Common variants in RYR1 are associated with left ventricular hypertrophy assessed by electrocardiogram

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Aims
To identify the genetic risk factors that influence the development of electrocardiographic (ECG) left ventricular hypertrophy (LVH), a major risk factor for cardiovascular (CV) morbidity and mortality.

Methods and results
We performed a genomewide association study (GWAS) of ECG-LVH, in which the community-based Korea Association REsource (KARE) study (8432 controls and 398 cases) was analysed by Affymetrix SNP array 5.0. The GWAS results were validated in hospital-based samples (597 controls and 207 cases). Fourteen single-nucleotide polymorphisms (SNPs) in eight genetic loci (5q35.1, 6p22.3-22.1, 8q24.2, 11p15, 11q21-22.1, 14q12, 17q11.2, and 19q13.1) were associated with ECG-LVH in the original GWAS study \( P < 1 \times 10^{-5} \). Of these SNPs, 12 were genotyped in the hospital sample. There was consistent association with the 19q13.1 region which contains RYR1 gene. The most significant SNP in the region was rs10500279, which had genomewide significance in the combined GWAS/replication sample \( \text{odds ratio} = 1.58 \) (confidence interval: 1.35–1.85), \( P = 1.0 \times 10^{-8} \). Mutations in RYR1, which encodes a major Ca\(^{2+}\) channel in the skeletal muscle, have been reported to correlate with CV diseases.

Conclusion
We performed the first GWAS for ECG-LVH, implicating the skeletal muscle Ca\(^{2+}\) channel protein RYR1 as a genetic risk factor. These results might increase our understanding of the development of ECG-LVH.

Keywords
Genomewide association study • Left ventricular hypertrophy • Electrocardiography • Ryanodine receptor • Cardiovascular disease

Introduction
Left ventricular hypertrophy (LVH) is a major risk factor for cardiovascular (CV) morbidity and mortality. Left ventricular hypertrophy is diagnosed by electrocardiography (ECG) and echocardiography.1–4 Echocardiography is a more sensitive and specific method of detecting LVH than ECG, but its use in large-scale population studies and clinical trials is limited by its prohibitive cost and operational considerations.5

In contrast, ECG is widely available, inexpensive, and less operator-dependent6; thus, ECG data are obtainable in nearly all patients and participants in epidemiological studies.7 Left ventricular hypertrophy is a multifactorial trait; its major determinants include blood pressure (BP), age, gender, and obesity.8 In addition, certain genetic factors, such as angiotensin-converting enzyme,9 guanine nucleotide-binding protein (GNB3),10 insulin-like growth factor,11 and neuropeptide Y,12 regulate the development of LVH. Several studies have reported

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a relationship between LVH and variations in genes that are associated with the renin–angiotensin–aldosterone system and nitric oxide synthase.

Recently, the EchoGen consortium (n = 16,706 subjects of European ancestry, based on five community cohorts) performed a seminal genomewide association study (GWAS) on cardiac structure, based on echocardiography measurements. The GWAS identified one locus (6q42) that correlated with LV diastolic dimensions and four loci (5q23, 12p12, 12q14, and 17p13) that were linked to the aortic root size. Its results, however, explained merely 1–3% of the trait variance that was observed. Considering that the heritability estimate of LV mass ranges between 0.17 and 0.59, many genetic factors remain to be identified.

Most studies that have sought to determine the genetic influence on LVH have used echocardiography to measure LV mass. Yet, a family study by Mayosi et al. estimated higher heritability rates for LVH detected by ECG (ECG-LVH) (39–41%) compared with LVH determined by echocardiography (ECHO-LVH) (21–29%), suggesting that there may be greater genetic susceptibility for ECG-LVH.

Here, we report the first GWAS on ECG-LVH using population-based community cohorts and replicate the results in hospital-based samples to identify genetic risk factors that influence the development of ECG-LVH.

Methods

Original study subjects

The Korea Association Resource (KARE) subjects were described previously. Briefly, the subjects came from two community-based cohorts—the rural Ansung community and the urban Ansan community—both located in KyungGi-Do province near Seoul, Korea. Initially, there were 5018 and 5020 individuals, aged 40–70 years, from Ansung and Ansan, respectively.

Subjects with genotype accuracies below 98% and high missing genotype call rates (>4%), high heterozygosity (>30%), or inconsistency in sex were excluded from subsequent analyses. Individuals who had a tumour were excluded, as were related individuals whose estimated identity-by-state values were high (>0.80). After these quality control steps, 8842 samples were selected, of whom 12 did not undergo ECG. Ultimately, 8830 samples were used for the GWAS.

Left ventricular hypertrophy was diagnosed by ECG, based on the Minnesota Code Classification System. If R amplitude is >26 mm in V5 or V6; R amplitude >20 mm in leads I, II, or III; or aVF or R amplitude >12 mm in the lead aVL (all criteria were measured on the penultimate complete normal beat).

Blood pressure was measured three times in the supine position, and the average value was used for the GWAS. Before the first measurement, participants rested for 5 min, and the three measurements were taken in one arm showing the higher BP at least 3 min apart. Other CV risk factors, such as cholesterol level and fasting glucose level, were measured from blood samples after overnight fasting.

Original study genotypes

Most DNA samples were isolated from the peripheral blood of participants and genotyped using the Affymetrix Genomewide Human SNP array 5.0 (Affymetrix, Inc., Santa Clara, CA, USA). The quality control steps of genotypes have been described elsewhere.

Briefly, the accuracy of the genotyping was determined by Bayesian Robust Linear Modeling using the Mahalanobis Distance (BRLMM) genotyping algorithm. Consequently, 333,651 single-nucleotide polymorphisms (SNPs) had a missing genotype call rate below 0.1%, a minor allele frequency (MAF) >0.1%, and no deviation from the Hardy–Weinberg equilibrium (HWE) (P > 1 × 10⁻⁶). To examine the population stratification, multidimensional scaling analysis and principal component analysis were performed using pruned 44,724 SNP markers among all KARE.

Replication study subjects

The replication study included 207 LVH patients and 597 normal controls, selected from the patient database at the Cardiovascular Genome Center, Yonsei University Health System, Seoul, Korea. Both case and control subjects were independent from those of the original GWAS study. The patient database comprises individuals aged 40–70 years who entered the outpatient clinic or were hospitalized between May 2002 and November 2007 in the Cardiology Division of Severance Cardiovascular Hospital. Electrocardiographic-left ventricular hypertrophy was diagnosed using the same criteria as in the original GWAS—the Minnesota Code Classification System.

The local Ethics Committee approved this study, and informed consent was obtained from all patients.

Replication study genotypes

Single-nucleotide polymorphism selection for the replication study was based on the significance with P-value (<1 × 10⁻⁶). The SNPs were genotyped by TaqMan™ fluorogenic 5’ nuclease assay (Applied Biosystems, Foster City, CA, USA). The final volume of each polymerase chain reaction (PCR) was 5 µL, containing 5 ng genomic DNA, 2.5 µL TaqMan™ Universal PCR Master Mix, and 0.13 µL 40× predesigned TaqMan probe Assay Mix.

Statistical analysis

The ECG-LVH cases and controls were analysed by logistic regression, controlling for covariates, such as antihypertensive drug treatment state, cohort, age, sex, body mass index (BMI), systolic BP (SBP), diastolic BP (DBP), and HDL, LDL, triglyceride, and fasting glucose levels. Statistical analyses were performed using PLINK, version 1.07, using default options and SPSS, v15.0. For the multicollinearity of covariates, we estimated the tolerance and variance inflation factor (VIF) by using the SPSS and described the results in Table 1. Multiple testing of association results was conducted by the Bonferroni correction criteria. The asymptotic HWE tests were conducted using the BRLMM algorithm. The results in the supine position were used to ensure the accuracy of the genotyping data.

Results

Baseline characteristics of subjects

Three hundred and ninety-eight individuals out of the 8830 community-based KARE subjects were diagnosed as ECG-LVH by the Minnesota Code Classification System. The demographics...
and clinical characteristics of the subjects are shown in Table 1. Antihypertensive treatment status, sex, age, BMI, SBP, DBP, and LDL levels differed significantly between the case and control groups of the KARE GWAS. Of the controls in the GWAS, 1217 (14%) subjects had taken antihypertensive medications compared with 72 (17%) cases.

In the hospital-based replication study, antihypertensive treatment status, age, HDL, LDL, and fasting glucose levels differed significantly between the cases and controls. Ninety-nine (17%) of the cases met the multiple comparison criteria (Bonferroni’s correction criterion), a less stringent P-value (\( < 1 \times 10^{-5} \)) was applied to select suggestive signals for further study in the replication sample.

The GWAS on ECG-LVH identified 14 SNPs in eight suggestive association loci: one SNP in 5q35.1 (rs265992, \( P = 2.1 \times 10^{-6} \)), one SNP in 6p22.3-22.1 (rs9295629, \( P = 9.0 \times 10^{-10} \)), five SNPs in 8q24.2 (the most significant SNP: rs4909705, \( P = 2.5 \times 10^{-7} \)), one SNP in 11q21-q22.1 (rs11225822, \( P = 9.7 \times 10^{-5} \)), one SNP in 14q12 (rs1956217, \( P = 9.9 \times 10^{-6} \)), one SNP in 17q11.2 (rs4239268, \( P = 9.5 \times 10^{-7} \)), and three SNPs in 19q13.1 (the best SNP: rs10500279, \( P = 9.5 \times 10^{-7} \)). The signal plots for each of the eight loci are shown in Supplementary material online, Figures S2–S9.

**Validation in replication sample**

Twelve of the 14 SNPs that we identified were genotyped in the replication sample (207 cases and 397 controls). All genotypes had low missing rate (0.1–3.2%) and none of SNPs failed to pass the quality control. The genomic inflation factors \( (\lambda) \) were all lower than 5, the suggested conservative threshold, suggesting the low multicollinearities of covariates.

### Table 1 Clinical characteristics of the KARE and replication study subjects

<table>
<thead>
<tr>
<th>Case vs. control, P-valuea</th>
<th>Collinearity statistics</th>
<th>Replication study subjects</th>
<th>Case vs. control, P-valuea</th>
<th>Collinearity statistics</th>
</tr>
</thead>
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<tr>
<td>Control</td>
<td>Case</td>
<td></td>
<td>Tolerance</td>
<td>VIF</td>
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<td>n</td>
<td>8432</td>
<td>398</td>
<td>597</td>
<td>207</td>
</tr>
<tr>
<td>Treated%</td>
<td>1217 (14)</td>
<td>72 (18)</td>
<td>4.3 ( \times 10^{-2} )</td>
<td>0.90</td>
</tr>
<tr>
<td>Men%</td>
<td>3916 (46)</td>
<td>261 (66)</td>
<td>3.0 ( \times 10^{-8} )</td>
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<td>Mean (SD)</td>
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<td>Age</td>
<td>52.1 (8.9)</td>
<td>55.1 (9.2)</td>
<td>2.2 ( \times 10^{-11} )</td>
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<td>Body mass index</td>
<td>24.6 (3.1)</td>
<td>23.6 (2.9)</td>
<td>1.1 ( \times 10^{-11} )</td>
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<td>Systolic blood pressure (mmHg)</td>
<td>117.1 (18.0)</td>
<td>128.0 (20.8)</td>
<td>1.7 ( \times 10^{-31} )</td>
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<td>Diastolic blood pressure (mmHg)</td>
<td>74.9 (11.5)</td>
<td>79.4 (11.7)</td>
<td>1.6 ( \times 10^{-14} )</td>
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<td>HDL cholesterol (mg/dL)</td>
<td>44.6 (10.1)</td>
<td>45.3 (10.6)</td>
<td>1.7 ( \times 10^{-1} )</td>
<td>0.80</td>
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<tr>
<td>LDL cholesterol (mg/dL)</td>
<td>116.0 (32.2)</td>
<td>110.3 (32.7)</td>
<td>6.8 ( \times 10^{-4} )</td>
<td>0.93</td>
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<td>Triglyceride (mg/dL)</td>
<td>163.0 (106.1)</td>
<td>162.6 (98.6)</td>
<td>9.4 ( \times 10^{-1} )</td>
<td>0.77</td>
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<tr>
<td>Fasting glucose level (mg/dL)</td>
<td>87.7 (22.0)</td>
<td>86.9 (19.4)</td>
<td>4.8 ( \times 10^{-3} )</td>
<td>0.94</td>
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</table>

**Electrocardiographic-left ventricular hypertrophy genomewide association study**

The ECG-LVH GWAS used KARE genotyped data previously reported by Cho et al. A GWAS of 333,651 SNPs was performed using community-based LVH cases (n = 398) and controls (n = 8432); a quantile–quantile (Q–Q) plot is shown in Supplementary material online, Figure S1A. The genomic inflation factor \( (\lambda) \) was 1.00, which was evidence against population stratification or inflated results.

Figure 1A illustrates the Manhattan plot of the GWAS results; the results that are based on P-values lower than \( 1 \times 10^{-3} \) are summarized in Table 2. None of the P-values for the associations met the multiple comparison criteria (Bonferroni’s correction criterion \( P < 1.5 \times 10^{-7} \)). Therefore, instead of Bonferroni’s correction criterion, a less stringent P-value \( (< 1 \times 10^{-5}) \) was applied to select suggestive signals for further study in the replication sample.

The GWAS on ECG-LVH identified 14 SNPs in eight suggestive association loci: one SNP in 5q35.1 (rs265992, \( P = 2.1 \times 10^{-6} \)), one SNP in 6p22.3-22.1 (rs9295629, \( P = 9.0 \times 10^{-10} \)), five SNPs in 8q24.2 (the most significant SNP: rs4909705, \( P = 2.5 \times 10^{-7} \)), one SNP in 11q21-q22.1 (rs11225822, \( P = 9.7 \times 10^{-5} \)), one SNP in 14q12 (rs1956217, \( P = 9.9 \times 10^{-6} \)), one SNP in 17q11.2 (rs4239268, \( P = 9.5 \times 10^{-7} \)), and three SNPs in 19q13.1 (the best SNP: rs10500279, \( P = 9.5 \times 10^{-7} \)). The signal plots for each of the eight loci are shown in Supplementary material online, Figures S2–S9.

**Validation in replication sample**

Twelve of the 14 SNPs that we identified were genotyped in the replication sample (207 cases and 397 controls). All genotypes had low missing rate (0.1–3.2%) and none of SNPs failed to pass the quality control. The genomic inflation factors \( (\lambda) \) were all lower than 5, the suggested conservative threshold, suggesting the low multicollinearities of covariates. Therefore, instead of Bonferroni’s correction criterion, a less stringent P-value \( (< 1 \times 10^{-5}) \) was applied to select suggestive signals for further study in the replication sample.

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Discussion

In this GWAS of ECG-LVH using community-based cohorts, three SNPs in RYR1 in the 19q13.1 locus approached significance; these were replicated in a hospital-based cohort. This GWAS of ECG-LVH contributes to the existing body of literature, which, until now, has focused on ECHO-LVH; studies on the ECG indices reflective of LVH may reflect disparate biological processes compared with anatomical measures by echocardiography.7

A report on the genomewide linkage of ECG-LVH by Mayosi et al.21 identified three suggestive loci: 10q23 for Sokolow–Lyon voltage, 17p13.3 for Cornell voltage product, and 12q14.1 for ECG LV mass. As shown in Figure 1B, no loci overlapped between this report and our findings, which might be attributed to disparate methods of establishing the LVH criteria (we used the Minnesota Code Classification System)23 and differences in the power of detection between linkage studies and GWASs.27 In addition, it was difficult to identify LVH-associated loci that overlapped between the EchoGen GWAS16 and this study, which might reflect the disparate biologies of ECG-LVH and ECHO-LVH.

Several limitations should be addressed with regard to the interpretation of our results. In this study, only Minnesota ECG criteria were used to diagnose ECG-LVH cases. However, Hsieh et al.28 suggested that compared with voltage-only criteria for detecting LVH, composite ECG criteria were more strongly predictive of CV mortality. Further, ECG voltage criteria detect LV wall thickness indirectly. Second, because the sample size of the replication study was not large, we could not rule out the possibility that other suggestive loci, such as DRD1, a known CV risk factor, are associated with ECG-LVH.29 To confirm other suggestive loci, they must be examined in a larger association study.

RYR1 has been well studied with regard to muscle contraction. Regulated increases in intracellular Ca^{2+} are required for many physiological functions, including muscle contraction, secretion, regulation of gene expression, and fertilization.30 Intracellular Ca^{2+} can be elevated via activation of plasma membrane-bound Ca^{2+}-permeable channels or the release of Ca^{2+} from intracellular stores.31 The rise in Ca^{2+} that is required for myocyte contraction is affected by the activation of RYRs, sarcoplasmic reticulum-bound Ca^{2+} release channels.32

Over the past 20 years, several mutations in RYR1 and RYR2 have been identified and linked to skeletal and cardiac diseases.33 Malignant hyperthermia,34 central core disease,34 and catecholaminergic polymorphic ventricular tachycardia35,36 have been associated genetically with mutations in RYR1 or RYR2. Further, several reports in animal models have demonstrated the involvement of RYRs in alterations in LVH, which observed that the density of RYRs decreased in hypertrophied rat hearts, resulting in impaired calcium flux,37 and that RYRs were distributed transmurally during LVH in dogs.38

Based on previous functional studies and the results observed in this study, it would be reasonable to speculate that RYRs are associated with LVH. It is difficult, however, to understand why RYR1, the predominant isoform in the skeletal muscle, has a stronger association with LVH than RYR2, the major isoform in the cardiac muscle [best SNP: rs3766884, OR = 0.81 (CI: 0.69–0.94), P = 0.006]. It is possible that RYR1 or its genetic variants have stronger influence on LVH compared with that of RYR2. Otherwise, RYR1 expression in the vascular smooth muscle...
Table 2  Logistic regression analysis results of the original genomewide association study and replication study, controlling for antihypertensive drug-treated states, cohort, age, sex, and cardiovascular risk factors as covariates

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Chr, chromosome; rsID, SNP ID in dbSNP database; BP, base position, based on the latest genome version (hg19); MAF, minor allele frequency; M, minor allele; OR, odds ratio; L95 and U95, confidence interval lower and upper 95%, respectively.

The cardiovascular risk factors are BMI, SBP, DBP, HDL, LDL, TG, and fasting glucose level.
(rather than cardiac muscle) might regulate BP and affect ECG-LVH secondarily. To examine this possibility, we performed an association analysis of RYR1 SNPs with SBP and DBP. However, there was no association found in this analysis, indicating that this possibility is low (data not shown).

Therefore, to better understand the mechanism responsible for the potential association between RYR1 and ECG-LVH, further examination through functional analysis of RYRs is necessary.

In conclusion, we have reported the first GWAS of ECG-LVH, with which variations in RYR1 were associated and this finding will increase our understanding of the aetiology of ECG-LVH.

Supplementary material
Supplementary material is available at European Heart Journal online.

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Conflict of interest: none declared.

References
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