2</td>
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<tr>
<td>1st event</td>
<td>11.1</td>
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<tr>
<td>2nd event</td>
<td>5.5</td>
<td>5.0</td>
<td>6.9</td>
</tr>
<tr>
<td>3rd event</td>
<td>3.2</td>
<td>3.6</td>
<td>3.6</td>
</tr>
<tr>
<td>Aborted cardiac arrest/ sudden cardiac death, %</td>
<td>0.1</td>
<td>0</td>
<td>0.2</td>
</tr>
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</table>

* P value for the comparison among the 3 genotype subgroups
† Data on polymorphism (any LQTS polymorphism found) in affected 1st degree family members were available for 218 patients.
Table 2. Multivariate analysis: Predictors of first syncope in the total study population.

<table>
<thead>
<tr>
<th></th>
<th>Hazard ratio</th>
<th>95% CI</th>
<th>P Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Female</td>
<td>1.60</td>
<td>1.19-2.15</td>
<td>0.002</td>
</tr>
<tr>
<td>QTc at baseline (every 100 msec)*</td>
<td>1.63</td>
<td>1.09-2.46</td>
<td>0.02</td>
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<tr>
<td>QTc at baseline ≥440 msec*</td>
<td>1.49</td>
<td>1.11-2.01</td>
<td>0.009</td>
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<tr>
<td>Time dependent family history of aborted cardiac arrest/ sudden cardiac death</td>
<td>1.89</td>
<td>1.26-2.83</td>
<td>0.002</td>
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<tr>
<td>Family LQT2 vs. Family LQT1</td>
<td>1.41</td>
<td>1.03-1.91</td>
<td>0.03</td>
</tr>
<tr>
<td>Family LQT2 vs. Family LQT3</td>
<td>1.77</td>
<td>1.14-2.76</td>
<td>0.01</td>
</tr>
<tr>
<td>Time dependent beta-blocker treatment</td>
<td>0.42</td>
<td>0.10-1.72</td>
<td>0.23</td>
</tr>
</tbody>
</table>

*The effects of QTc at baseline (continuous measure) and QTc >440 msec on outcome were evaluated in separate models; findings for other covariates are reported from the model in which QTc was assessed as a continuous measure.
Table 3. Multivariate analysis: Predictors of recurrent syncope events among 218 patients with data on family polymorphism.

<table>
<thead>
<tr>
<th>Predictor</th>
<th>Hazard ratio</th>
<th>95% CI</th>
<th>P Value</th>
</tr>
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<tr>
<td>Any polymorphism</td>
<td>8.31</td>
<td>2.69-25.70</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Multiple polymorphisms vs. no polymorphism</td>
<td>8.85</td>
<td>2.79-28.05</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Single polymorphism vs. no polymorphism</td>
<td>7.73</td>
<td>2.18-27.46</td>
<td>0.002</td>
</tr>
<tr>
<td>$K897T$ vs. no polymorphism</td>
<td>11.10</td>
<td>2.79-44.12</td>
<td>0.001</td>
</tr>
<tr>
<td>$G38S$ vs. no polymorphism</td>
<td>7.98</td>
<td>1.97-32.32</td>
<td>0.004</td>
</tr>
<tr>
<td>$H558R$ vs. no polymorphism</td>
<td>1.69</td>
<td>0.22-13.08</td>
<td>0.616</td>
</tr>
<tr>
<td>Time dependent beta-blocker treatment</td>
<td>0.29</td>
<td>0.10-0.86</td>
<td>0.02</td>
</tr>
</tbody>
</table>

Adjusted also for gender, QTc at baseline, and time dependent family history of aborted cardiac arrest or sudden cardiac death.

Table 4. Clinical characteristics of patients with aborted cardiac arrest

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Patient 1</th>
<th>Patient 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>QTc at enrollement, msec</td>
<td>400</td>
<td>454</td>
</tr>
<tr>
<td>Number of cardiac events</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>Age of first cardiac event, years</td>
<td>14</td>
<td>6</td>
</tr>
<tr>
<td>Trigger for first cardiac event</td>
<td>Playing Volleyball</td>
<td>Vigorous physical activity sledding accident</td>
</tr>
<tr>
<td>Age of aborted cardiac arrest, years</td>
<td>14</td>
<td>24</td>
</tr>
<tr>
<td>Trigger for aborted cardiac arrest</td>
<td>Playing Volleyball</td>
<td>Pregnancy Event at time of delivery</td>
</tr>
<tr>
<td>Family mutation</td>
<td>G601S (in $KCNH2$)</td>
<td>W568fsX593 (in $KCNH2$)</td>
</tr>
<tr>
<td>Genes tested in patient</td>
<td>$KCNQ1$, $KCNH2$, SCN5A, KCNE1, KCNE2</td>
<td>$KCNQ1$, $KCNH2$, SCN5A, KCNE1, KCNE2</td>
</tr>
<tr>
<td>Polymorphism in patient</td>
<td>Data unavailable</td>
<td>$K897T$ (in $KCNH2$)</td>
</tr>
<tr>
<td>Polymorphism in 1st degree relative</td>
<td>$K897T$ (in $KCNH2$) $G38S$ (in $KCNE1$)</td>
<td>$K897T$ (in $KCNH2$)</td>
</tr>
<tr>
<td>Deafness</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Life threatening cardiac event in 1st degree relative</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Other diagnoses</td>
<td>Mitral valve prolapse</td>
<td>Asthma</td>
</tr>
<tr>
<td>Treatment with beta blockers</td>
<td>After aborted cardiac arrest</td>
<td>Never</td>
</tr>
<tr>
<td>Implantable cardioverter defibrillator</td>
<td>After aborted cardiac arrest</td>
<td>Never</td>
</tr>
</tbody>
</table>
Figure Legends:

**Figure 1.** Incidence rate of syncope by age and gender.

The incidence rate of first syncope event per 1000 person-years was calculated by dividing the number of subjects with syncope by the total number of person-years of follow-up in each gender-age subgroup.

**Figure 2.** Probability of syncope by clinical risk factors.

Kaplan-Meier estimates of the probability of syncope from birth to 40 years of age by (A) gender; (B) family long QT syndrome genotype; and (C) QTc duration.

**Figure 3.** Probability of syncope by family history of life threatening cardiac event.

Mantel-Byar graph cumulative probability of syncope by time-dependent family history (1st degree relative) of life threatening cardiac event. This analysis accrues patients over time in the positive family history group, and thus the early events, when relatively few patients are at risk, impact the trajectory of the curve somewhat disproportionately.

**Figure 4.** Kaplan-Meier cumulative probability of syncope by LQTS family polymorphism.

Data regarding the presence of an LQTS gene polymorphism in a first degree relative were collected among 218 study subjects.
Unadjusted P=0.004

Family Polymorphism

No polymorphism

Patients at Risk
Family Polymorphism 154
No polymorphism 64

Years

0 10 20 30 40

Probability of Syncope
0.00 0.05 0.10 0.15 0.20 0.25 0.30 0.35

131 (0.06) 92 (0.17) 63 (0.23) 45 (0.25)
54 (0.02) 34 (0.02) 27 (0.05) 23 (0.05)
Risk of Syncope in Family Members Who Are Genotype Negative for a Family-Associated Long QT Syndrome Mutation

Alon Barsheshet, Arthur J. Moss, Scott McNitt, Slava Polonsky, Coeli M. Lopes, Wojciech Zareba, Jennifer L. Robinson, Michael J. Ackerman, Jesaia Benhorin, Elizabeth S. Kaufman, Jeffrey A. Towbin, G. Michael Vincent, Ming Qi and Ilan Goldenberg

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Table 1S. Distribution of LQTS gene polymorphism among affected first degree relatives of study subjects.

<table>
<thead>
<tr>
<th>Polymorphism in 1st degree relative</th>
<th>All subjects (n=218)</th>
<th>Family mutation</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>LQT1 (n=44)</td>
</tr>
<tr>
<td>K897T (KCNH2)</td>
<td>82</td>
<td>14</td>
</tr>
<tr>
<td>H558R (SCN5A)</td>
<td>60</td>
<td>22</td>
</tr>
<tr>
<td>A572D (SCN5A)</td>
<td>9</td>
<td>0</td>
</tr>
<tr>
<td>F2004L (SCN5A)</td>
<td>14</td>
<td>14</td>
</tr>
<tr>
<td>G38S (KCNE1)</td>
<td>121</td>
<td>21</td>
</tr>
<tr>
<td>D85N (KCNE1)</td>
<td>29</td>
<td>2</td>
</tr>
</tbody>
</table>

Data on LQTS gene polymorphism among affected first degree relatives of study subjects were available for 218 subjects. A hundred and one subjects had more than one type of family LQTS gene polymorphism. LQTS gene polymorphism was evaluated for the 5 most common LQTS genes: KCNQ1, KCNH2, SCN5A, KCNE1, and KCNE2.