ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals

**BACKGROUND:** QT interval, measured through a standard ECG, captures the time it takes for the cardiac ventricles to depolarize and repolarize. JT interval is the component of the QT interval that reflects ventricular repolarization alone. Prolonged QT interval has been linked to higher risk of sudden cardiac arrest.

**METHODS AND RESULTS:** We performed an ExomeChip-wide analysis for both QT and JT intervals, including 209,449 variants, both common and rare, in 17,341 genes from the Illumina Infinium HumanExome BeadChip. We identified 10 loci that modulate QT and JT interval duration that have not been previously reported in the literature using single-variant statistical models in a meta-analysis of 95,626 individuals from 23 cohorts (comprised 83,884 European ancestry individuals, 9,610 blacks, 1,382 Hispanics, and 750 Asians). This brings the total number of ventricular repolarization associated loci to 45. In addition, our approach of using coding variants has highlighted the role of 17 specific genes for involvement in ventricular repolarization, 7 of which are in novel loci.

**CONCLUSIONS:** Our analyses show a role for myocyte internal structure and interconnections in modulating QT interval duration, adding to previous known roles of potassium, sodium, and calcium ion regulation, as well as autonomic control. We anticipate that these discoveries will open new paths to the goal of making novel remedies for the prevention of lethal ventricular arrhythmias and sudden cardiac arrest.

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Prolonged QT interval has been associated with increased risk of sudden cardiac arrest (SCA), a major cause of mortality, with between 180,000 and 450,000 cases of sudden cardiac arrest in the United States of America annually. Because the vast majority of sudden cardiac arrest occurs in the absence of clinical features that would bring a victim to medical attention, identifying additional risk factors and dissecting the pathogenesis of disease are of high importance. In this study, we conduct ExomeChip-wide analyses in 95,626 population-based multiethnic individuals to interrogate the role of a largely unstudied class of variation on ventricular repolarization in the population—coding single nucleotide variants. These variants fill in the gap between the extremely rare large-effect coding variants that result in the Mendelian long- and short-QT syndromes and the common small-effect largely noncoding variation identified through genome-wide association studies. The focus on exons and coding variants has an added benefit of directly implicating genes. Our approach of focusing on coding variants and both QT and JT intervals measures has identified 10 novel loci associated with ventricular repolarization and has implicated 17 specific genes, 7 of which are in novel loci. Our analyses show a role for myocyte internal structure and interconnections in modulating QT interval duration, adding to previous known roles of potassium, sodium, and calcium ion regulation, as well as autonomic control. We anticipate that these discoveries will open new paths to the goal of making novel remedies for the prevention of lethal ventricular arrhythmias and sudden cardiac arrest.

Heritability estimates of QT interval are between 30% and 40%, indicating that genetic variants play a large role in modulating QT interval in the general population. Mendelian syndromes of QT interval (long- and short-QT syndrome), which lead to increased risk of cardiac arrhythmias and SCA, occur in ≈1 in 2000 individuals and are caused by variants in ion channels or their interacting proteins. Previous candidate gene and genome-wide association studies (GWAS), largely screening common noncoding variants, have identified 35 loci containing variants that modestly influence QT interval, the largest of these studies, the QT Interval International GWAS Consortium (QT-IGC), included a discovery population of 760,61 European ancestry individuals.

In this study, we conduct ExomeChip-wide analyses in population-based samples to interrogate the role of a largely unstudied class of variation on ventricular repolarization in the population—coding single nucleotide variants (SNVs). These variants fill in the gap between the extremely rare large-effect coding variants that result in the Mendelian long- and short-QT syndromes and the common small-effect largely noncoding variation identified through GWAS. The focus on exons and coding variants has an added benefit of directly implicating genes. By contrast, noncoding variation typically implicates a region of the genome, often containing multiple genes, and therefore requiring extensive functional experiments to implicate a specific gene. Furthermore, in this study, we examine both QT and JT interval to more comprehensively examine ventricular repolarization. We have previously observed that variation in specific loci can influence ventricular depolarization and repolarization in a concordant fashion.

We performed a meta-analysis of 23 cohorts including 95,626 multiethnic individuals comprised 83,884 European ancestry individuals, 9610 blacks, 1382 Hispanics, and 750 Asian individuals (Table I in the in the Data Supplement). Each individual was genotyped for 191,740 coding SNVs in 17,341 genes using the Illumina Infinium HumanExome BeadChip (ExomeChip), along with 17,709 noncoding SNVs of known importance from previous GWAS and variants tiling across the genome. These variants were chosen by evaluating ≥12,000 exome sequences for coding variants that appeared in at least 3 individuals.

**METHODS**

The data, analytic methods, and study materials will be made available to other researchers for purposes of reproducing the results, subject to Data Use/Sharing Agreements adopted by individual participating cohorts. GWAS summary results will be available through the CHARGE Consortium Summary Results webpage available at dbGaP (phs000930). This study was approved by local institutional review boards, and all participating subjects gave informed consent (detailed ethics statements in the Data Supplement).

**SNV Association Tests and Meta-Analysis**

Detailed methods are provided in the Data Supplement. Briefly, all cohorts excluded individuals with QRS intervals ≥120 ms, heart rate <40 beats per minute or >120 beats per
RESULTS

QT Interval ExomeChip Analysis Identifies 6 Novel Loci

Meta-analysis identified SNVs in 25 loci associated with QT interval at ExomeChip-wide significance ($P<2\times10^{-7}$; Figure I in the Data Supplement). Of these, 19 loci were previously associated with QT interval, and 6 loci were novel (Table 1). At 4 of these novel loci (PM20D1, SLC4A3, CASR, and NRAP), the top hit is a nonsynonymous variant. For the 2 novel loci where the index SNV is a noncoding variant, no genes in these loci harbored coding SNVs associated with QT interval. Analyses stratified by ethnicity found similar effect sizes between European ancestry individuals and blacks and same general direction of effects in the much smaller Hispanic (n=1382) and Chinese (n=750) cohorts (Table II and Figure II in the Data Supplement).

Nineteen of the 25 loci associated with QT interval at ExomeChip-wide significance in our study had been associated with QT interval in prior European ancestry GWAS studies (Table 2, *P value). Table 2 detail the 35 known QT loci identified from prior GWAS of European ancestry individuals. Of the 14 previously identified loci for which the most significant SNV in our current study is a coding variant (Table 2, A), 3 loci reached ExomeChip-wide significance in our study (*P value). Of the 21 previously identified loci for which the most significant SNV in our study is a noncoding variant not in LD ($r^2>0.8$) with a nearby coding variant, 16 loci exceeded the significance threshold in our study (Table 2, B, *P value). For 5 of these 16 loci where the top signal was a noncoding SNV, they nonetheless harbored coding variants in ≥1 nearby genes that also reached ExomeChip-wide significance (Table II in the Data Supplement).

| Nearby Gene | SNV | Chr | Coded/Noncoded Allele | CAF  | Effect in ms (SE) | P Value  | Function  | Gene(s) With Independent Coding Variation | DEPICT Implicated Gene(s) | eQTL |
|-------------|-----|-----|-----------------------|------|------------------|---------|-----------|------------------------------------------|---------------------------|------|
| PM20D1      | rs1361754 | 1   | G/A                  | 0.511 | 0.47 (0.08)      | 1E-09   | Nonsynonymous | PM20D1                                  | PM20D1, *NUCKS1, RAB7L1, *SLC4A1   |      |
| SLC4A3      | rs55910611 | 2   | AVG                  | 0.006 | -3.06 (0.61)     | 2E-07   | Nonsynonymous | SLC4A3                                  |                           |      |
| CASR        | rs1801725 | 3   | T/G                  | 0.126 | -0.58 (0.12)     | 4E-08   | Nonsynonymous | CASR                                    | CSTA                      |      |
| ZNF37A      | rs4934956 | 10  | T/C                  | 0.497 | 0.58 (0.10)      | 2E-10   | Intergenic  | NRP, NRAP                                |                           |      |
| NRP         | rs3189030 | 10  | A/G                  | 0.299 | -0.48 (0.09)     | 4E-08   | Nonsynonymous | NRAP                                    | CASP?*                    |      |
| GOSR2       | rs17608766 | 17  | C/T                  | 0.123 | 0.72 (0.12)      | 3E-09   | UTR3                   |                                          | RRPM1                     |      |

Significance was determined from analysis of inverse rank normal transformed residuals to avoid P value inflation from the analysis of rare variants. Effect size estimates in milliseconds (ms) are reported from untransformed analyses. n=95 626 number of samples. DEPICT* genes pass FDR <5% cutoff. Expression quantitative trait loci (eQTL) genes are pulled from the Genotype-Tissue Expression portal (GTEX) using the representative SNV and GWiS independent SNVs. CAF indicates coded allele frequency; DEPICT, Data-driven Expression-Prioritized Integration for Complex Traits; FDR, false discovery rate; GWiS, genome-wide significance; SNV, single-nucleotide variants; and UTR3, three prime untranslated region.

*Gene if the eQTL is in the left ventricle.
Table 2. Thirty-Five Loci Previously Associated With QT Interval

| Nearby Gene | SNV        | Chr | Coded/Noncoded Allele | CAF   | Effect in ms (SE) | P Value | Function | QT-IGC Implicated Gene(s) | Gene(s) With Independent Coding Variation | DEPICT Implicated Gene(s) | eQTL |
|-------------|------------|-----|-----------------------|-------|------------------|---------|----------|--------------------------|---------------------------------------------|--------------------------|------|
| A, Known QT loci with coding variant as top SNV |
| RNF207  | rs709209  | 1   | G/A                   | 0.379 | 1.23 (0.09)      | 1E-48*  | Nonsynonymous | RNF207(c) | RNF207 | GPR153                  |
| SP3      | rs1047640 | 2   | C/T                   | 0.120 | 0.60 (0.12)      | 3E-06   | Nonsynonymous |           | SP3                           |
| TTN-CCDC141 | rs72648998  | 2   | T/C                   | 0.054 | 1.00 (0.18)      | 3E-09* | Nonsynonymous | CCDC141(i),TTN    | TTN                          | FEBP7, PRKRA               |
| SPT52L   | rs192861441 | 2   | A/G                   | 0.004 | −2.22 (0.67)     | 3E-04   | Nonsynonymous | SMTS52L(t),SGOL2L(p) |                               |
| C3ORF75  | rs2276853  | 3   | G/A                   | 0.411 | −0.36 (0.08)     | 2E-05   | Nonsynonymous | KHL18(0),PTPN23(0),SCAP(0),SETD2(0),MYL3(3) | NBEAL2                           |
| SMARCAD1 | rs7439869  | 4   | T/C                   | 0.378 | 0.41 (0.08)      | 8E-07   | Nonsynonymous |           | SMARCAD1                         |
| GMPR     | rs1042391  | 6   | T/A                   | 0.551 | −0.42 (0.09)     | 3E-06   | Nonsynonymous | GMPR(k),ATXN1(p) | GMPR | GMPR                          |
| KCNH2    | rs1805123  | 7   | G/T                   | 0.214 | −1.47 (0.10)     | 7E-51*  | Nonsynonymous | KCNH2(3) | KCNH2                         |
| LAPT4M8  | rs17831160 | 8   | A/G                   | 0.030 | −0.64 (0.24)     | 3E-03   | Nonsynonymous |           |                               |
| AZIN1    | rs143025416 | 8   | A/G                   | 0.001 | 4.90 (1.55)      | 2E-03   | Nonsynonymous |           |                               |
| GBF1     | rs143226354 | 10  | T/C                   | 8.89E-05 | 14.18 (4.66)    | 4E-03   | Splicing/  | ACTR1A(i)                         |
| ATP2A2   | rs11068997 | 12  | A/G                   | 0.040 | −0.94 (0.21)     | 4E-07   | Nonsynonymous | VPS29(t),GPAT23(t),ARPC3(t),C12ORF24(t),ATP2A2(p) | GIT2, TCTN1, ATP2A2, PPTC7 |
| USP50-TRPM7 | ns042919   | 15  | A/G                   | 0.097 | −0.57 (0.14)     | 4E-05   | Nonsynonymous |   |                               |
| CREBBP   | rs143903106 | 16  | T/G                   | 0.001 | 4.10 (1.46)      | 5E-03   | Nonsynonymous | TRAP1(i)                         |
| B, Known QT loci with noncoding variant as top SNV |
| TCEA3     | rs1077514  | 1   | G/A                   | 0.179 | −0.58 (0.11)     | 4E-08*  | Intronic | TCEA3(3)                         | TCEA3†, ASAP3               |
| NOS1AP    | rs12143842 | 1   | T/C                   | 0.240 | 3.18 (0.10)      | 3E-255* | Intergenic |           |                               |
| ATPB1     | rs10919071 | 1   | G/A                   | 0.115 | −1.37 (0.13)     | 3E-30*  | Intronic | ATPB1(3),NME7(1)          | NME7                          |
| SLCBA1    | rs2540226  | 2   | T/G                   | 0.482 | 0.24 (0.08)      | 2E-03   | Intergenic | SLCBA1(p)                       | THUMPD2                      |
| SCN5A-SCN10A | rs12053903  | 3   | C/T                   | 0.379 | −0.88 (0.09)     | 1E-26*  | Intrinsic | SCN5A(p),SCN10A             | SCN5A, SNORA6, SCN5A§            |
| SLC4A4    | rs7689609  | 4   | C/T                   | 0.212 | 0.64 (0.12)      | 4E-08*  | Intronic |                               |                               |
| GFRA3     | rs4835768  | 5   | G/A                   | 0.485 | 0.34 (0.08)      | 7E-05   | Intergenic | FAM138(t),ETF1(p)          | MYOT, FAM138               |
| SLC35F1-PLN | rs111537300 | 6  | C/T                   | 0.467 | 1.41 (0.08)      | 5E-74*  | Intergenic | PLN(i)                          | S5X10                         |
| CAV1      | rs3807989  | 7   | A/G                   | 0.429 | 0.54 (0.08)      | 4E-12*  | Intrinsic | CAV1(p),CAV2(p)            | ACC002066.1                  |
| NCOA2     | rs2926707  | 8   | G/T                   | 0.348 | 0.31 (0.09)      | 3E-04   | Intrinsic |                               |                               |
| KCNQ1     | rs2074238  | 11  | T/C                   | 0.074 | −3.58 (0.16)     | 8E-130* | Intrinsic | C110RF21(t),PHEMXI(t),TSPM32(t),KCNQ1(3) | KCNQ1, KCNQ1                   |
| FEN1-FADS2 | rs1535     | 11  | G/A                   | 0.325 | −0.48 (0.09)     | 8E-10*  | Intronic | FADS1(0),FADS2(0),FADS3(0) | FAD2,1, FADS1, TMEM258          |
| KLF12     | rs1886512  | 13  | A/T                   | 0.381 | 0.57 (0.09)      | 2E-10*  | Intrinsic | KLF12(1)                         | KLF121                       |
| ANKRD9    | rs11704    | 14  | C/G                   | 0.291 | 0.35 (0.09)      | 7E-05   | UTR3      | ANKRD9(0)                         | ANKRD9, ZNF839                |

(Continued)
JT Interval Association Identifies 4 Novel Loci

Although ventricular depolarization and repolarization are often coregulated, this is not universally true. Therefore, to more specifically examine ventricular repolarization, we also investigated genetic associations with JT interval, defined mathematically by subtracting the QRS interval (ventricular depolarization and conduction) from the QT interval, which primarily reflects ventricular repolarization. Among the 15,590 ARIC participants, the correlations ($r^2$) among the intervals were 0.84 for QT and JT; 0.02 for QRS and JT; and 0.08 for QT and QRS. We analyzed JT interval as described above for QT interval while adding QRS interval as an additional covariate to further remove the effect of ventricular depolarization on the analysis. Thirty coding variants in 14 loci were associated with JT interval (Table III in the Data Supplement). Four of these 14 loci were not identified as QT interval loci (Table 3). Hence, at these loci, variants that prolong the QRS interval (depolarization) shorten the JT interval (repolarization). Analyses run stratified by ethnicity found similar effect sizes between European ancestry individuals and blacks (Table III in the Data Supplement).

Use of Coding Variants to Implicate Specific Genes

Leveraging information from nominally significant coding SNVs, we sought to implicate causative genes in each locus by demonstrating that putatively functional coding variants are associated with ventricular repolarization independently of noncoding SNVs. We have previously shown that several QT loci contain multiple independent genetic effects, including some loci harboring multiple significant coding variants (Tables II and III in the Data Supplement). Thus, even if not the top hit at a locus, putative functional SNVs can still implicate a specific gene at a locus. We used the GWIS$^3$ algorithm to determine the number of independent effects in all 45 ventricular repolarization associated loci from Tables 1 through 3 and to identify the SNV that best represents each independent effect in European ancestry individuals (n=83,884; Table IV in the Data Supplement). The SCN5A-SCN10A locus is a particularly illustrative example of the use of this approach. Although coding variants in DLECT, SCN5A, and SCN10A are each ExomeChip-wide significant, after using GWIS, the...
signal coming from the coding variants in DLEC1 and SCN5A is explained by noncoding variants, and only the SCN10A coding variant signal remains (Table V in the Data Supplement). In the Gene(s) with independent coding variation column in Tables 1 through 3, we list the 17 genes in 16 loci that have an independent effect represented by a coding variant.

For the loci listed in Table 2 B, such as the SCN5A-SCN10A locus, where intronic and intergenic variants were included in the analyses, the independent associations in coding SNVs identified by GWIS are independent of the noncoding variants in the region. This analysis implicates 2 genes for involvement in cardiac repolarization among those of European descent: SCN10A and KCNQ1. For the novel loci in Table 1 where a coding SNV is the most significant association in our study, it is unlikely that noncoding variants of importance are present in those loci because the loci were not found during the QT-IGC efforts, a study of similar sample size.

In contrast, for the 14 previously identified QT loci where the top SNV in our study was a coding variant (Table 2, A), the GWIS findings are less conclusive because intronic and intergenic SNVs were largely not examined in these regions. Therefore, to determine whether the associated coding variants are independently associated with QT interval and hence implicate a causal gene, or alternatively, are associated simply because of LD with a more strongly associated noncoding variant not genotyped with the ExomeChip, we performed additional analyses in a subset of the data set, ARIC, that includes both the QT-IGC top SNV, as well as the top SNV, from the current study. We performed conditional analyses at the 7 loci in Table 2, A where significant associations were identified by GWIS (the remaining 7 loci did not have any SNVs identified as significant by GWIS after accounting for multiple testing), by including both the QT-IGC and ExomeChip variants in the same regression model in the ARIC Europeans data set (n=9537; Table VI in the Data Supplement). Conditional analyses demonstrate that the coding variant in SP3 is independent of the top noncoding SNV at this locus discovered from QT-IGC, implicating this gene in QT interval modulation. For GMPR, the coding variant is in almost perfect linkage disequilibrium with the noncoding QT-IGC variant (r²=0.99 in ARIC), suggesting that the coding variant may be the causal variant explaining the QT-IGC signal. For a third locus, RNF207, although conditional analysis suggested that the QT-IGC SNV accounts for the association at this locus, both the top QT-IGC SNV as well as the top SNV from this study are coding variants in high LD, thus implicating the RNF207 gene in myocardial repolarization. For the remaining 4 loci, 1 coding variant is associated because of the stronger noncoding QT-IGC signal (KCNH2); 2 were not properly tested because of no effect in ARIC of the ExomeChip variant (ATP2A2) or the QT-IGC variant (TTM), although there was low LD (r²<0.04) between the coding and noncoding variants, suggesting independence; and 1 was unclear (SMARCAD1), as putting both SNVs in the model significantly altered the β estimates for both SNVs.

In Silico Analyses to Implicate Causal Genes

To further decode the role these loci might play in regulating ventricular repolarization, Data-driven Expression-Prioritized Integration for Complex Traits9 was used to investigate whether identified loci contain genes from functional annotated gene sets/pathways. Included in Tables 1 through 3 in the DEPICT Implicated Gene(s) column is a list of genes with a false discovery rate <5%. Furthermore, we looked up each of the Tables 1 through 3 SNVs in the Genotype-Tissue Expression Portal to identify single-tissue expression quantitative trait loci10,11 (left ventricle expression quantitative trait loci, represented by footnote symbols in tables). Findings for
DISCUSSION

Our approach of focusing on coding variants and both QT and JT intervals has identified 10 novel loci associated with ventricular repolarization and has implicated 17 specific genes, 7 of which are in novel loci. Previous studies have implicated roles for potassium ion regulation, sodium ion regulation, calcium ion regulation, and autonomous control of QT interval, and our results provide support for each of these pathways. SLC12A7 (KCC4), which is highly expressed in the left ventricle, is a potassium chloride cotransporter involved in potassium efflux. CASR is a G protein–coupled receptor that maintains circulating calcium ion homeostasis via parathyroid hormone secretion in the parathyroid and kidney tubule ion handling.

In addition to previously implicated pathways, our analyses highlight a role for genes involved in generating the physical force of contraction inside of cardiomyocytes and for conducting electric signal between cardiomyocytes across the heart. Pathway enrichment analyses using Data-driven Expression-Prioritized Integration for Complex Traits (detailed methods in the Data Supplement) identified the GO category GO:0005916, which comprised the genes that code for fascia adherens, the structure that links myofibrils between cardiomyocytes, and contains N-cadherin. NRAP, found to have a significant independent coding variant, likely anchors terminal actin filaments of myofibrils to other protein complexes beneath the sarcolemma and is expressed exclusively in skeletal muscle and heart. skNAC (skeletal NACA) knockout mice, a muscle-specific isoform of NACA, which was found to have a significant independent coding variant, die between embryonic days 10.5 and 12.5 because of cardiac defects, showing interventricular septal defects and a thin myocardial wall. With these 3 points of evidence combined with the previously known locus and GWAS-implicated gene, TTN, a clear class of genes emerge that influence ventricular repolarization through their effect on myocyte structure.

It is important to note that the intercalated disc, which is the interface between cardiomyocytes, contains fascia adherens, desmosomes, and gap junctions, the last of which is known to play a role in ion-mediated relaying of action potentials between cardiomyocytes and, in combination with the gene NOSTAP, has been implicated as regulating QT interval. In contrast, we implicate a nonion-dependent structural/mechanical interconnect between cardiomyocytes mediated by the fascia adherens.

By looking specifically at ventricular repolarization (JT interval) without the influence of depolarization (QRS interval), we detected additional loci related to ventricular repolarization while teasing apart the differential regulation of the various phases of ventricular conduc- tion. Our current results are consistent with our prior findings that variation in some loci influence ventricular depolarization and repolarization in a discordant fashion, and still other loci are associated with one phenotype and not the other. Although ventricular depolarization and repolarization are often coregulated, the difference in genetic effect indicates this is not universally true. Several limitations should be noted. First, we did not have an additional sample to perform replication studies although results were consistent across the diverse cohorts included in our study (Figures IV–XIII in the Data Supplement). Second, correlation of effect sizes was weak between the European ancestry and Hispanic and Asian populations, limiting extrapolation of findings to these populations.

In summary, we have identified 10 loci newly associated with ventricular repolarization. This brings the total number of ventricular repolarization–associated loci to 45. In addition, we have directly implicated 17 specific genes contained in these loci as likely affecting ventricular repolarization and outlined a class of genes that mechanically control QT interval. These new discoveries will likely allow for the development of novel vectors for the prevention of lethal ventricular arrhythmias and SCA.

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DISCLOSURES

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Footnotes

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