Common Genetic Variants, QT Interval and Sudden Cardiac Death in a Finnish Population-Based Study

Running title: Noseworthy, et al.; Common variants, QT and SCD

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Abstract:

Background - Although sudden cardiac death (SCD) is heritable, its genetic underpinnings are poorly characterized. The QT interval appears to have a graded relationship to SCD and 35-45% of its variation is heritable. We examined the relationship among recently reported common genetic variants, QT interval and SCD.

Methods and Results - We genotyped 15 common (minor allele frequency >1%) candidate SNPs, based on association to the QT interval in prior studies, in individuals in 2 cohort studies (Health 2000, n=6,597; Mini-Finland, n=801). After exclusions, we identified 116 incident SCDs from the remaining sample (n=6,808). We constructed a QT genotype score (QTscore) using the allele copy number and previously reported effect estimates for each SNP. Cox proportional hazards models adjusting for age, sex, and geographical area were used time to SCD analyses. The QTscore was a continuous independent predictor of the heart rate-corrected QT interval (P<10^{-107}). Comparing the top to the bottom quintile of QTscore there was a 15.6 msec higher group mean QT interval (P<10^{-84}). A 10 msec increase in the observed QT was associated with an increased risk of SCD (HR 1.19, 95% CI 1.07-1.32, P=0.002). There was no linear relationship between QTscore and SCD risk; although, in post-hoc secondary analysis there was increased risk in the top compared with the middle QTscore quintile (HR of 1.92, 95% CI 1.05-3.58, P=0.04).

Conclusions - Our study strongly replicates the relationship between common genetic variants and the QT interval, confirms the relationship between the QT interval and SCD, but does not show evidence for a linear relationship between QTscore and SCD risk.

Key words: death, sudden; genetics; QT interval, electrocardiography; mortality; electrophysiology
Introduction:

Sudden cardiac death (SCD) is a leading cause of mortality worldwide.\textsuperscript{1,2} Rare genetic syndromes are well described but their contribution to total burden of SCD is low, accounting for fewer than 5\% of deaths.\textsuperscript{3,4} There is interest in understanding the role of common genetic variants in SCD risk, but, to date, reproducible examples have been difficult to identify.\textsuperscript{3,5-8} Common variants are expected to confer only a small increase in SCD risk individually, since they would otherwise be subject to strong negative selection. As a complement to primary genetic discovery in SCD samples, we hypothesized that common variants that are associated with SCD risk factors may influence the risk of SCD. Consistent with this hypothesis are recent observations that common variants associated with electrocardiographic QT interval or with myocardial infarction (MI) are also associated with SCD.\textsuperscript{5-7}

Prolongation of the QT interval is associated with increasing risk of SCD\textsuperscript{9} and 35-45\% of its variation can be attributed to additive genetic factors,\textsuperscript{10-12} therefore offering a tractable intermediate phenotype for the study of SCD genetics. Through large multicenter genome-wide association studies, we and other investigators have identified several common variants that impact inter-individual variability in QT interval duration.\textsuperscript{11,13} While individual common variants would be expected to result in only modest increments in SCD risk, these common variants could, in aggregate, increase SCD through influencing susceptibility to arrhythmogenic triggers such as myocardial ischemia, electrolyte disturbances, or QT-prolonging medications.

In this study, we studied a large, population-based cohort in Finland: (1) to attempt to replicate the association of these common genetic variants to QT interval, (2) to confirm the relationship between QT interval and SCD, and (3) to explore the association between these variants in a score reflecting the joint influence of the variants and the risk of SCD.
Methods:

Study Population:

The Health 2000 Study population is a cross-sectional cohort drawn from the Finnish Population Information System (http://www.vaestorekisterikeskus.fi/vrk/home.nsf www/populationinformationystem). The survey was carried out in Finland in 2000-2001. The implementation of the survey is described in detail elsewhere (http://www.terveys2000.fi/doc/methodologyrep.pdf). The study involved a two-stage stratified cluster sample representative of the whole adult Finnish population aged ≥30 years. The Health 2000 sample comprised 8,028 individuals, of whom 79% (6,354 individuals; 2,876 men and 3,478 women) participated in a comprehensive health examination including questionnaires, measurements (e.g. blood pressure, resting ECG), and doctor’s physical examination. DNA samples were collected from 6,597 subjects and digital ECGs were available from 6,295 subjects.

The Mini-Finland Health Survey was carried out from 1978 to 1980. The study involved a two-stage stratified cluster sample representing the whole Finnish population aged 30 years or over. The sample size was 8,000 individuals. Of the original sample 1,286 individuals living in seven cities (Helsinki, Kuopio, Lahti, Oulu, Salo, Tampere, Turku) were invited to a health re-examination in 2001, and 985 (77%) participated in the follow-up study. DNA samples were available from 801 subjects of the Mini-Finland Health Survey.

Subjects >80 years old at baseline in either the Health 2000 or Mini-Finland study were excluded from the current investigation. For analysis of the association of the QT score with the observed QT interval, subjects were excluded if QT interval was not available, if the study ECG
showed atrial fibrillation (n=55), QRS ≥ 120 msec (n=148), or if the subject was using QT-prolonging (n=1,692) or -shortening (digoxin, n=90) medications. Subjects taking QT-altering medications were not excluded from analyses of the association of the QT score with SCD. A drug was considered to potentially prolong the QT interval if it was listed in any of the four categories in the list maintained at http://www.qtdrugs.org. Digoxin was classified as the sole QT-shortening medication. Mini-Finland participants were not included in analyses of QT interval, because ECG intervals had not been measured.

**Study samples and data sources**

Follow-up data were obtained using national active surveillance and health care registers in Finland. The National Causes-of-Death register (maintained by Statistics Finland) includes data on the underlying and immediate cause of death as well as up to two contributing causes of death for all deaths in Finland. The Finnish Hospital Discharge Register, maintained by the National Institute for Health and Welfare, includes date of admission, date of discharge, and diagnoses associated with admission. The National Drug Reimbursement Register, maintained by the National Social Insurance Institute, catalogues diagnosis codes submitted for medication reimbursement. All records were linked using personal ID codes, which are unique to each permanent resident of Finland. The follow up is 100% for all residents of Finland.

The Health 2000 and Mini-Finland Study protocols were approved by both the Institutional Ethical Committee and by the Epidemiology Ethics Committee of the Helsinki and Uusimaa Hospital Region and carried out according to the recommendations of the Declaration of Helsinki.


**Disease and cause of death definitions**

Cause of death was adjudicated by two independent physicians based on information from Health 2000 and Mini-Finland examinations and the national registers: the National Causes-of-Death register, the Finnish Hospital Discharge Register which includes date of admission, date of discharge, and diagnosis associated with admission, and the National Drug Reimbursement Register. When the primary reviewers disagreed on the cause of death, cases were reviewed by two additional independent physicians and a final adjudication was achieved by consensus. In total, 490 deaths were adjudicated. There was agreement in 439/495 (90%) and the remaining 51 cases were adjudicated with two additional reviewers. Adjudication of cause of death was blinded to genotyping data.

Deaths were adjudicated as probable sudden cardiac death, possible sudden cardiac death, unlikely sudden cardiac death, and unknown cause of death. Eligible deaths for adjudication included out-of-hospital deaths and deaths within 10 days of hospitalization. Probable sudden cardiac death was defined as a death in which a cardiac cause was listed as the immediate or underlying cause of death and death was not known to be unrelated to arrhythmia. Possible sudden cardiac death was defined as a death in which the immediate or underlying cause of death was non-cardiac, but cardiac disease was present, and could reasonably have contributed to arrhythmia based on mechanism (e.g. unexpected death due to aspiration in a patient with a prior MI), or deaths that could have been arrhythmic based on circumstance (e.g. death of a driver in a motor vehicle crash, death while swimming). Unlikely arrhythmic cause was defined as death from an explained medical cause unrelated to cardiac disease (e.g. cancer death, massive blood loss, sepsis, pulmonary embolism, stroke) or from a cardiac cause that was known to be non-sudden or unrelated to lethal arrhythmia (e.g. death due to myocardial rupture after MI, death due
to endocarditis). Unknown cause of death included deaths for which insufficient data were available. We excluded deaths in individuals who had been hospitalized for more than 10 days prior to death. After exclusions, in total there were 84 probable cardiac deaths, 32 possible cardiac deaths, 347 unlikely cardiac deaths, and 30 unknown etiology deaths. Probable and possible sudden cardiac deaths were pooled in the SCD analyses. Autopsies were performed in 38.9% of all deaths, 62.6% of SCDs, and 73.0% of out-of-hospital SCDs. The median observational time was 8.1 years for Health2000 and 7.8 years for Mini-Finland health.

Prevalent coronary heart disease (CHD) was defined as one of the following: (a) physician diagnosis during the survey health examination of previous MI or coronary disease requiring surgical or percutaneous revascularization; (b) previous hospital discharge with a diagnosis of MI (ICD-8 or ICD-9 code 410 or ICD-10 codes I21-I22); (c) pathologic Q-waves or Minnesota code 1.1, or 1.2 together with 5.1-2 in the ECG; or (d) history of coronary revascularization procedure in the hospital discharge records.

**QT interval**

The QT interval was measured from 12-lead digital ECGs (recorded with Marquette MAC 5000, GE Marquette Medical Systems, Milwaukee, WI, USA) using a validated automated algorithm. As previously reported, the QT interval from QRS onset to T-wave end was measured in each lead from the median QRS-T complex, which is a digitally averaged complex from the full 10-second recording and is automatically produced for each lead by the software (QT Guard, GE Marquette Medical Systems). In this study, the QT interval was defined as the mean of these 12 measurements. The QT intervals were corrected for heart rate using a validated nomogram-correction (QTNC) method. The nomogram-corrected
QT interval = measured QT interval + [394.04 msec – (a × heart rate + b)], where “a” and “b” were determined separately for each 10 beats per min heart rate range. Example: for HR 60-68 “a” = -2.18 and “b” = 525.01 msec, for HR 69-78 “a” = -1.64 and “b” = 489.94 msec (see supplementary table).

Genotyping

A total of 15 independent SNPs were reported in 2 GWA studies\textsuperscript{11,13} to have genome-wide significant association with QT duration (P < 5x10^{-8}). Multiple SNPs at a given locus were included only if they were in low linkage disequilibrium with each other. Since the primary NOS1AP SNP is known to have a very strong effect and there is extensive linkage disequilibrium across the region, we only included the top SNP at NOS1AP. Genotyping of genomic DNA was performed using the Sequenom iPLEX Gold assay (MALDI-TOF-mass spectrometry, MassARRAY Analyzer Compact, Sequenom Inc., San Diego, CA, USA) according to the manufacturer’s instructions. Assays were designed using MassARRAY Assay Design 3.1 software. Gender markers were included in the iPLEX design for detection of plate swaps. Genotypes were automatically assigned and manually confirmed using MassARRAY TyperAnalyzer 4.0 software. Passing SNPs were required to have at least 80% genotyping success and Hardy-Weinberg equilibrium P > 0.0001; one SNP failed. Individuals with successful genotype calls for fewer than 8 out of 14 SNPs were excluded from analyses.
Statistical Analysis

Three primary analyses were performed: (1) association between the QT genotype score (QT\text{score}, see definition below) and the QT\text{NC}, (2) observed QT\text{NC} as a predictor of SCD, and (3) QT\text{score} as a predictor of SCD.

A QT genotype score (QT\text{score}) was constructed using the allele copy number and the previously established\textsuperscript{13,19} effect estimates for the 14 SNPs using the following formula: \[\text{QT}\text{score} = [(\text{SNP1 allele copy number}) \times (\text{SNP1 effect estimate in predicted msec})] + [(\text{SNP2 allele copy number}) \times (\text{SNP2 effect estimate in predicted msec})] + \ldots \text{ through SNP14}.\]

SNP genotypes that were missing were imputed to have allele copy number equal to 2 times the coded allele frequency in the total sample. The genotype score was expressed in “predicted msec” of expected change in the QT interval.

All analyses included adjustment for age, sex, and geographic region. In analyses of SCD risk, additional adjustments were performed for use of QT-altering medications and prevalent CHD. To determine the referent quintile in these analyses, we first plotted the QT\text{NC} or QT\text{score} against SCD by undecile (11 equal groups) to determine whether a non-linear U- or J-shaped relationship existed. Multivariable linear regression models were used for cross-sectional association of genotype or QT\text{score} with QT\text{NC} and Cox proportional hazards model for association with time to SCD. Age was accounted for in the time scale of the Cox proportional hazards models for all SCD analyses. For single SNP to QT interval analyses, the threshold for significance was set at \textit{P} < 0.007 (0.05/14 x 2 for a one-sided test of association in the same direction as the original report). For other primary analyses significance was defined as two-sided \textit{P} < 0.05; secondary analyses were exploratory.
Results:

Demographic and clinical descriptive data for the total sample and SCD cases for Health 2000 and Mini-Finland are shown in Table 1.

**QT SNP association with QT interval**

All SNPs but one (SNP rs17779747) were independently associated with QT interval in the same direction as in the QTGEN or QTSCD studies (P < 0.007, Table 2). The correlation of effect estimates in Health2000 to the original QTGEN and QTSCD effect sizes was 0.99. The QT score weighted by the effect sizes observed in QTGEN and QTSCD was a continuous independent predictor of QT_NC in a linear regression model after adjustment for age, sex, and geographic study region (P < 10^-10, Figure 1). The mean QT_NC in the top quintile was 15.6 msec higher than the bottom quintile (P < 10^-84). The QT_score explained 8.6% of variation in QT_NC, after adjustment for age, sex and geographic study region.

**QT interval as a risk factor for SCD**

A 10 msec increase in QT_NC was associated with an increased risk of possible or probable SCD in Cox proportional hazards model after adjustment for sex and geographic study region (HR 1.19, 95% CI 1.07-1.32, P = 0.002) and after additional adjustment for prevalent CHD and QT-altering medication use (HR 1.07, 95% CI 1.054-1.30, P = 0.003). The relationship between QT_NC and SCD appeared to be roughly linear across the range of QT_NC quintiles (Figure 2). Results were unchanged using age- and sex-adjusted residuals (data not shown).
SCD risk was also assessed using a dichotomous previously reported threshold for QT prolongation (QT\textsubscript{NC} > 450 msec for men or > 470 msec for women).\textsuperscript{9} The risk of SCD was 1.3% below and 24% above this threshold (HR 13.3, 95% CI 4.7-37.7, P=1x10\textsuperscript{-6}, after adjustment for sex and geographic region; HR 12.7, 95% CI 4.2-38.6, P=7x10\textsuperscript{-6} after additional adjustment for prevalent CHD and QT-altering drugs). Significance testing using Fisher’s exact test without covariate adjustment was similar (P = 6x10\textsuperscript{-5}).

\textit{QT\textsubscript{score} and risk for SCD}

None of the SNPs that contributed to the QT\textsubscript{score} were associated with SCD risk, when considered individually (Table 2). The continuous QT\textsubscript{score} as a predictor of possible or probable SCD showed a non-significant increase in SCD risk for increasing QT\textsubscript{score} (HR 1.30 per 10 predicted msec increase in QT\textsubscript{score}, 95% CI 0.87-1.94, P = 0.20, after adjustment for sex and geographic region). Conditioning on identical exclusion criteria applied to the QT\textsubscript{NC}to SCD analyses (ECG unavailable, >80 yo, pacer, LBBB, RBBB, QRS >120, using QT-prolonging drug, using digoxin) did not change the finding.

In secondary post-hoc analyses, the QT\textsubscript{score} plotted against SCD by QT\textsubscript{score} quintile suggested a U-shaped relationship (Figure 3) so the middle quintile was considered as the referent category. The risk of SCD was higher in top QT\textsubscript{score} quintile compared with the middle quintile (HR of 1.92, 95% CI 1.05-3.58, P = 0.04 with adjustment for sex and geographic region; and HR 1.90, 95% CI 1.02-3.55, P = 0.04 with additional adjustment for CHD and QT-altering drugs).

\textbf{Discussion:}
We strongly replicated the association between several recently identified common genetic variants and the electrocardiographic QT interval individually and in aggregate. We confirmed the relationship between the QT interval and SCD. There was no evidence for a linear relationship between and SCD risk. In post-hoc secondary analysis, there appeared to be a non-linear relationship between a QT\textsubscript{score} and SCD with increased SCD risk at fourth and fifth QT\textsubscript{score} quintile compared with the median quintile.

More generally, our findings support the strategy of studying common variants that contribute to a dichotomous trait by harnessing the relationship between common variants and an intermediate phenotype. It is well established that the rare Mendelian diseases of extremes of QT duration, the long QT syndrome (LQTS)\textsuperscript{3,20,21} and short QT syndrome (SQTS)\textsuperscript{22-26} are risk factors for SCD, but this is the first illustration that multiple common variants that contribute to repolarization, together, affect risk of SCD in the general population. Of note, none of the individual SNPs that constitute the score were independently associated with SCD, so they would not have been detectable in primary analyses based on association to SCD risk.

In our study, the QT genotype score was highly associated with the observed QT interval, strongly replicating the findings of the QTGEN\textsuperscript{11} and QTSCD\textsuperscript{13} studies. In the QTGEN study, the top quintile of QT genotype score was associated with an approximately 9-12 msec higher QTc compared with nearly 16 msec in our study.

The strength of the QT score effect in our study in comparison to prior reports was somewhat surprising. One would typically expect to see smaller effects in a replication cohort than those observed in the discovery cohorts due to a tendency to overestimate effect sizes ("winner’s curse") in initial discoveries. However, this bias is most pronounced for effects of
borderline significance, whereas most discoveries in QTGEN and QTSCD greatly exceeded genome-wide significance thresholds.

The increased effect of QTscore on observed QT in our study may have resulted from more precise QT measurements and possibly more accurate adjustment for heart rate than in the prior studies. The measurement methods used in the Health 2000 have shown high reproducibility.27 Alternately, Finnish individuals may have a simpler genetic architecture,28 attributable to a founder effect resulting in loss of some rare variants with comparatively strong effect. The comparatively strong effects could also be due to chance alone.

Consistent with prior reports,9 prolonged QT interval was associated with increased risk of SCD. The QT interval was a continuous predictor of SCD risk across the range of QT intervals, but, most strikingly, there was a more than 10-fold increase in SCD risk above one published threshold for prolonged QT.9

Despite QTscore being a strong predictor of QT interval, a significant linear relationship between the score and SCD was not observed (HR 1.30 per 10 predicted msec increase in QTscore, 95% CI 0.87-1.94, P = 0.20). However, in exploratory analysis, the genotype-based QTscore was associated with an increased SCD risk in the fourth and fifth QTscore quintile compared with the median quintile. The comparatively weak effect of the QT genotype score on SCD risk (compared with the QT interval itself) may result from lack of power, lack of true effect, or may arise because not all QT-prolonging alleles actually increase SCD risk. In future studies, the association of each individual SNP with SCD risk could be assessed, and a genotype-based score could be derived for SCD risk rather than QT effect, but this would need to be tested in an independent sample. How might a QT genotype score offer additional risk prediction to the observed QT? Rather than simply reflecting the repolarization time, the QTscore may be a
measure of susceptibility to arrhythmogenic stimuli. Uniform repolarization is maintained by multiple redundant mechanisms, a concept termed “repolarization reserve”.29,30 A single defect in one of these redundant pathways may reduce repolarization reserve but remain subclinical (and not reflected in the measured QT interval) until a “second hit” such as a drug exposure or myocardial ischemia un masks the defect and provides the substrate for fatal arrhythmia. Indeed, many SCD cases in our study occurred on a background of risk factors for myocardial ischemia. The QTscore also may represent a subject’s lifelong exposure to genetically determined QT prolongation, and may be more strongly associated with SCD than the QT interval measured in the resting, unperturbed state at one point in time.

Common variants in NOS1AP have been previously reported to be associated with the QT interval,11,13,31-39 in individuals with congenital LQTS,40,41 and more recently with SCD in unselected populations.5,6 Specifically, two independent signals have been associated with SCD: rs16847548 which is also associated with the QT interval, and rs12567209, which is associated with SCD only. The NOS1AP variant in our study (rs12143842) is correlated to rs16847548 ($r^2 = 0.818$) but not to rs12567209 ($r^2 = 0.027$). Though the NOS1AP SNP in our study did not reach statistical significance for association with SCD on its own (HR 1.31, P=0.06), it has previously been shown to be associated with SCD with nearly identical hazard ratios of 1.26-1.33.6,34 Of note, in prior studies, adjustment for QT interval attenuated but did not eliminate the association between rs16847548 and SCD, indicating that at least some of the effect of the rs16847548 (or its proxies) is mediated through its QT-prolonging effect.

Aside from these NOS1AP variants, relatively few common variants that contribute to SCD risk have been identified. Common SCD variants may be difficult to identify because SCD is a heterogeneous phenotype, representing the downstream end product of diverse underlying
causes, case adjudication is challenging and often retrospective, and studies are generally underpowered because of the challenge of enrolling large SCD cohorts. The use of intermediate phenotypes can prove fruitful as in the relationship of common variants to low density lipoprotein which are also generally related to MI.42

The methodologic advantages of this study are its use of large, population-based cohorts, prospective ascertainment of clinical data, a high rate of autopsies among SCD cases, and complete follow-up. The major limitations of this study are its low power to detect individual SNP effects due to small sample size, possible survivor bias resulting from the older age at time of DNA collection in the Mini-Finland study, and imprecision in the case adjudication for SCD that relied on administrative data sources. Misclassification of non-cardiac deaths as SCD could bias towards the null hypothesis of finding no association. Additionally, the SCD definition employed relies heavily on the presence of concomitant heart disease and thus may under-sample primary arrhythmic sudden deaths, a group in whom genetic causes are potentially more important. Lastly, not all QT prolongation is associated with increased SCD, such as that associated with amiodarone or ranolazine use. Analogously, it is possible that some variants that alter repolarization are arrhythmogenic while others are not.

In conclusion, our study strongly replicates the association between common genetic variants and the QT interval and suggests a relationship between these variants in aggregate and SCD. As additional QT interval variants are identified, these may add additional prognostic information to such genotype scores.

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**Conflict of Interest Disclosures:** None

**References:**


34. Eijgelsheim M, Aarnoudse AL, Rivadeneira F, Kors JA, Witteman JC, Hofman A, van Duijn CM, Uitterlinden AG, Stricker BH. Identification of a common variant at the


Table 1: Demographic and clinical characteristics of study participants and SCD cases in the Health 2000 and Mini-Finland surveys.

<table>
<thead>
<tr>
<th></th>
<th>Entire cohort</th>
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<tbody>
<tr>
<td></td>
<td>Health 2000</td>
<td>Mini-Finland</td>
</tr>
<tr>
<td></td>
<td>(n=6,091)</td>
<td>(n=717)</td>
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<tr>
<td>Age yrs, mean ± SD</td>
<td>52 ± 13</td>
<td>63 ± 8</td>
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<tr>
<td>Female, n</td>
<td>3,261</td>
<td>421</td>
</tr>
<tr>
<td></td>
<td>(54%)</td>
<td>(59%)</td>
</tr>
<tr>
<td>Hypertension, n</td>
<td>2,736</td>
<td>459</td>
</tr>
<tr>
<td></td>
<td>(45%)</td>
<td>(64%)</td>
</tr>
<tr>
<td>Dyslipidemia,* n</td>
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<td>640</td>
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<tr>
<td></td>
<td>(86%)</td>
<td>(89%)</td>
</tr>
<tr>
<td>Diabetes, n</td>
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<td></td>
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<td>(11%)</td>
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<tr>
<td>Current smoker, n</td>
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<td></td>
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<td>Coronary heart disease, n</td>
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<td>QT prolonging meds, n</td>
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<td>Heart rate bpm, mean ± SD</td>
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<td>QT msec, mean ± SD</td>
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<td>QTnc msec, mean ± SD</td>
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</tr>
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</table>

*dyslipidemia defined as LDL cholesterol >3.0 mmol/L, triglycerides >2.0 mmol/L, or HDL cholesterol <1.0 mmol/L in men or HDL cholesterol <1.2 mmol/L in women
Table 2: Individual SNP effects and genotyping success. SNP effects are represented as the change in QT (in msec) per copy of the coded allele (for SNP vs. QTNC), selected based on a positive QT interval effect in the QTGEN or QTSCD publications, and hazard ratio for SCD per copy of the coded allele (for SNP vs. SCD). Values represent the additive effect of each coded allele.

<table>
<thead>
<tr>
<th>Nearest gene</th>
<th>Chr</th>
<th>Pos.*</th>
<th>SNP</th>
<th>Genotyping</th>
<th>SNP vs. QTnc</th>
<th>SNP vs. SCD</th>
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<tbody>
<tr>
<td></td>
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<td>coded allele</td>
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Chr = chromosome; Pos = genome position; Cod. freq. = coded allele frequency; HWE, Hardy-Weinberg equilibrium
*SNP positions are shown in reference to NCBI reference sequence 36, †call rates are shown for each individual SNP after exclusion of individuals with <80% genotyping success for each genotyping pool separately; ‡ HR estimated using Cox proportional hazards model with age as the time scale
Figure Legends:

**Figure 1.** The observed difference in QT<sub>NC</sub> by QT<sub>score</sub> quintile (n = 1,103 per quintile) in comparison to the lowest quintile (Q1) and the predicted difference in QT<sub>NC</sub>. Error bars represent 95% confidence intervals. Note, QT<sub>score</sub> quintile includes exclusion for unavailable ECGs (ECG needed for QT<sub>NC</sub> calculation).

**Figure 2.** A graded relationship was observed between QT<sub>NC</sub> quintile (n = 1,175 subjects per quintile) and hazard ratio for SCD after adjustment for sex, geographic region, prevalent CHD, and use of QT-altering medications. Error bars represent the 95% CIs of the HR for SCD.

**Figure 3.** There was a non-linear relationship with hazard ratio for SCD across the range of QT<sub>score</sub> by quintile (n = 1,289 subjects per quintile). Error bars represent the 95% CIs of the HR for SCD. * p ≤ 0.05. Note, QT<sub>score</sub> quintile does not include exclusion for unavailable ECGs (hence quintiles slightly larger than shown in Figure 1).
Common Genetic Variants, QT Interval and Sudden Cardiac Death in a Finnish Population-Based Study
Peter A. Noseworthy, Aki S. Havulinna, Kimmo Porthan, Annukka M. Lahtinen, Antti Jula, Pekka J. Karhunen, Markus Perola, Lasse Oikarinen, Kimmo K. Kontula, Veikko Salomaa and Christopher Newton-Cheh

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SUPPLEMENTAL MATERIAL

Supplementary table 1. Nomogram-corrected QT interval

Nomogram-corrected QT interval = measured QT interval + correction value

correction value (ms) = 394.039219191961 – (a × heart rate + b)

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