Genetic loci associated with prevalent and incident myocardial infarction and coronary heart disease in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium

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Abstract

Background

Genome-wide association studies have identified multiple genomic loci associated with coronary artery disease, but most are common variants in non-coding regions that provide limited information on causal genes and etiology of the disease. To better understand etiological pathways that might lead to discovery of new treatments or prevention strategies, we focused our investigation on low-frequency and rare sequence variations primarily residing in coding regions of the genome while also exploring associations with common variants.

Methods and Results

Using samples of individuals of European ancestry from ten cohorts within the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium, both cross-sectional and prospective analyses were conducted to examine associations between genetic variants and myocardial infarction (MI), coronary heart disease (CHD), and all-cause mortality following these events. Single variant and gene-based analyses were performed separately in each cohort and then meta-analyzed for each outcome. A low-frequency intronic variant (rs988583) in *PLCL1* was significantly associated with prevalent MI (OR=1.80, 95% confidence interval: 1.43, 2.27; $P=7.12 \times 10^{-7}$). Three common variants, rs9349379 in *PHACTR1*, and rs1333048 and rs4977574 in the 9p21 region, were significantly associated with prevalent CHD. Four common variants (rs4977574, rs10757278, rs1333049, and rs1333048) within the 9p21 locus were significantly associated with incident MI. We conducted gene-based burden tests for genes with a cumulative minor allele count (cMAC) $\geq$ 5 and variants with minor allele frequency (MAF) < 5%. *TMPRSS5* and *LDLRAD1* were significantly associated with prevalent MI and CHD, respectively, and *RC3H2* and *ANGPTL4* were significantly associated with incident MI and CHD, respectively. No loci were significantly associated with all-cause mortality following a MI or CHD event.

Conclusion

87 This study confirmed previously reported loci influencing heart disease risk, and one single variant and

88 three genes associated with MI and CHD were newly identified and warrant future investigation.

Introduction

Coronary heart disease (CHD) is a leading cause of morbidity and mortality worldwide, accounting for one of every seven deaths in the United States in 2016. (1) In addition to major modifiable risk factors such as dyslipidemia, hypertension, diabetes, and cigarette smoking (2), genetic susceptibility to CHD has also been investigated extensively through family-based studies, candidate gene studies, and more recently genome-wide association studies (GWAS). (3-9) With progressively expanded sample sizes in recent GWAS, at least 160 loci have been associated with the risk of coronary artery disease. (10-13) Most of these loci are represented by common variants located in noncoding regions, resulting in limited implications for causal genes and etiological pathways. Further, while most available data are derived from genome-wide analysis of prevalent CHD, data are sparse from prospective studies of incident cardiovascular events in populations free of baseline cardiovascular disease.

Low-frequency and rare coding sequence variations across the genome have been investigated in studies of cardiovascular disease risk factors (14-18), with the goal of better understanding the etiology of these risk factors and to advance the discovery of the treatment and prevention of diseases. (19) We previously published the results from a prospective analysis of CHD among individuals of European ancestry from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium, and identified low-frequency and common variants associated with incident CHD. (20)

In this current study of individuals of European ancestry, we implemented both a cross-sectional and prospective study design in the setting of the CHARGE Consortium to examine the association between genetic variants and the risk of prevalent and incident myocardial infarction (MI) and CHD. Study of incident cardiovascular events is enabled by the rigorous prospective design of population cohorts contributing to the CHARGE Consortium. We also investigated whether these genetic variants are associated with all-cause mortality after incident MI and CHD.

Materials and Methods

Study design and participants

Ten cohorts within the CHARGE Consortium Subclinical Working Group were included in this study: Age, Gene, Environment, Susceptibility Study (AGES), Atherosclerosis Risk in Communities (ARIC) Study, Cardiovascular Health Study (CHS), Family Heart Study (FamHS), Framingham Heart Study (FHS), the GeneSTAR Study (GeneSTAR), Multi-Ethnic Study of Atherosclerosis (MESA), Rotterdam Study (RS), Study of Health in Pomerania (SHIP), and the Women's Genome Health Study (WGHS). Detailed characteristics of the participating cohorts and study participant are shown in the **Supporting Document.** All study participants provided written informed consent to participate in genetic studies, and all study sites received approval to conduct this research from their local Institutional Review Boards (IRB) respectively.

Genotype calling and quality control

Participants from WGHS were genotyped by the HumanHap300 Duo+ (Illumina, Inc., San Diego, CA), and all other study participants were genotyped by the HumanExome BeadChip (v1.0-1.2, Illumina, Inc., San Diego, CA) which contains more than 240,000 variants including those discovered through exome sequencing in ~12,000 individuals and other non-coding common variants such as previously-reported GWAS signals and ancestry-informative markers. Data for AGES, ARIC, CHS, FamHS, FHS, MESA, and RS were jointly called at the University of Texas Health Science Center at Houston (21); SHIP was called in Illumina GenomeStudio using the CHARGE Consortium joint calling cluster file; GeneSTAR used the Illumina GenomeStudio and zCall software (22); and WGHS data was called using the Illumina BeadStudio v.3.3. Variant quality control (QC) was performed centrally (21) and by the individual studies, including checking concordance with previous GWAS data, and excluding participants with missing >5% genotypes, population clustering outliers, individuals with high inbreeding coefficients or heterozygote rates, gender mismatches, duplicated pairs, and unexpectedly high proportion of identity-by-descent sharing for family studies.

Cardiovascular outcome definition

Two cardiovascular outcomes were examined for association in this study: 1) MI: fatal or non-fatal MI; and 2) CHD: fatal or non-fatal MI, fatal CHD, sudden death within one hour of onset of symptoms, or revascularization (percutaneous coronary artery intervention such as stent or balloon angioplasty, or coronary artery bypass grafting). No exclusions were applied for the cross-sectional analysis of prevalent MI and prevalent CHD. For analysis of incident events, participants with a history of MI, CHD or revascularization at the baseline examination were excluded. All-cause mortality after MI or CHD was also investigated with follow-up time from first MI or CHD incident events until death, loss to follow-up, or the end of study.

Statistical analysis

Single variant and gene-based analyses were conducted in each participating cohort respectively, followed by meta-analysis performed for each cardiovascular outcome to summarize results. All autosomal variants were coded to the minor allele observed in the CHARGE jointly called data (21) and assumed log-additive genetic effect in the analyses. The minor allele frequency (MAF) thresholds were defined using the European allele frequencies derived from the CHARGE jointly called data. (21) Variant annotation was performed centrally within CHARGE using dbNSFP. (23, 24) Variants with MAF $\geq$ 1% were included in single variant tests for prevalent MI and CHD and for incident MI. Single variant results for incident CHD followed the same analytic approach and are reported in Morrison et al. (20) and are not reported in detail here. Gene-based tests were evaluated for MI and CHD outcomes: the Sequence Kernel Association Test (SKAT) (25) and a burden test (26). Only functional coding variants (missense, stop-gain, stop-loss, or splice-site changes) with MAF < 5% were aggregated by gene, and we only analyzed genes with a cumulative minor allele count (cMAC) $\geq$ 5.

For both single variant and gene-based burden tests of prevalent events, we performed Firth's logistic regression model to test the association between each variant and cardiovascular outcome using the "logistf" package in R (27-29) to account for the possible inflated type one error in the rare variant

association analysis in a case-cohort study design.(30) Meta-analysis for prevalent events was conducted with METAL (31) and applied the genomic control correction. For the single variant and two gene-based tests of incident events, a Cox proportional hazards regression model implemented in the seqMeta package in R was used to test the association between each variant and the incident event or post-event all-cause mortality. SeqMeta was used both at the study-specific analysis and meta-analysis levels. (32) All study-specific analyses (single variant and gene-based tests) were adjusted for cohort-specific design variables (e.g. study sites, family structure) and for population substructure using principal components as needed. We applied a Bonferroni corrected threshold to determine statistical significance in each analysis as described below.

Results

Prevalent MI and CHD association

A total of 27,349 participants of European ancestry from seven cohorts including 1831 prevalent MI cases (6.7%) and 2518 prevalent CHD cases (9.2%) were used in the meta-analyses of prevalent events (**S1 Table**). We examined individually a total of 36,406 variants, combining both low-frequency and common variants (MAF ≥ 1%), across all autosomal chromosomes corresponding to a Bonferroni corrected significance threshold of $P=1.37 \times 10^{-6}$. A low-frequency (MAF=1.64%) intronic variant (rs988583) in the phospholipase C like 1 gene (*PLCL1*) was significantly associated with prevalent MI ($P=7.12 \times 10^{-7}$; OR=1.80, 95% confidence interval=1.43 to 2.27; **Table 1**). Three common variants were significantly associated with prevalent CHD: rs9349379 in *PHACTR1* and rs1333048 and rs4977574 in the 9p21 region (**Table 1**).

Table 1. Low-frequency and common variants associated with prevalent MI and CHD.

Outcome	Variant	Chromosome and Position*	Allele 1 / Allele 2	Locus	Function	Frequency of Allele 2 (%)	Odds Ratio (95% Confidence Interval)	p-value

MI	rs988583	2:198987935	C/A	*PLCL1*	Intronic	1.64	1.80 (1.43, 2.27)	7.12×10^{-7}
CHD	rs9349379	6:12903957	A/G	*PHACTR1*	Intronic	39.99	0.84 (0.79, 0.89)	2.96×10^{-8}
CHD	rs1333048	9:22125347	A/C	9p21	Intergenic	48.98	0.85 (0.80, 0.91)	3.25×10^{-7}
CHD	rs4977574	9:22098574	A/G	9p21	Intronic	48.24	0.86 (0.87, 0.91)	1.03×10^{-6}

*Chromosome and nucleotide positions are based on genome build GRCh37.

In the gene-based burden tests, we analyzed 16,628 autosomal genes that contained functional low-frequency or rare variants with MAF < 5% and with a cumulative minor allele count (cMAC) ≥ 5; therefore, the Bonferroni corrected p-value threshold was $P=3.01\times10^{-6}$. The transmembrane serine protease 5 gene (*TMPRSS5*) on chromosome 11, containing nine nonsynonymous rare variants (**S2 Table**), was significantly associated with prevalent MI ($P=2.59\times10^{-6}$, OR=3.00, 95% confidence interval: 1.90, 4.73; **Table 2**). The low-density lipoprotein receptor class A domain containing 1 gene (*LDLRAD1*) on chromosome 1 contained seven rare variants (**S2 Table**) and was significantly associated with prevalent CHD ($P=1.30\times10^{-6}$, OR=4.48, 95% confidence interval: 2.44, 8.23; **Table 2**).

Table 2. Genes associated with prevalent MI and CHD in gene-based analysis.

Outcome	Gene	Chromosome and Position*	cMAC**	Variants (n)^	Test	Odds Ratio (95% Confidence Interval)	p-value
MI	*TMPRSS5*	11:113558268-113577151	152.02	9	Burden	3.00 (1.90, 4.73)	2.59×10^{-6}
CHD	*LDLRAD1*	1:54472971-54483859	60.05	7	Burden	4.48 (2.44, 8.23)	1.30×10^{-6}

*Chromosome and nucleotide positions are based on genome build GRCh37.
**cMAC = overall cumulative minor allele count.
^Variants (n) = number of variants included in the analysis; variants were restricted to those with MAF < 5% and annotated as nonsynonymous, splice-site, or stop loss/gain function.

Incident MI and CHD association

Nine cohorts contributed a total of 55,736 participants of European ancestry to the analyses of incident events, where 3,031 incident MI cases (5.4%) were reported during an average of 15.0 years of

follow-up and 5,425 incident CHD cases (9.73%) were reported during an average of 15.6 years of follow-up (**S3 Table**). A total of 37,109 low frequency and common autosomal variants (MAF ≥ 1%) were individually tested for association with incident MI, with adjustment of age, sex, and population substructure. The Bonferroni corrected p-value threshold for single variant analysis of incident MI was $P=1.35 \times 10^{-6}$. Four common variants in the noncoding region at the 9p21 locus were significantly associated with incident MI (**Table 3**). As previously stated, single variant results for incident CHD are reported in Morrison et al. (20) and are not reported here.

Table 3. Low-frequency and common variants associated with incident MI.

Outcome	Variant	Chromosome and Position*	Allele 1 / Allele 2	Locus	Function	Frequency of Allele 2 (%)	Odds Ratio (95% Confidence Interval)	p-value
MI	rs4977574	9:22098574	A/G	9p21	Intronic	48.55	1.13 (1.08, 1.19)	1.21×10^{-6}
MI	rs10757278	9:22124477	A/G	9p21	Intergenic	48.00	1.16 (1.10, 1.22)	6.61×10^{-9}
MI	rs1333049	9:22125503	G/C	9p21	Intergenic	48.06	1.16 (1.11, 1.22)	5.92×10^{-9}
MI	rs1333048	9:22125347	A/C	9p21	Intergenic	49.13	1.15 (1.09, 1.21)	7.27×10^{-8}

*Chromosome and nucleotide positions are based on genome build GRCh37.

For the gene-based analyses, we examined 17,574 genes across all autosomal chromosomes for association with incident MI, and the Bonferroni corrected significance level was $P=2.85 \times 10^{-6}$. The ring finger and CCCH-Type domains 2 gene (*RC3H2*) on chromosome 9 was significantly associated with incident MI in the burden test ($P=2.99 \times 10^{-6}$, OR=0.35, 95% confidence interval=0.23, 0.55; **Table 4**) and contained 12 nonsynonymous and one splice-site rare variants (**S4 Table**). No genes were significantly associated with incident MI using SKAT. For the gene-based analyses of incident CHD, 16,620 genes were evaluated and the Bonferroni significance levels was $P=3.01 \times 10^{-6}$. Angiopoietin-like 4 (*ANGPTL4*) on chromosome 19 was significantly associated with incident CHD using SKAT ($P=1.29 \times 10^{-6}$; **Table 4**) and contained 10 variants (**S4 Table**), and no gene was significantly associated using the burden test.

Table 4. Genes associated with incident MI and CHD in gene-based analysis.

Outcome	Gene	Chromosome and Position*	cMAC**	Variants (n)^	Test	Odds Ratio (95% Confidence Interval)	p-value
MI	*RC3H2*	9:125606835-125667562	356.02	13	Burden	0.35 (0.23, 0.55)	2.99×10^{-6}
CHD	*ANGPTL4*	19:8429011-843925	2830.07	10	SKAT	-	1.29×10^{-6}

*Chromosome and nucleotide positions are based on genome build GRCh37.
**cMAC = overall cumulative minor allele count.
^Variants (n) = number of variants included in the analysis; variants were restricted to those with MAF < 5% and annotated as nonsynonymous, splice-site, or stop loss/gain function.

Post MI and CHD mortality analysis

Among the 3,751 MI and CHD cases from six cohorts that contributed to the analysis of all-cause mortality, there were 1,860 all-cause deaths over a mean 10.9 years of follow-up (**S5 Table**). We examined 36,685 autosomal variants with MAF ≥ 1% in the single variant analysis (Bonferroni corrected significant level of $P=1.36 \times 10^{-6}$) and 17,574 genes in the gene-based analysis (Bonferroni corrected significant level of $P=2.85 \times 10^{-6}$). No single variant or gene reached the significance threshold in the analysis of all-cause mortality among survivors of MI or CHD. We examined the significant variants and genes reported in Tables 1-4 for their relationship with mortality following a MI or CHD event (**S6 Table**). While these loci were significantly associated with prevalent and incident MI or CHD events, only the 9p21 common variants were nominally associated with all-cause mortality ($P < 0.05$). The 9p21 variants that were associated with reduced risk of prevalent CHD (rs1333048 and rs4977574; **Table 1**), and with increased risk of incident MI (rs1333048, rs4977574, rs10757278, and rs1333049; **Table 3**) were all associated with modestly reduced risk of all-cause mortality (**S6 Table**).

Discussion

Our study evaluated genetic susceptibility to MI and CHD in cross-sectional and prospective settings among individuals of European ancestry. We confirmed several previously reported loci and

newly identified one low-frequency variant and three genes harboring low-frequency and rare coding variants that warrant investigation in future studies.

Single variant analysis of prevalent cardiovascular outcomes revealed a low-frequency (MAF=1.64%) intronic variant, rs988583, in *PLCL1* significantly associated with increased risk of MI (P=7.12 × 10^{-7}). *In silico* replication was conducted by a look up of rs988583 and its association with prevalent MI in the Myocardial Infarction Genetics and CARDIoGRAM exome chip meta-analysis public release (33), and there was no significant association with MI (P=0.34). A GWAS of MI and coronary artery disease (CAD) in a Saudi Arab population identified an intergenic variant, rs7421388, near *PLCL1* associated with CAD (P = 4.31 × 10^{-6}) and replicated in an independent sample of Saudi Arabs (P = 5.37 × 10^{-7}). (34) In another study of an ethnic Arab population, rs1147169 in *PLCL1* was protective against a low level of high density lipoprotein-cholesterol levels (P = 2.87 × 10^{-7}). (35) In individuals of European ancestry, rs988583 and rs1147169 are in linkage equilibrium (R^2= 0.0043). In addition to these studies, *PLCL1* has been implicated in coronary artery aneurysm in Kawasaki disease and *PLCL1* might play a role in the regulation of vascular endothelial cell inflammation via interference with proinflammatory cytokine expression. (36)

A burden test aggregating low-frequency and rare coding variants in genes showed a significant positive association between *TMPRSS5* and prevalent MI (P=2.59 × 10^{-6}) and *LDLRAD1* and prevalent CHD (P=1.30 × 10^{-6}), and a significant protective association between *RC3H2* and incident MI (P=2.99 × 10^{-6}). A significant association between *ANGPTL4* and incident CHD was identified using SKAT (P=1.29 × 10^{-6}). The relationship between *ANGPTL4* and CHD has been previously reported, with the rs116843064 missense variant playing a major role in reducing lipid levels and risk of CHD. (33, 37) Serine proteases, such as *TMPRSS5*, are known to be involved in many physiological and pathological processes, and *TMPRSS5* has been implicated in impaired hearing function. (38) Little is known about *LDLRAD1*, with most marked gene expression in lung and fallopian tube (39), and a rare variant in this gene has been associated with breast cancer. (40) Roquin-2 is encoded by *RC3H2* and has been shown to play a key role in posttranscriptional regulation of autoimmunity and inflammatory response. (41) Each of

these genes associated with prevalent or incident cardiovascular outcomes has rare and low-frequency variants underlying the gene burden tests (**S2 and S4 Table**). We identified 11 putative driving variants of these gene-based associations (i.e. those with p<0.05 in **S2 and S4 Table**; rs201233178, rs200417674, and rs116913282 in *TMPRSS5*; rs150560713, rs202234131, rs142900519, and rs76122098 in *LDLRAD1*; rs201920127, rs144714368, and rs199901510 in *RC3H2*; and rs116843064 in *ANGPTL4*). An *in silico* replication was not possible due to the rare frequency of these coding variants and their absence in the public release of the Myocardial Infarction Genetics and CARDIoGRAM exome chip meta-analysis or the analysis of CAD in the UK Biobank and the UK Biobank and CARDIoGRAMplusC4D meta-analysis (10, 33) However, it is important to note that rs116843064 of *ANGPTL4* is the same variant found in the single variant analysis conducted for incident CHD by Morrison et al., and this gene is likely to be driving the significant association found in the SKAT analysis of incident CHD. (20) It is of interest that the effect sizes of the gene-based tests (**Tables 2 and 4**) are larger than the single variant test effect sizes (**Tables 1 and 3**), supporting the notion that low-frequency and rare variants may have a more substantial impact on disease risk.

Although there was no statistically significant result found for all-cause mortality after MI or CHD, after accounting for multiple testing, the protective direction of effect for many of our mortality results suggests that genetic variants might contribute differently in various stages of disease manifestation. Specifically, our results highlight differences in the direction of effect for common variants at the 9p21 locus associated with decreased risk of prevalent CHD, increased risk of incident MI, and a nominally significant reduced risk of all cause-mortality following a cardiovascular event. Generally, the loci identified for prevalent disease were not the same as those identified for incident disease, as has been observed in previous studies. (9) Indeed, comparison of prevalent and incident findings (**S6 Table**) shows that the single variant (*PLCL1* locus) and gene-based (*TMPRSS5* locus) results for prevalent MI were not significantly associated with incident MI, and the direction of effects were consistent for *PLCL1* but not *TMPRSS5*. Similarly, the significant gene, *LDLRAD1*, identified for increased risk of prevalent CHD was not significantly associated with incident CHD, but the direction of effect was consistent. The *RC3H2*

gene, which showed an inverse association with incident MI, was not significantly associated with prevalent MI and it exhibited an opposite direction of effect. A possible explanation for these observed differences is that genetic studies of cardiovascular diseases are usually conducted with the cross-sectional study design, which has the potential to oversample participants with longer post-event survival (42) and the results do not always replicate in the prospective studies for disease onset and vice versa. (9) Given the limited statistical power of our findings for post-event survival, our study supports the need for substantially larger well-phenotyped cohorts to differentiate effects of variants associated with CHD from post-event mortality.

An advantage of this study is that within the setting of the CHARGE Consortium we are able to evaluate and make comparisons between cross-sectional and prospective study designs, and to investigate all-cause mortality following cardiovascular events. There are differing, but overlapping, sample sizes across the various study designs: 27,349 participants from seven cohorts for prevalent outcomes, 55,736 participants from nine cohorts for incident outcomes, and 3,751 MI and CHD cases from six cohorts that contributed to the analysis of all-cause mortality. These differing sample sizes influence our power to detect associations, and inferences about similarities and differences across study designs could be due to biological differences or differences in sample sizes. This investigation of low-frequency and rare variants was limited to the variants included on the genotyping platforms (HumanHap300 Duo+ and HumanExome BeadChip, v1.0-1.2, Illumina, Inc., San Diego, CA) and was also limited to individuals of European ancestry. Additionally, although the variants on the genotyping platform and included in our gene-based tests were enriched for coding variants predicted to be causal, we cannot attribute causality to the variants or genes with novel associations. A strength of this study is that the quality of rare variant genotype calling was maximized by the joint clustering performed within CHARGE on thousands of samples (21).

In conclusion, this study comprehensively evaluated the relationship between autosomal genetic variation and prevalent and incident cardiovascular outcomes in participants of European ancestry in the

context of the CHARGE consortium. We confirmed previously reported loci influencing heart disease risk as well as newly identified several loci associated with MI and CHD that warrant future investigation.

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References

1. Benjamin EJ, Muntner P, Alonso A, Bittencourt MS, Callaway CW, Carson AP, et al. Heart Disease and Stroke Statistics—2019 Update: A Report From the American Heart Association. Circulation. 2019;139(10):e56-e528.
2. Anderson KM, Odell PM, Wilson PWF, Kannel WB. Cardiovascular disease risk profiles. American Heart Journal. 1991;121(1, Part 2):293-8.
3. Swerdlow DI, Holmes MV, Harrison S, Humphries SE. The genetics of coronary heart disease. British Medical Bulletin. 2012;102(1):59-77.
4. O'Donnell CJ, Nabel EG. Genomics of Cardiovascular Disease. New England Journal of Medicine. 2011;365(22):2098-109.
5. Lloyd-Jones DM, Nam BH, D'Agostino RB, Levy D, Murabito JM, Wang TJ, et al. Parental cardiovascular disease as a risk factor for cardiovascular disease in middle-aged adults: a prospective study of parents and offspring. JAMA. 2004;291(18):2204-11.
6. Marenberg ME, Risch N, Berkman LF, Floderus B, de Faire U. Genetic Susceptibility to Death from Coronary Heart Disease in a Study of Twins. New England Journal of Medicine. 1994;330(15):1041-6.
7. Murabito JM, Pencina MJ, Nam B-H, D'Agostino RB, Wang TJ, Lloyd-Jones D, et al. Sibling Cardiovascular Disease as a Risk Factor for Cardiovascular Disease in Middle-aged Adults. JAMA. 2005;294(24):3117-23.
8. Dai X, Wiernek S, Evans JP, Runge MS. Genetics of coronary artery disease and myocardial infarction. World journal of cardiology. 2016;8(1):1-23.
9. Dehghan A, Bis JC, White CC, Smith AV, Morrison AC, Cupples LA, et al. Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. PloS one. 2016;11(3):e0144997-e.
10. van der Harst P, Verweij N. Identification of 64 Novel Genetic Loci Provides an Expanded View on the Genetic Architecture of Coronary Artery Disease. Circulation research. 2018;122(3):433-43.
11. Klarin D, Zhu QM, Emdin CA, Chaffin M, Horner S, McMillan BJ, et al. Genetic analysis in UK Biobank links insulin resistance and transendothelial migration pathways to coronary artery disease. Nature genetics. 2017;49(9):1392-7.
12. Nikpay M, Goel A, Won H-H, Hall LM, Willenborg C, Kanoni S, et al. A comprehensive 1000 Genomes–based genome-wide association meta-analysis of coronary artery disease. Nature Genetics. 2015;47:1121.
13. Nelson CP, Goel A, Butterworth AS, Kanoni S, Webb TR, Marouli E, et al. Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics. 2017;49:1385.
14. Natarajan P, Bis JC, Bielak LF, Cox AJ, Dörr M, Feitosa MF, et al. Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics. 2016;9(6):511-20.
15. Yu B, Pulit Sara L, Hwang S-J, Brody Jennifer A, Amin N, Auer Paul L, et al. Rare Exome Sequence Variants in CLCN6 Reduce Blood Pressure Levels and Hypertension Risk. Circulation: Cardiovascular Genetics. 2016;9(1):64-70.
16. Flannick J, Mercader JM, Fuchsberger C, Udler MS, Mahajan A, Wessel J, et al. Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. Nature. 2019;570(7759):71-6.
17. Liu DJ, Peloso GM, Yu H, Butterworth AS, Wang X, Mahajan A, et al. Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics. 2017;49:1758.
18. Warren HR, Evangelou E, Cabrera CP, Gao H, Ren M, Mifsud B, et al. Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature genetics. 2017;49(3):403-15.

19. Stein EA, Mellis S, Yancopoulos GD, Stahl N, Logan D, Smith WB, et al. Effect of a Monoclonal Antibody to PCSK9 on LDL Cholesterol. New England Journal of Medicine. 2012;366(12):1108-18.
20. Morrison AC, Fu Y, O'Donnell C. Variants in ANGPTL4 and the Risk of Coronary Artery Disease. New England Journal of Medicine. 2016;375(23):2303-6.
21. Grove ML, Yu B, Cochran BJ, Haritunians T, Bis JC, Taylor KD, et al. Best Practices and Joint Calling of the HumanExome BeadChip: The CHARGE Consortium. PLOS ONE. 2013;8(7):e68095.
22. Goldstein JI, Crenshaw A, Carey J, Grant GB, Maguire J, Fromer M, et al. zCall: a rare variant caller for array-based genotyping: genetics and population analysis. Bioinformatics (Oxford, England). 2012;28(19):2543-5.
23. Liu X, Jian X, Boerwinkle E. dbNSFP: a lightweight database of human nonsynonymous SNPs and their functional predictions. Human mutation. 2011;32(8):894-9.
24. Liu X, Jian X, Boerwinkle E. dbNSFP v2.0: a database of human non-synonymous SNVs and their functional predictions and annotations. Human mutation. 2013;34(9):E2393-E402.
25. Wu MC, Lee S, Cai T, Li Y, Boehnke M, Lin X. Rare-variant association testing for sequencing data with the sequence kernel association test. American journal of human genetics. 2011;89(1):82-93.
26. Li B, Leal SM. Methods for detecting associations with rare variants for common diseases: application to analysis of sequence data. American journal of human genetics. 2008;83(3):311-21.
27. Conti E, Izaurralde E. Nonsense-mediated mRNA decay: molecular insights and mechanistic variations across species. Current Opinion in Cell Biology. 2005;17(3):316-25.
28. Firth D. Bias Reduction of Maximum Likelihood Estimates. Biometrika. 1993;80(1):27-38.
29. Heinze G, Schemper M. A solution to the problem of separation in logistic regression. Statistics in Medicine. 2002;21(16):2409-19.
30. Wang X. Firth logistic regression for rare variant association tests. Frontiers in Genetics. 2014;5(187).
31. Willer CJ, Li Y, Abecasis GR. METAL: fast and efficient meta-analysis of genomewide association scans. Bioinformatics (Oxford, England). 2010;26(17):2190-1.
32. Voorman A, Brody JB, Chen H, Lumley T, Davis B. seqMeta: Meta-Analysis of Region-Based Tests of Rare DNA Variants. R package version 1.6.7. 2017 [Available from: https://CRAN.R-project.org/package=seqMeta.
33. Stitziel NO, Stirrups KE, Masca NGD, Erdmann J, Ferrario PG, König IR, et al. Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. The New England journal of medicine. 2016;374(12):1134-44.
34. Wakil SM, Ram R, Muiya NP, Mehta M, Andres E, Mazhar N, et al. A genome-wide association study reveals susceptibility loci for myocardial infarction/coronary artery disease in Saudi Arabs. Atherosclerosis. 2016;245:62-70.
35. Wakil SM, Ram R, Muiya NP, Andres E, Mazhar N, Hagos S, et al. A common variant association study reveals novel susceptibility loci for low HDL-cholesterol levels in ethnic Arabs. Clinical Genetics. 2016;90(6):518-25.
36. Lin Y-J, Chang J-S, Liu X, Tsang H, Chien W-K, Chen J-H, et al. Genetic variants in PLCB4/PLCB1 as susceptibility loci for coronary artery aneurysm formation in Kawasaki disease in Han Chinese in Taiwan. Scientific reports. 2015;5:14762-.
37. Folsom AR, Peacock JM, Demerath E, Boerwinkle E. Variation in ANGPTL4 and risk of coronary heart disease: the Atherosclerosis Risk in Communities Study. Metabolism: clinical and experimental. 2008;57(11):1591-6.
38. Guipponi M, Toh M-Y, Tan J, Park D, Hanson K, Ballana E, et al. An integrated genetic and functional analysis of the role of type II transmembrane serine proteases (TMPRSSs) in hearing loss. Human Mutation. 2008;29(1):130-41.
39. Gene expression for LDLRAD1 (ENSG00000203985.10) [Internet]. Available from: https://gtexportal.org/home/gene/LDLRAD1.

40. Haiman CA, Han Y, Feng Y, Xia L, Hsu C, Sheng X, et al. Genome-wide testing of putative functional exonic variants in relationship with breast and prostate cancer risk in a multiethnic population. PLoS genetics. 2013;9(3):e1003419-e.
41. Pratama A, Ramiscal Roybel R, Silva Diego G, Das Souvik K, Athanasopoulos V, Fitch J, et al. Roquin-2 Shares Functions with Its Paralog Roquin-1 in the Repression of mRNAs Controlling T Follicular Helper Cells and Systemic Inflammation. Immunity. 2013;38(4):669-80.
42. Anderson CD, Nalls MA, Biffi A, Rost NS, Greenberg SM, Singleton AB, et al. The effect of survival bias on case-control genetic association studies of highly lethal diseases. Circulation Cardiovascular genetics. 2011;4(2):188-96.

Supporting information

S1 Document. Characteristics of the participating cohorts.

S1 Table. Study participants' characteristics for prevalent MI and CHD analysis.

S2 Table. Low-frequency and rare variants underlying top signals from gene-based analysis for prevalent events.

S3 Table. Study participants' characteristics for incident MI and CHD analysis.

S4 Table. Low-frequency and rare variants underlying top signals from gene-based analysis for incident events.

S5 Table. Study participants' characteristics for post MI and CHD mortality analysis.

S6 Table. Prevalent and incident findings in relation to corresponding outcomes.