Common Genetic Variation Near the Phospholamban Gene Is Associated with Cardiac Repolarisation: Meta-Analysis of Three Genome-Wide Association Studies

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Abstract

To identify loci affecting the electrocardiographic QT interval, a measure of cardiac repolarisation associated with risk of ventricular arrhythmias and sudden cardiac death, we conducted a meta-analysis of three genome-wide association studies (GWAS) including 3,558 subjects from the TwinsUK and BRIGHT cohorts in the UK and the DCCT/EDIC cohort from North America. Five loci were significantly associated with QT interval at P < 1 × 10⁻⁶. To validate these findings we performed an in silico comparison with data from two QT consortia: QTSCD (n = 15,842) and QTGEN (n = 13,685). Analysis confirmed the association between common variants near NOS1AP (P = 1.4 × 10⁻⁸) and the phospholamban (PLN) gene (P = 1.9 × 10⁻²⁸). The most associated SNP near NOS1AP (rs12143842) explains 0.82% variance; the SNP near PLN (rs11153730) explains 0.74% variance of QT interval duration. We found no evidence for interaction between these two SNPs (P = 0.99). PLN is a key regulator of cardiac diastolic function and is involved in regulating intracellular calcium cycling, it has only recently been identified as a susceptibility locus for QT interval. These data offer further mechanistic insights into genetic influence on the QT interval which may predispose to life threatening arrhythmias and sudden cardiac death.
Introduction

The QT interval on the electrocardiogram (ECG) represents the period of ventricular depolarization and subsequent repolarisation. Individuals with delayed cardiac repolarisation show a longer QT interval and this predisposes them to the development of cardiac arrhythmias. Patients with the rare Mendelian Long QT Syndrome (LQTS) are at risk of sudden cardiac death [1]. Lengthening of the heart-rate corrected QT interval within the normal range is associated with increased coronary heart disease incidence and mortality, as well as all-cause mortality [2,3]. QT prolongation is the most common cause for withdrawal or restriction of drugs that have already been marketed. Furthermore, many potentially valuable drugs fail to be approved or are downgraded to second-line status because they prolong QT and increase risk of serious life threatening arrhythmias, especially torsade de pointes [4].

QT interval length is known to be influenced by various parameters such as heart rate [5], age [6], sex [7], and medications.
and studies have suggested that QT interval at the population level is a genetically influenced quantitative trait with up to 52% heritability [9-11]. Until recently, research into genetic factors influencing QT interval was limited to candidate genes known to have a role in arrhythmogenesis on the basis of their involvement in Mendelian Long or Short-QT Syndrome (LQTS or SQTS) [12–17].

However, an early genome-wide association (GWA) study [18] identified a common genetic variant (rs10494366) in the nitric oxide synthase 1 adaptor protein (NOS1AP) gene region, which has been consistently associated with QT-interval variation across many independent replication studies [19–24]. The NOS1AP variant has been estimated to explain up to 1.5% of QT variance [18], therefore larger GWA studies of QT interval have the potential to detect additional common genetic variants, likely of more modest effect size.

Recently, two consortia (QTGEN [25] and QTSCD [26]) reported meta-analyses of GWAS of QT interval duration in population-based cohorts; these papers describe a number of new loci [25,26]. We report a meta-analysis of three GWA studies totalling 3,558 individuals and test for association between QT interval duration and polymorphisms (SNPs). Subsequently, we performed an in silico association analysis of approximately 2.4 million genotyped or imputed single nucleotide polymorphisms (SNPs). One SNP (rs885170) near NBEA on chromosome 13 exceeded the genome-wide significance threshold, P = 5 × 10−8 based on recent estimations of the genome-wide testing burden for common sequence variation [29,30]. Four other SNPs had P < 1 × 10−6. The first was rs12143842 (P = 2.1 × 10−6), it is located on chromosome 1, upstream of NOS1AP, a gene already identified as prolonging QT interval [18]. The second SNP rs2832357 (P = 2.3 × 10−6) is located on chromosome 21, near GRIK1, the third rs1153750 (P = 6.4 × 10−7) is located on chromosome 6 in an intergenic region in a cluster of SNPs near three genes SLC35F1, C6orf204 and PLN. The final locus, rs6038729 (P = 6.3 × 10−7) is located on chromosome 20, near the BMP2 gene.

Results and Discussion

Meta-analysis results from TwinsUK, BRIGHT and DCCT/EDIC cohorts

The characteristics of the 3,558 individuals included in the meta-analysis are shown in Table 1. Genome wide genotyping was performed using a variety of platforms; therefore we imputed genotypes using the HapMap CEU sample. A total of 2,399,142 genotyped or imputed SNPs met the inclusion criteria for our study; we tested these for association with QT interval using an additive model. We observed highly associated SNPs in five chromosomal regions 1q23.3, 6q22.31, 13q13, 20p13 and 21q21.3 (Figure 1). Possible bias caused by population stratification was checked by calculating the genomic inflation factor λ of the meta-analysis [27,28]. The λ was 1.016 indicating our samples showed little evidence for population stratification and therefore the results of the meta-analysis were not adjusted (Figure 2). Table 2 shows the results by cohort of the most significant SNP for each associated region, Table S1 shows the results for all SNPs with P < 1 × 10−6. One SNP (rs885170) near NBEA on chromosome 13 exceeded the genome-wide significance threshold, P = 5 × 10−8 based on recent estimations of the genome-wide testing burden for common sequence variation [29,30]. Four other SNPs had P < 1 × 10−6. The first was rs12143842 (P = 2.1 × 10−6), it is located on chromosome 1, upstream of NOS1AP, a gene already identified as prolonging QT interval [18]. The second SNP rs2832357 (P = 2.3 × 10−6) is located on chromosome 21, near GRIK1, the third rs1153750 (P = 6.4 × 10−7) is located on chromosome 6 in an intergenic region in a cluster of SNPs near three genes SLC35F1, C6orf204 and PLN. The final locus, rs6038729 (P = 6.3 × 10−7) is located on chromosome 20, near the BMP2 gene.

Results for known LQTS and SQTS candidate genes

There are 11 genes identified to date as being causative for Mendelian single gene forms of LQTS and SQTS. Notably, both of the recent GWAS meta-analyses [25,26] found that common variants in a subset of these genes encoding ion channels, known to cause the Mendelian LQTS, were the most strongly associated with QT interval. We looked up the SNP with the lowest P-value in each of these genes and up to 20 kb upstream and downstream. Only one SNP in KCNE1 (LQT5; rs5787730 A>G; frequency allele A: 31.7%; β = −1.6 ms/allele A; P = 0.00045; Table S2) was found to be significantly associated with QT interval, although not genome-wide significant. This SNP was in linkage disequilibrium with the polymorphisms D6S5N (rs1805128; r² = 0.011;
within 1 Mb of the most significant SNPs of our five associated regions for all SNPs (black diamonds) and for all SNPs except those located within this threshold were used for calculating the variance of QT interval in our meta-analysis.

Figure 2. Quantile-quantile plots of association results of the meta-analysis from TwinsUK, BRIGHT and DCCT/EDIC cohorts. Based on 2,399,142 SNPs in 3,558 individuals from the combined cohorts. The −log10(P) plot of association test for QT interval is shown for all SNPs (black diamonds) and for all SNPs except those located within 1 Mb of the most significant SNPs of our five associated regions (dark grey) [26]. Genomic Control λ was 1.016 [25]. The lower horizontal line denotes the 95% percentile of the results of all SNPs, values lower than this threshold were used for calculating the λ. The upper line indicates the point from where P-values of the complete dataset deviate from the expected line.

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P = 0.87) and rs727957 \((r^2 = 0.010; P = 0.090)\), which were previously found to be associated with prolonged QT interval in a general population [14,31]. None of the other genes showed evidence for association with QT interval in our study.

Follow-up of the top 5 loci

To validate potential associations with QT interval we selected the most associated SNP in each of the five regions from the primary meta-analysis and conducted an in silico comparison with data from the QTSCD and QTGEN consortia (Table 3). This confirmed two of our five loci as being significantly associated with QT interval in the replication at \(P = 5 \times 10^{-8}\); the strongest evidence of association was with a SNP near NOS1AP, rs12143842 (\(P = 1.4 \times 10^{-29}\)). rs10494366 is the NOS1AP polymorphism most commonly associated with QT interval in previous studies [19–24], it reached a P-value of 0.035 in our data-set. This SNP is not strongly correlated to rs12143842 in the HapMap CEU samples \((r^2 = 0.102)\). The rs12143842 polymorphism explains 0.82% variance of QT interval in our meta-analysis.

The second significantly associated locus was at chromosome 6q22.31, near the SLC35F1/C6orf204/PLN loci [rs11153730; P = 1.9 \times 10^{-29}; Table 3; Figure 3]. This SNP is intergenic in a region with only a few genes. Little is known about SLC35F1 and C6orf204, however the most plausible candidate gene is phospholamban (PLN), an inhibitor of the Ca\(^{2+}\)-ATPase isoform 2a (SERCA2a), a Ca\(^{2+}\) transporting intracellular pump located in the sarcoplasmic reticulum (SR) of cardiac muscle cells. The most associated SNP rs11153730 is strongly correlated with two intrinsic SNPs (rs3752581 and rs13192336) in PLN \((r^2 = 0.7\) in HapMap CEU samples). Both SNPs are associated with QT interval \(P = 7.3 \times 10^{-4}\); both imputed.

The frequency of the C allele of rs11153730 near PLN was consistent across studies (49.4% in TwinsUK; 48.1% in BRIGHT; 49.0% in DCCT/EDIC). Each C allele prolongs the standardized QT interval by 0.122 units (corresponding to \(\sim 2.5\) ms) and explains 0.74% variance of QT interval duration (Table 2). The effect size from combining all studies was lower, 0.09 with 0.40% explained variance (Table 3). This decrease in effect size is not unexpected and may be attributed to the “winner’s curse” phenomenon [32].

The effects of the NOS1AP and PLN loci did not show significant heterogeneity between the three studies as tested by the Q test \((P > 0.05, \text{Table S1})[33]\, in total the two most significant loci in our initial meta-analysis explain c. 1.6% of the variance in QT interval duration. We also investigated whether there was any evidence for a gene-gene interaction between the two most significantly associated SNPs in the NOS1AP (rs12143842) and PLN (rs11153730) genes. Analysis revealed no evidence to suggest this \((P = 0.99)\).

Phospholamban and QT interval length

Phospholamban (in its unphosphorylated state) is an inhibitor of the Ca\(^{2+}\)-ATPase isoform 2a (SERCA2a), a Ca\(^{2+}\) transporting intracellular pump located in the SR of cardiac muscle cells. The SR controls contraction and relaxation by regulating intracellular calcium levels. Phosphorylation of PLN reduces inhibition of SERCA2a, leading to activation of the Ca\(^{2+}\) pump, enhanced muscle relaxation rates and decreased Ca\(^{2+}\) levels, thereby contributing to the contractile response elicited by beta-agonists [34,35].

PLN knock-out mice exhibit increased rates of basal myocardial contraction as well as increased rates of basal myocardial relaxation [34,35]. However, the enhanced contractility observed with PLN knockout mice is in contrast to humans lacking PLN who develop a lethal cardiomyopathy. Indeed, several rare (non-HapMap) mutations in the human PLN gene have been associated with either dilated [36] or hypertrophic cardiomyopathy [37], presumably caused by PLN mediated over-inhibition [38,39] or chronic activation of SERCA2a [37] respectively. Interestingly, some of the individuals in the study of Haghhighi et al. [40] who were heterozygous for an Arg14Del mutation presented with ventricular extra systolic beats and ventricular tachycardia.

It has previously been shown that prolongation of cardiac repolarization elevates intracellular Ca\(^{2+}\), potentially increasing the risk of arrhythmias [41]. Del Monte et al. [42] reported that over-expression of SERCA2a in rats reduced ventricular arrhythmias in an ischemia/reperfusion model. Recent evidence showed that intracellular Ca\(^{2+}\) may also influence K\(^{+}\) currents and, thus duration of the action potential [43]. Suppression of SERCA2a by PLN may reduce SR Ca\(^{2+}\) content and lead to QT interval shortening through calmodulin kinase II-dependent alternations in K\(^{+}\) currents [44], whereas SERCA2a over-expression may result in an increased Ca\(^{2+}\) content and QT interval prolongation as shown in mice without underlying cardiac disease [43].

In addition to PLN, neuronal nitric oxide synthase (NOS1) is also involved in regulating intracellular calcium cycling [45]. NOS1AP is a regulator of NOS1. Furthermore, a recent study of transgenic mice with cardiomyocyte-specific NOSI over-expression suggested that the greater intracellular Ca\(^{2+}\) transients, and SR Ca\(^{2+}\) load in these mice following treatment to induce cardiac hypertrophy could be explained, at least in part, by modulation of PLN phosphorylation status [46]. In fact, nNOS-derived NO has
**Table 2.** Results of the most significant SNP from the five regions associated with QT interval in GWAS meta-analysis of TwinsUK, BRIGHT and DCCT/EDIC cohorts.

<table>
<thead>
<tr>
<th>SNP ID</th>
<th>Cohort</th>
<th>Coded Allele Frequency (%)</th>
<th>HWE (P)</th>
<th>Genotyped</th>
<th>Beta (SE)</th>
<th>R² (%)*</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs12143842, chr 1</td>
<td>TwinsUK</td>
<td>24.4</td>
<td>0.11</td>
<td>No</td>
<td>0.22 (0.053)</td>
<td>1.76</td>
<td>3.2×10⁻⁵</td>
</tr>
<tr>
<td></td>
<td>coded allele: T</td>
<td>BRIGHT</td>
<td>26.6</td>
<td>0.89</td>
<td>0.15 (0.046)</td>
<td>0.83</td>
<td>0.0015</td>
</tr>
<tr>
<td></td>
<td>non-coded allele: C</td>
<td>DCCT/EDIC</td>
<td>25.3</td>
<td>0.68</td>
<td>0.085 (0.049)</td>
<td>0.27</td>
<td>0.082</td>
</tr>
<tr>
<td><strong>Meta</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.15 (0.028)</td>
<td>0.82</td>
<td>2.1×10⁻⁷</td>
</tr>
<tr>
<td>rs11153730, chr 6</td>
<td>TwinsUK</td>
<td>48.4</td>
<td>0.024</td>
<td>No</td>
<td>0.21 (0.145)</td>
<td>2.19</td>
<td>3.6×10⁻⁶</td>
</tr>
<tr>
<td></td>
<td>coded allele: C</td>
<td>BRIGHT</td>
<td>48.1</td>
<td>0.45</td>
<td>0.096 (0.004)</td>
<td>0.46</td>
<td>0.017</td>
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<tr>
<td></td>
<td>non-coded allele: T</td>
<td>DCCT/EDIC</td>
<td>49</td>
<td>0.75</td>
<td>0.075 (0.042)</td>
<td>0.28</td>
<td>0.076</td>
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<tr>
<td><strong>Meta</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.12 (0.024)</td>
<td>0.74</td>
<td>6.4×10⁻⁷</td>
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<tr>
<td>rs885170, chr13</td>
<td>TwinsUK</td>
<td>18.7</td>
<td>0.28</td>
<td>No</td>
<td>0.17 (0.058)</td>
<td>0.84</td>
<td>0.0045</td>
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<tr>
<td></td>
<td>coded allele: G</td>
<td>BRIGHT</td>
<td>19.7</td>
<td>0.41</td>
<td>0.22 (0.051)</td>
<td>1.58</td>
<td>1.2×10⁻⁵</td>
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<tr>
<td></td>
<td>non-coded allele: A</td>
<td>DCCT/EDIC</td>
<td>17.6</td>
<td>0.76</td>
<td>0.14 (0.057)</td>
<td>0.55</td>
<td>0.016</td>
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<tr>
<td><strong>Meta</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.18 (0.032)</td>
<td>0.99</td>
<td>1.8×10⁻⁵</td>
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<tr>
<td>rs6038729, chr20</td>
<td>TwinsUK</td>
<td>32.3</td>
<td>0.98</td>
<td>Yes</td>
<td>0.064 (0.046)</td>
<td>0.18</td>
<td>0.16</td>
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<td>coded allele: C</td>
<td>BRIGHT</td>
<td>30.1</td>
<td>0.14</td>
<td>0.21 (0.044)</td>
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<td>non-coded allele: A</td>
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<td>32.3</td>
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<td>0.11 (0.046)</td>
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<td>0.015</td>
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<tr>
<td><strong>Meta</strong></td>
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<td></td>
<td></td>
<td></td>
<td>0.13 (0.026)</td>
<td>0.73</td>
<td>6.3×10⁻⁷</td>
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<tr>
<td>rs2832357, chr21</td>
<td>TwinsUK</td>
<td>2.7</td>
<td>0.77</td>
<td>Yes</td>
<td>0.27 (0.16)</td>
<td>0.37</td>
<td>0.088</td>
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<td>coded allele: G</td>
<td>BRIGHT</td>
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<td>0.2</td>
<td>0.49 (0.12)</td>
<td>1.29</td>
<td>5.3×10⁻⁵</td>
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<td>non-coded allele: A</td>
<td>DCCT/EDIC</td>
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<td>0.40 (0.076)</td>
<td>0.82</td>
<td>2.3×10⁻⁷</td>
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</table>

HWE: Hardy-Weinberg equilibrium test; SE: standard error; N/A: not applicable.
*Percentage of explained variance.
doi:10.1371/journal.pone.0006138.t002

**Table 3.** Results of the five most significant loci from GWAS meta-analysis of TwinsUK, BRIGHT and DCCT/EDIC cohorts and *in silico* comparison with the QTGEN and QTSCD consortia data.

<table>
<thead>
<tr>
<th>SNP</th>
<th>Chr</th>
<th>Position*</th>
<th>Flanking genes (distance to SNP in kb)</th>
<th>Coded Allele</th>
<th>Meta-analysis of TwinsUK, BRIGHT and DCCT/EDIC</th>
<th>QTSCD</th>
<th>QTGEN</th>
<th>META</th>
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<tr>
<td>rs12143842</td>
<td>1</td>
<td>160,300,514</td>
<td>OLFML2B; NOS1AP</td>
<td>Freq T (%)</td>
<td>26</td>
<td>24</td>
<td>26</td>
<td>25</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Beta</td>
<td>0.15</td>
<td>0.16</td>
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<td>0.18</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td>P-value</td>
<td>2.1×10⁻⁷</td>
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<tr>
<td>rs11153730</td>
<td>6</td>
<td>118,774,215</td>
<td>SLC35F1;C6orf204;PLN</td>
<td>Freq C (%)</td>
<td>48</td>
<td>50</td>
<td>50</td>
<td>50</td>
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<tr>
<td></td>
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<td></td>
<td></td>
<td>Beta</td>
<td>0.12</td>
<td>0.091</td>
<td>0.08</td>
<td>0.09</td>
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<td>P-value</td>
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<td>rs885170</td>
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<td>34,095,789</td>
<td>RFC3; NBEA</td>
<td>Freq G (%)</td>
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<td>P-value</td>
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<td>0.28</td>
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<tr>
<td>rs6038729</td>
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<td>7,085,757</td>
<td>BMP2; FUSIP1P2</td>
<td>Freq C (%)</td>
<td>31</td>
<td>32</td>
<td>31</td>
<td>32</td>
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<td>Beta</td>
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<td>0.76</td>
<td>0.0071</td>
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<td>BACH1; GRKI</td>
<td>Freq G (%)</td>
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<td>0.0075</td>
<td>0.022</td>
<td>0.053</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>P-value</td>
<td>2.3×10⁻⁷</td>
<td></td>
<td>0.58</td>
<td>0.031</td>
</tr>
</tbody>
</table>

Freq: allele frequency.
*NCBI Genome build 36.3.
doi:10.1371/journal.pone.0006138.t003
been shown to regulate myocardial relaxation and intracellular Ca\(^{2+}\) decay by promoting PKA-mediated PLN phosphorylation [47] and in nNOS\(^{-/-}\) myocytes, decreased PLN phosphorylation has been shown to decrease the rate of SR Ca\(^{2+}\) reuptake and impair relaxation by inhibiting SERCA2a activity. Whether abovementioned mechanisms are similar in humans awaits confirmation in future studies.

In addition to interaction with the SERCA genes (\textit{ATPT2A1} and \textit{ATP2A2}) and NOS1, it has also been suggested that PLN interacts at the protein level with a number of molecules involved in ATP-dependent transport of Ca\(^{2+}\) (Figure S1). Furthermore, PLN is highly expressed in muscle and heart tissue and is co-expressed with muscle, or heart specific genes (Figures S2 and S3). Together with the data described above these observations suggest that PLN is most likely to influence QT interval through regulation of myocellular calcium cycling.

The current findings indicate that maintaining normal homeostatic calcium cycling is crucial as when imbalanced it can lead to human heart failure. However, PLN may also play a role in cardiac repolarization, which again if disturbed leads to serious arrhythmias. Earlier studies have suggested screening for \textit{PLN} mutations in individuals with dilated cardiomyopathy [48,49]. In view of the fact that both super-inhibition, as well as, over-expression of SERCA2a by PLN may lead to cardiomyopathy and heart failure, it maybe that any therapies directed at PLN will be challenging to develop without disturbing the fine balance between SERCA2a and PLN.

Apart from the discovery of variants in genes causing LQTS and SQTS [13,14,25,26,50] and \textit{NOS1AP} [18–26], very few variants have thus far been consistently associated with QT interval duration in the general population. Our study with 3,558 individuals illustrates the potential of GWAS to identify novel variants playing a role in determining QT interval duration. Our results highlight the consistent role of \textit{NOS1AP} genetic variants in modulating QT interval and confirm the recently identified \textit{PLN} locus. Despite only two loci reaching genome-wide significance overall, and their effects, although positive are modest (<1% of variance), these results must be considered in the context of our sample size. Meta-analyses of larger datasets will no doubt identify additional SNPs with smaller effects or with rarer allele frequencies associated with QT interval.

In summary, our study is amongst the first to report common variants near \textit{PLN} associated with QT interval. Functional relevance of PLN to QT interval duration is supported, it has a well documented role in myocellular calcium cycling, our results suggest that further molecular and functional analyses of this gene is warranted to pursue its role in regulating QT interval duration. Furthermore, genetic variation in the \textit{NOS1AP} gene has also been
associated with risk of mortality in patients using both cardiac and non-cardiac drugs [51,52]. Therefore the observed association between \( \text{PLN} \) and QT interval may also have implications for cardiac and non-cardiac drug development, as QT prolongation is a very common reason for cessation of development or withdrawal of drugs. Further investigation into the potential interaction between \( \text{PLN} \) variants and drug-induced QT prolongation would also be of great interest.

**Materials and Methods**

**Ethics Statement**

All subjects involved in the study gave fully informed written consent for the collection of samples and subsequent analysis. The TwinsUK study received written ethical approval for this study from the National Research Ethics Service (St. Thomas’ Research Ethics Committee Ref, EC04/015). The BRIGHT study received written ethical approval from The London Multicentre Research Ethics Committee. The DCCT/EDIC study received written ethical approval from The Hospital for Sick Children Research Ethics Board.

**Study subjects and SNP genotyping**

**The TwinsUK Study.** Samples from the TwinsUK cohort were genotyped with the Infinium assay (Illumina, San Diego, USA) across three fully compatible SNP arrays, the Hap300 Duo, Hap500, and Hap550 [53]. SNP calling was performed using the Illuminus software [54]. SNPs were excluded if they violated Hardy–Weinberg equilibrium (HWE) \( p<1.0 \times 10^{-6} \), had genotype call rates \(<90\%\); or had a minor allele frequency (MAF) of less than \( 0.01 \). Individuals were excluded if the sample call rate was less than \( 95\% \), autosomal heterozygosity was not between \( 33 \) and \( 37\% \), genotype concordance was over \( 97\% \) with another sample and the sample was of lesser call rate, non-caucasian ancestry either self-identified or identified by cluster analysis in STRUCTURE [55], or unexplained relatedness (estimated proportion of allele shared identical by descent \( >0.05 \) [56]) to >120 other samples. This resulted in GWAS data being available on 305,912 SNPs for 2,256 individuals from 595 dizygotic (DZ) twin pairs and 1066 singletons (among them twins from monozygotic (MZ) twin pairs) from the TwinsUK cohort. This cohort was previously shown to be representative of the general (singleton) UK population [57]. ECG data were available on 1,104 of these individuals. Eight hundred and sixty had automated measurements of the QT interval by the Cardiofax ECG-9020K (Nihon Kohden UK Ltd., Middlesex, UK) and 244 were scored manually using a high-resolution digitizing board (GTCO CalComp Peripherals, USA).

Fifty six individuals were removed from the data set because of atrial fibrillation, QT duration >120 ms or presence of a heart condition (i.e. ischemic heart disease, stroke or bypass surgery). None of the genotyped twins had a pacemaker or used anti-arrhythmic drugs. The dataset for analyses consequently included 1,048 twins, the variances of the regression coefficients were corrected for the uncertainty of the genotypes that were imputed.

**The BRIGHT study.** Two thousand unrelated white European hypertensive individuals from the BRIGHT study (www.brightstudy.ac.uk) were genotyped with the GeneChip Human Mapping 500K Array Set (Affymetrix). Only individuals and SNPs passing WTCCC thresholds for quality control [58] were included in the analysis. Briefly, individuals were excluded if they had >3% missing data or evidence of non-Caucasian ancestry under Eigenstrat analysis [59]. SNPs were excluded if they showed deviation from HWE (\( p<5 \times 10^{-7} \), high levels of missing data (capture rate \(<95\%\) or low MAF \(<1\%\). Twelve-lead ECG recordings (Siemens-Sicard 440; http://www.brightstudy.ac.uk/info/sop04.html), which produces an automated measurement of the QT interval, were available for all subjects. All data were transferred from each recruitment centre by electronic modem to electrophysiologists from the West of Scotland Primary Prevention Study (Professor Peter MacFarlane) for central reporting. Thirteen hundred and ninety two individuals remained in the analysis after exclusion of those having ischemic disease, stroke, or bypass, atrial fibrillation, or QRS duration >120 ms and having full covariate information.

**The DCCT/EDIC Study.** The Diabetes Control and Complications Trial (DCCT)/Epidemiology of Diabetes Interventions and Complications (EDIC) study was a clinical trial and follow-up of subjects with type 1 diabetes. Fourteen hundred forty one patients with type 1 diabetes were recruited for the DCCT [60] and followed-up in EDIC [61]. Genome-wide genotyping in subjects from the DCCT/EDIC was performed using the Illumina 1 M beadchip assay (Illumina, San Diego, USA) of which 841,342 SNPs with a MAF >1% were subsequently analyzed statistically. Autosomal SNPs showing significant association with gender \( (p<10^{-8}) \) or deviating from HWE \( (p<10^{-8}) \) were excluded from the analysis. To reduce the possibility of population stratification, we limited the analysis to individuals who self-identified as white, and excluded individuals who were determined to be admixed between Caucasian and other ethnic groups through population genetic approaches, using Eigenstrat [59] seeding with genotype data from the three major populations genotyped in HapMap Phase II [62].

Twelve-lead resting ECGs were obtained by a certified technician or research nurse at 29 clinics, measured digitally and read according to the revised Minnesota Code at the Central ECG Reading Unit (University of Minnesota, under the direction of Dr. Richard S. Crow) [63]. In brief, at least 1 full min of ECG tracing was obtained consisting of 5 s of each of the leads I, II, III, aVR,aVL, aVF, and V1–V6). Additionally, individuals having ischemic disease, stroke, or bypass, atrial fibrillation, or QRS duration >120 ms were excluded, therefore in total 323 individuals were excluded from the analysis.

**Imputation**

As all three cohorts used different platforms for genome wide genotyping, non-genotyped autosomal SNPs were imputed. For TwinsUK and BRIGHT individuals imputation was performed using Phase II CEU HapMap data (release 22, build 36) as the reference database using IMPUTE version 0.3.2 [64]. For DCCT/EDIC individuals imputation was performed using Phase II CEU HapMap data (release 22, build 36) using MACH v 1.0.16 [62,65].

**Statistical Analyses**

Using regression analysis, we adjusted QT interval for RR interval, age, sex, height, body mass index, hypertension, and QT interval shortening or prolonging drugs (if available) within each cohort. For the TwinsUK sample, an extra covariate for the method of measurement (automatically vs. manually scored) of the QT interval was incorporated. Standardized QT interval residuals were used for further analyses. For the TwinsUK and BRIGHT cohorts, association between standardized corrected QT interval data and autosomal SNPs was tested with an F-test in SNPTEST version 1.1.4 using an additive model and the proper option to account for the uncertainty of the genotypes that were imputed [64]. As the TwinsUK cohort data consisted partly of dizygotic twins, the variances of the regression coefficients were corrected
for the sibship relations using the Huber-White method for robust variance estimation in R [66,67]. In the DCCT/EDIC cohort, SNPs were tested for association with corrected QT interval using an additive model in MACH2QTl version 1.04 [62,65]. Genomic control was performed to check for population stratification [27]. A meta-analysis was conducted in R using the inverse variance-weighted fixed effects method on the beta estimates relative to a constant reference allele to combine the results of TwinsUK, BRIGHT, and DCCT/EDIC cohorts (own software). Only SNPs with MAF > 1%, P > 10^{-6} for the HWE test calculated using the genotypes inferred after imputation by maximum likelihood expectation and an imputation quality score reflecting the observed by expected variance ratio > 0.5 for TwinsUK and BRIGHT (IMPUTE proper_info) and > 0.3 for DCCT/EDIC (MACH r^2) were included in the analysis. Heterogeneity of observed effects was tested by the Q test [33].

QTSCD and QTGEN ‘in silico’ cohorts: description, genotyping and analysis

The QTSCD consortium conducted a meta-analysis of results of GWAS on QT interval from the ARIC, SardiNIA, KORA, GenNOVA and HNR cohorts comprising in total 15,842 individuals (in press [26]). The QTGEN consortium combined the results of GWAS on QT interval from the Framingham Heart Study, the Rotterdam Study, and the Cardiovascular Health study in a meta-analysis including in total 13,685 individuals (in press [25]). Both studies imputed genotype data in order to facilitate the comparison of genotyping results across different platforms. Further details of materials and methods of both consortia can be found elsewhere (in press [25,26]).

We performed a meta-analysis combining our results with those of the QTSCD and the QTGEN consortia for our five most statistically significant independent SNPs using methods as described above.

Supporting Information

Figure S1 PLN protein-protein interaction network. This protein-protein interaction network was generated by the STRING program (http://string.embl.de) after querying the PLN gene using a high confidence score (0.700). Data supporting the interactions illustrated were derived from experimental studies (purple lines), databases (blue lines) and text mining (green lines). The genes that are involved in the calcium signaling pathway are indicated in red, the nodes with purple stars indicate the genes that are associated with cardiovascular diseases as based on functional annotation by DAVID (http://david.abcc.ncifcrf.gov). Only for large nodes are 3D protein structures available in STRING. The colour of the nodes does not encode any information.

Found at: doi:10.1371/journal.pone.0006138.s001 (0.22 MB DOC)

Figure S2 PLN co-expression network. This network is retrieved from the gene co-expression database COXPRESdb (http://coxpresdb.hgc.jp) using the PLN Entrez ID (5350) as the query. The co-expression network is drawn based on rank of correlation from 123 Human microarray experiments released by the NCBI GEO database. The bold grey lines indicate average ranks from 1 to 4. The normal light gray lines indicate average ranks from 5 to 29. The orange lines indicate conserved co-expression based on evidence from the NCBI HomoloGene database and COXPRESdb. The gene names in red indicate muscle or heart specific expression and nodes with purple stars refer to genes that are associated with cardiovascular diseases as based on functional annotation by DAVID (http://david.abcc.ncifcrf.gov). For large nodes 3D protein structures are available in STRING. The colour of the nodes does not encode any information.

Found at: doi:10.1371/journal.pone.0006138.s002 (0.13 MB DOC)

Table S1 All SNPs with p<10^{-6} for the additive model from the meta-analysis of the TwinsUK, BRIGHT and DCCT/EDIC cohorts.

Found at: doi:10.1371/journal.pone.0006138.s003 (0.04 MB DOC)

Table S2 Most significant SNPs from the meta-analysis of TwinsUK, BRIGHT and DCCT/EDIC cohorts within an area 20 kb upstream and downstream of the 11 known candidate genes for LQTS and SQTS.

Found at: doi:10.1371/journal.pone.0006138.s005 (0.04 MB XLS)

Appendix S1 Consortium members and affiliations

Found at: doi:10.1371/journal.pone.0006138.s006 (0.06 MB DOC)

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For the BRIGHT study: We are extremely grateful to all the patients who participated in the study and the BRIGHT nursing team, and to Abisholm Oushpina.

For the DCCT/EDIC study: The content of this article is solely the responsibility of the authors and does not necessarily represent the official views of the National Institute of Diabetes and Digestive and Kidney Diseases or the National Institutes of Health.

For QTSCD: We gratefully acknowledge all participants in the community based studies of ARIC, KORA, SardiNIA, GenNOVA and Heinz Nixdorf Recall Study, and all Study investigators for study design and helpful discussion.

For QTGEN: The QTGEN consortium thanks the participants of the Framingham Heart Study, Rotterdam Study and Cardiovascular Health Study.

Author Contributions

Conceived and designed the experiments: CW MJC HS AP PM YJ. Analyzed the data: IMN CW SJN DW JF NS EZ LVW MDT HS AP PM YJ. Wrote the paper: IMN CW SJN DW JF NS EZ LVW MDT HS AP PM YJ. We thank the staff from the Genotyping Facilities at the Wellcome Trust Sanger Institute for sample preparation, Quality Control and Genotyping led by Leena Peltonen and Panos Deloukas; Le Centre National de Genotypage, France, led by Mark Lathrop, for genotyping; Duke University, North Carolina, USA, led by David Goldstein, for genotyping; and the Finnish Institute of Molecular Medicine, Finnish Genome Center, University of Helsinki, led by Aarno Palotie.

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Author Contributions

Conceived and designed the experiments: CW MJC HS AP PM YJ. Analyzed the data: IMN CW SJN DW JF NS EZ LVW MDT HS AP PM YJ. Wrote the paper: IMN CW SJN DW JF NS EZ LVW MDT HS AP PM YJ. We thank the staff from the Genotyping Facilities at the Wellcome Trust Sanger Institute for sample preparation, Quality Control and Genotyping led by Leena Peltonen and Panos Deloukas; Le Centre National de Genotypage, France, led by Mark Lathrop, for genotyping; Duke University, North Carolina, USA, led by David Goldstein, for genotyping; and the Finnish Institute of Molecular Medicine, Finnish Genome Center, University of Helsinki, led by Aarno Palotie.
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