Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease

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IMPORTANCE The activity of lipoprotein lipase (LPL) is the rate-determining step in clearing triglyceride-rich lipoproteins from the circulation. Mutations that damage the LPL gene (LPL) lead to lifelong deficiency in enzymatic activity and can provide insight into the relationship of LPL to human disease.

OBJECTIVE To determine whether rare and/or common variants in LPL are associated with early-onset coronary artery disease (CAD).

DESIGN, SETTING, AND PARTICIPANTS In a cross-sectional study, LPL was sequenced in 10 CAD case-control cohorts of the multinational Myocardial Infarction Genetics Consortium and a nested CAD case-control cohort of the Geisinger Health System DiscovEHR cohort between 2010 and 2015. Common variants were genotyped in up to 305,699 individuals of the Global Lipids Genetics Consortium and up to 120,600 individuals of the CARDioGRAM Exome Consortium between 2012 and 2014. Study-specific estimates were pooled via meta-analysis.

EXPOSURES Rare damaging mutations in LPL included loss-of-function variants and missense variants annotated as pathogenic in a human genetics database or predicted to be damaging by computer prediction algorithms trained to identify mutations that impair protein function. Common variants in the LPL gene region included those independently associated with circulating triglyceride levels.

MAIN OUTCOMES AND MEASURES Circulating lipid levels and CAD.

RESULTS Among 46,891 individuals with LPL gene sequencing data available, the mean (SD) age was 50 (12.6) years and 51% were female. A total of 188 participants (0.40%; 95% CI, 0.35%-0.46%) carried a damaging mutation in LPL, including 105 of 32,646 control participants (0.32%) and 83 of 14,245 participants with early-onset CAD (0.58%). Compared with 46,703 noncarriers, the 188 heterozygous carriers of an LPL damaging mutation displayed higher plasma triglyceride levels (19.6 mg/dL; 95% CI, 4.6-34.6 mg/dL) and higher odds of CAD (odds ratio = 1.84; 95% CI, 1.35-2.51; P < .001). An analysis of 6 common LPL variants resulted in an odds ratio for CAD of 1.51 (95% CI, 1.39-1.64; P = 1.1×10^-22) per 1-SD increase in triglycerides.

CONCLUSIONS AND RELEVANCE The presence of rare damaging mutations in LPL was significantly associated with higher triglyceride levels and presence of coronary artery disease. However, further research is needed to assess whether there are causal mechanisms by which heterozygous lipoprotein lipase deficiency could lead to coronary artery disease.


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The enzymatic activity of lipoprotein lipase (LPL) serves as the rate-determining step in the postprandial clearance of circulating triglyceride-rich lipoproteins. Homozygous LPL deficiency, known as familial chylomicronemia syndrome, is associated with marked elevations in chylomicrons, severe hypertriglyceridaemia, and recurrent pancreatitis. However, an increased risk of coronary artery disease (CAD) in this condition has not been observed, potentially because the large circulating chylomicrons are unable to penetrate the arterial wall. By contrast, in heterozygous LPL deficiency, the attenuated capacity for lipolysis leads to a buildup of circulating chylomicron remnants and intermediate-density lipoproteins that are rich in both triglycerides and cholesterol. A study of 9 such individuals suggested an increased risk of CAD, but this association has not been confirmed.

In this study, the LPL gene (LPL; RefSeq NM_000237.2) was sequenced to test the hypothesis that rare damaging mutations leading to heterozygous LPL deficiency are associated with differences in circulating lipid levels as well as higher odds of early-onset CAD. In addition, to provide complementary evidence, independent common variants (allele frequency >1%) in the LPL gene region were also tested for association with CAD.

Methods

Study Populations

Gene sequencing of LPL was performed in participants of 10 previously described CAD case-control cohorts (eTable 1 in the Supplement). Studies included the Atherosclerosis, Thrombosis, and Vascular Biology Italian Study; the Exome Sequencing Project Early-Onset Myocardial Infarction study; a nested case-control of the Jackson Heart Study; the South German Myocardial Infarction study; the Ottawa Heart Study; the Precocious Coronary Artery Disease study; the Pakistan Risk of Myocardial Infarction Study; the Registre Gironi del COR (Gerona Heart Registry) study; the Leicester Myocardial Infarction study; and the North German Myocardial Infarction study. Clinical data were assessed in each study. The majority of CAD cases in this analysis (97.5%) were ascertained with onset at an early age (defined as ≤50 years in men and ≤60 years in women). Written informed consent was obtained from all participants of contributing studies, each of which received ethical approval from respective institutional review boards. Approval for this analysis was obtained from the institutional review board of Partners HealthCare.

Replication of the observed associations with regard to lipid levels and CAD was performed via analysis of the previously described DiscovEHR study. DiscovEHR study participants were recruited as part of the MyCode Community Health Initiative of the Geisinger Health System and Regenon Genetics Center. The present analysis was restricted to early-onset CAD cases and CAD-free controls (aged <55 years for men or <65 years for women for both cases and controls). Median values for serially measured laboratory and anthropometric traits were calculated for all individuals with 2 or more measurements in the electronic health record (EHR) following removal of likely spurious values that were more than 3 SDs from the intraindividual median value. Participants were considered to have CAD if they had a history of coronary revascularization in the EHR, or history of acute coronary syndrome, ischemic heart disease, or exertional angina (International Classification of Diseases, Ninth Revision codes 410*, 411*, 412*, 413*, and 414*) with angiographic evidence of obstructive coronary atherosclerosis (>50% stenosis in ≥1 major epicardial vessel from catheterization report). The CAD-free controls were defined as individuals without any case criteria or any single encounter or problem list diagnosis code indicating CAD.

Across all studies, the effect of lipid-lowering therapy in individuals reporting use at the time of lipid measurement was taken into account by dividing the measured total cholesterol and low-density lipoprotein cholesterol (LDL-C) by 0.8 and 0.7, respectively. Because remnant cholesterol was not measured in study cohorts, values were estimated according to the following formula: remnant cholesterol = total cholesterol minus high-density lipoprotein cholesterol minus LDL-C.

To extend the analysis to common variants in LPL, summary statistics of 2 large genome-wide association studies were analyzed. The effect of common LPL variants on circulating triglyceride levels was used as a proxy for influence on LPL activity. The relationship of common LPL variants with triglyceride levels was assessed in an analysis of up to 305,699 individuals from 73 cohorts of the Global Lipids Genetics Consortium genotyped using the Illumina HumanExome BeadChip between 2012 and 2014. These same variants were subsequently linked to CAD in up to 120,600 individuals also genotyped between 2012 and 2014 in the previously reported CARDioGRAM Exome Consortium study.

Gene Sequencing

Whole-exome sequencing of the Myocardial Infarction Genetics Consortium participants was performed between...
2010 and 2015 at the Broad Institute as previously described.\(^9\) In brief, sequence data of all participants were aligned to a human reference genome build GRCh37.p13 using the Burrows-Wheeler Aligner algorithm. Aligned non-duplicate reads were locally realigned and base qualities were recalibrated using Genome Analysis Toolkit software.\(^{21}\)

Variants were jointly called using Genome Analysis Toolkit HaplotypeCaller software. The sensitivity of the selected variant quality score recalibration threshold was 99.6% for single-nucleotide polymorphisms and 95% for insertion or deletion variants as empirically assessed using HapMap controls with known genotypes included in the genotyping call set. LPL sequence data from the Geisinger Health System DiscovEHR participants were extracted from exome sequences generated at the Regeneron Genetics Center between 2014 and 2015 as previously described.\(^{16}\)

**Damaging LPL Variant Ascertainment**

The positions of genetic variants were based on the complementary DNA reference sequence for LPL (RefSeq NM_000237.2). Rare LPL variants (minor allele frequency <1%) were annotated with regard to the following 3 classes in a sequential fashion: (1) loss-of-function variants, ie, single base changes that introduce a stop codon leading to premature truncation of a protein (nonsense), insertions or deletions (indels) of DNA that disrupt the translated protein’s amino acid sequence beyond the variant site (frameshift), or point mutations at sites of pre-messenger RNA splicing that alter the splicing process (splice-site); (2) variants annotated as pathogenic in ClinVar, a publicly available archive of genetic variations associated with clinical phenotypes; and (3) missense variants predicted to be damaging or possibly damaging by each of 5 computer prediction algorithms (LRT score, MutationTaster, PolyPhen-2 HumDiv, PolyPhen-2 HumVar, and SIFT) as performed previously.\(^{2,23}\) Software used to annotate observed variants included Variant Effect Predictor version 81 and its associated Loss-of-Function Transcript Effect Estimator (LOFTEE) plugin,\(^{24,25}\) and the dbNSFP database version 3.0b1.\(^{26}\)

**Statistical Analysis**

The association of rare damaging LPL mutations with lipid phenotypes in the Myocardial Infarction Genetics Consortium and the DiscovEHR studies was estimated using linear regression with adjustment for age, age squared, sex, study cohort, and the first 5 principal components of ancestry. Principal components of ancestry were based on observed genotypic differences across subpopulations (eg, race or ethnicity) in the overall study. Inclusion of principal components as covariates in linear regression analyses increases statistical power for true relationships and minimizes confounding by ancestry.\(^{27}\)

The association of LPL mutations with odds of CAD was determined via meta-analysis using Cochran-Mantel-Haenszel statistics for stratified 2-by-2 tables without continuity correction as implemented previously.\(^{3,8,28}\)

Common variants (allele frequency >1%) at the LPL locus independently associated with circulating triglyceride levels were ascertained via analysis of the Global Lipids Genetics Consortium cohorts. The association of variants with inverse normal transformed residuals of natural log of triglyceride levels was determined in a model adjusted for age, age squared, sex, and up to 4 principal components of ancestry. For any given genetic locus, such as LPL, multiple variants may be associated with circulating triglyceride levels in an independent fashion. Sequential forward selection provides a statistical framework to identify such independent variants.\(^{29,30}\)

The relationship of all genetic variants in the LPL locus with triglyceride levels was first determined. This analysis was then repeated using regression conditional on the most strongly associated variant, continuing the process until the top result was no longer significant at a prespecified threshold of \(P < 5 \times 10^{-8}\) (to represent genome-wide significance). To aid in interpretability, the beta coefficients derived from this analysis were converted into units of milligrams per deciliter using data from the National Health and Nutrition Examination Survey from 2005 through 2012, in which a similar transformation was used (replacing self-reported race for principal components of ancestry) to yield a conversion factor of 60.7-mg/dL change in triglyceride level per 1-unit change in inverse normal transformed values.

These same common LPL variants were linked to CAD using summary-level test statistics in the previously reported CARDIoGRAM Exome Consortium study.\(^{15}\) The cumulative association of these variants with odds of CAD was determined, standardized per genetic 1-SD increase in triglyceride levels. Explicitly, if \(x\) is the association of each variant with the outcome of interest, and \(y\) the association of each variant with triglyceride levels, then the estimated association of a 1-SD increase in triglycerides mediated by LPL locus variants is calculated as a fixed-effects meta-analysis of \(x/y\) for all variants. This method is mathematically equivalent to a previously reported approach.\(^{31}\)

Analyses were performed using R version 3.2.2 software (The R Foundation). All reported \(P\) values were 2-tailed, with \(P < .05\) used as a threshold for statistical significance unless otherwise specified.

**Results**

Gene sequencing of LPL was performed in 22,533 participants of the Myocardial Infarction Genetics Consortium, including 12,395 controls and 10,138 cases with CAD (Table 1). A total of 123 loss-of-function or missense variants in LPL with minor allele frequency less than 1% were identified. Of these 123 variants, 52 were classified as damaging (Table 2). Eight of these 123 variants led to loss of function, including 5 premature stop (nonsense) codons, 2 splice acceptor or donor variants, and 1 frameshift mutation. Only about 25% of missense variants in any given gene have a strongly damaging effect on protein function;\(^{32}\) additional annotation algorithms were thus needed for the 115 missense variants. Six were previously deemed pathogenic based on ClinVar annotation. In addition, 38 of the 109 remaining missense variants were predicted to be damaging...
The presence of a rare damaging LPL mutation was associated with an odds ratio for CAD of 1.96 (95% CI, 1.30-2.96; P = .001) in a combined analysis of the Myocardial Infarction Genetics Consortium studies (Figure 2). This association was most pronounced in those with a loss-of-function mutation in LPL (Table 2). Within the subgroup of 2592 CAD cases and 5341 controls free of CAD with an observed LDL-C level lower than 130 mg/dL (to convert to millimoles per liter, multiply by 0.80855) or hemoglobin A1c level greater than 6.5% (to convert to proportion of total hemoglobin, multiply by 0.01), an increased odds of CAD among carriers of a damaging LPL mutation remained apparent (odds ratio = 2.15; 95% CI, 1.14-4.06; P = .02).

Independent replication of the increased circulating triglyceride levels and CAD was performed in 24 358 individuals from the Geisinger Health System DiscovEHR cohort (Table 1). This cohort included 4107 individuals with early-onset CAD (age <55 years in men or <65 years in women) as ascertained based on medical records as well as 20 251 CAD-free controls. Ninety-one individuals were heterozygous carriers of a damaging LPL mutation, including 23 individuals with CAD (0.56%; 95% CI, 0.36% to 0.85%) and 68 CAD-free controls (0.34%; 95% CI, 0.26% to 0.43%). Circulating triglyceride levels were 17.2 mg/dL (95% CI, 0.5 to 34.9 mg/dL; P = .06) higher in mutation carriers as compared with noncarriers (Figure 1 and Table 2). The mutation carriers had increased odds of early-onset CAD (odds ratio = 1.67; 95% CI, 1.04 to 2.69; P = .03).

In a combined analysis of the Myocardial Infarction Genetics Consortium and DiscovEHR cohorts, among 46 891

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Myocardial Infarction Genetics Consortium</th>
<th>Geisinger Health System DiscovEHR Cohort*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Participants With CAD (n = 10 139)</td>
<td>CAD-Free Controls (n = 12 395)</td>
</tr>
<tr>
<td>Age, median (IQR), y</td>
<td>45 (41-50)</td>
<td>60 (48-68)</td>
</tr>
<tr>
<td>Female, No. (%)b</td>
<td>1294 (28)</td>
<td>4276 (19)</td>
</tr>
<tr>
<td>BMI, median (IQR)</td>
<td>26 (24-29)</td>
<td>27 (25-31)</td>
</tr>
<tr>
<td>Current smoker, No. (%)b</td>
<td>4322 (47)</td>
<td>2406 (21)</td>
</tr>
<tr>
<td>Medical history, No. (%)b</td>
<td>2190 (25)</td>
<td>1942 (19)</td>
</tr>
<tr>
<td>Hypertension</td>
<td>2918 (47)</td>
<td>3741 (42)</td>
</tr>
<tr>
<td>Lipid-lowering medicationc</td>
<td>2739 (31)</td>
<td>473 (5)</td>
</tr>
<tr>
<td>Total cholesterold</td>
<td>216 (181-252)</td>
<td>197 (168-228)</td>
</tr>
<tr>
<td>LDL cholesterold</td>
<td>138 (107-171)</td>
<td>120 (96-147)</td>
</tr>
<tr>
<td>HDL cholesterol</td>
<td>37 (31-45)</td>
<td>42 (33-53)</td>
</tr>
<tr>
<td>Triglycerides</td>
<td>166 (116-246)</td>
<td>133 (90-198)</td>
</tr>
<tr>
<td>Remnant cholesterol</td>
<td>33 (23-48)</td>
<td>28 (19-40)</td>
</tr>
</tbody>
</table>

Abbreviations: BMI, body mass index (calculated as weight in kilograms divided by height in meters squared); CAD, coronary artery disease; HDL, high-density lipoprotein; IQR, interquartile range; LDL, low-density lipoprotein.

* Total and LDL cholesterol values were divided by 0.8 and 0.7, respectively, in those receiving lipid-lowering medication to estimate untreated values.

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Individuals with LPL gene sequencing data available, the mean (SD) age was 50 (12.6) years and 51% were female. A damaging LPL mutation was present in 188 of 46891 individuals (0.40%; 95% CI, 0.35% to 0.46%), including 105 of 32 646 control participants (0.32%) and 83 of 14 245 participants with early-onset CAD (0.58%). A meta-analysis of the association with lipid levels demonstrated that compared with 46 703 noncarriers, the 188 heterozygous carriers of an LPL damaging mutation displayed higher plasma triglyceride levels; these mutations were associated with a circulating triglycerides increase of 19.6 mg/dL (95% CI, 4.6 to 34.6 mg/dL), a high-density lipoprotein cholesterol decrease of 3.6 mg/dL (95% CI, −5.7 to −1.5 mg/dL), and a remnant cholesterol increase of 5.6 mg/dL (95% CI, 2.3 to 9.0 mg/dL) (Figure 1). These beta coefficients can be interpreted to suggest, for example, that an individual with a damaging LPL mutation would be predicted to have a 19.6-mg/dL higher level of circulating triglycerides as compared with an individual without such a mutation after correction for potential confounding related to age, sex, study cohort, and ancestry. These mutations were additionally associated with increased odds of early-onset CAD (odds ratio = 1.84; 95% CI, 1.35 to 2.51; P < .001) (Figure 2).

Beyond rare damaging mutations, common variants at the LPL locus were analyzed to assess for a similar link to triglyceride levels and CAD. In an analysis of up to 305 699 individuals, 6 common variants (minor allele frequency ranging from 1%-29%) were robustly (P < 5 × 10⁻⁸) and independently associated with plasma triglyceride levels. The minor (less common) alleles of 4 of these variants were associated with decreased triglyceride levels, suggesting gain of lipoprotein lipase activity, and 2 were linked to increased triglyceride levels, consistent with decreased activity. In an analysis of up to 120 600 individuals of CAD case-control studies, each of these variants was confirmed to be associated with odds of CAD (P < .002 for each) with the expected directionality. A roughly linear relationship was noted in this data set between association with triglyceride levels and odds of CAD (eFigure in the Supplement). A weighted analysis that combined these 6 variants demonstrated an odds ratio for CAD of 1.51 (95% CI, 1.39-1.64; P = 1.1 × 10⁻⁹) per 1-SD increase in triglycerides mediated by LPL locus variants.

Table 2. Association of Damaging Lipoprotein Lipase Gene (LPL) Mutations With CAD by Rare Variant Class in the Myocardial Infarction Genetics Consortium Studies and Early-Onset CAD DiscovEHR Study

<table>
<thead>
<tr>
<th>Outcome</th>
<th>Variant Classa</th>
<th>Myocardial Infarction Genetics Consortium</th>
<th>Gelseinger Health System DiscovEHR Cohort</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Carriers, No. (%)</td>
<td>Carriers, No. (%)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Participants with CAD (n = 10138)</td>
<td>Participants with CAD (n = 4107)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Participants with CAD (n = 12 395)</td>
<td>Participants with CAD (n = 20 251)</td>
</tr>
<tr>
<td></td>
<td>Loss-of-Function</td>
<td>7 (0.07)</td>
<td>1 (0.02)</td>
</tr>
<tr>
<td></td>
<td>ClinVar Pathogenic</td>
<td>15 (0.15)</td>
<td>6 (0.15)</td>
</tr>
<tr>
<td></td>
<td>Predicted Damaging Missense</td>
<td>38 (0.37)</td>
<td>16 (0.39)</td>
</tr>
<tr>
<td></td>
<td>Combined</td>
<td>60 (0.59)</td>
<td>23 (0.56)</td>
</tr>
<tr>
<td></td>
<td>Beta coefficient for difference in triglyceride concentrations (95% CI), mg/dLb</td>
<td>.41 (−4.8 to 119.4)</td>
<td>.01 (92.7 to 296.4)</td>
</tr>
<tr>
<td></td>
<td>P Value</td>
<td>.001</td>
<td>.001</td>
</tr>
<tr>
<td></td>
<td>Odds ratio for CAD (95% CI)c</td>
<td>4.33 (0.85 to 21.96)</td>
<td>2.47 (0.22 to 27.2)</td>
</tr>
<tr>
<td></td>
<td>P Value</td>
<td>.08</td>
<td>.46</td>
</tr>
</tbody>
</table>

Abbreviation: CAD, coronary artery disease.

a Rare variants refer to those with minor allele frequency less than 1% in the sequenced population. Loss-of-function variants were defined as single base changes that introduce a stop codon leading to premature truncation of a protein (nonsense), insertions or deletions (indels) of DNA that disrupt the translated protein's amino acid sequence beyond the variant site (frameshift), or point mutations at sites of pre-messenger RNA splicing that alter the splicing process (splice-site). Predicted damaging variants refer to those predicted to be deleterious or possibly deleterious by each of 5 in silico prediction algorithms (LRT score, MutationTaster, PolyPhen-2 HumDiv, PolyPhen-2 HumVar, and SIFT).

b Beta coefficients reflective of the difference in triglyceride concentrations between carriers of a damaging LPL mutation and noncarriers were derived from linear regression analysis that included adjustment for age, age squared, sex, cohort, and the first 5 principal components of ancestry. Principal components of ancestry were based on observed genotypic differences across subpopulations (eg, race or ethnicity) in the overall study. Inclusion of principal components as covariates in linear regression analyses increases statistical power for true relationships and minimizes confounding by ancestry.27

c The association of LPL mutations with risk of CAD was determined via meta-analysis implementing Cochran-Mantel-Haenszel statistics for stratified 2-by-2 tables.
Discussion

The protein-coding exons of LPL were sequenced in 46 891 individuals from an international collaboration of CAD case-control cohorts and patients of a large health care organization. In this study, approximately 0.40% of individuals carried a rare damaging mutation in LPL. These carriers had increased circulating triglyceride levels (19.6 mg/dL) and an odds ratio of 1.84 for early-onset CAD. An analysis using common variants in LPL similarly demonstrated a significant association with CAD.

These results permit several conclusions. First, heterozygous LPL deficiency was associated with the presence of early-onset CAD. By identifying 188 carriers of a rare damaging mutation, an association with higher levels of triglycerides and remnant cholesterol and lower levels of high-density lipoprotein cholesterol was established along with an odds ratio for early-onset CAD of 1.84. This susceptibility to CAD may be due to impaired lipolysis of triglyceride-rich lipoproteins. Triglyceride-rich lipoproteins penetrate directly into the arterial wall and are selectively retained in the intima, thus promoting the development of cholesterol-rich foam cells and an inflammatory response that accelerates atherosclerosis.33

Second, a complementary common variant analysis involving 6 independent LPL variants confirmed the association of genetic variation in LPL with CAD. In an analysis in more than 300 000 individuals, each common variant’s association with triglyceride levels was used as a proxy for influence on LPL activity. Association of these same variants with CAD in more than 120 000 individuals demonstrated an odds ratio for CAD of 1.51 per 1-SD increase in triglyceride levels and an odds ratio of 1.84 for early-onset CAD. By using common variants in LPL, similarly demonstrated a significant association with CAD.

Fixed-effects meta-analysis was used to combine results across cohorts (P for heterogeneity > .50 for each lipid phenotype). The number of participants from each study cohort with lipid fraction values available is displayed. HDL indicates high-density lipoprotein; IQR, interquartile range; and LDL, low-density lipoprotein. To convert cholesterol to millimoles per liter, multiply by 0.0259; triglycerides to millimoles per liter, multiply by 0.0113.

Beta coefficients reflective of the difference in lipid concentrations between carriers of a damaging LPL mutation and noncarriers were derived from linear regression models that included adjustment for age, age squared, sex, cohort, and the first 5 principal components of ancestry. Principal components of ancestry were based on observed genotypic differences across subpopulations (eg, race or ethnicity) in the overall study. Inclusion of principal components as covariates in linear regression analyses increases statistical power for true relationships and minimizes confounding by ancestry.37
In each study, the relationship of rare damaging mutations in \( LPL \) with risk of CAD was determined. P values for association tests and confidence intervals were determined using exact methods. A meta-analysis across studies was performed using Cochran-Mantel-Haenszel statistics for stratified 2-by-2 tables. This method combines score statistics and is particularly useful when some observed odds ratios are 0. An odds ratio in the Jackson Heart Study (JHS) cohort was not available (NA) owing to absence of identified carriers of a damaging \( LPL \) mutation. ATVB indicates Atherosclerosis, Thrombosis, and Vascular Biology Italian Study; DiscovEHR, DiscovEHR project of the Regeneron Genetics Center and Geisinger Health System; ESP-EOMI, Exome Sequencing Project Early-Onset Myocardial Infarction study; Leicester, Leicester Myocardial Infarction study; North German, North German Myocardial Infarction study; OHS, Ottawa Heart Study; PROCARDIS, Precocious Coronary Artery Disease study; PROMIS, Pakistan Risk of Myocardial Infarction Study; REGICOR, Registre Gironí del COR (Gerona Heart Registry) study; South German, South German Myocardial Infarction study; and dashed line, overall meta-analysis effect estimate.

A key strength of the present analysis is that \( LPL \) was sequenced in a large number of individuals to analyze the entire spectrum of damaging mutations, each of which was rare in the population. Second, concordant results were demonstrated between CAD case-control studies of the Myocardial Infarction Genetics Consortium and the DiscovEHR study participants from the Geisinger Health System, in whom CAD status was ascertained based on EHRs. This reinforces the potential utility of ongoing efforts such as the UK Biobank and the All of Us Research Program (a cohort study within the Precision Medicine Initiative), which will facilitate large-scale interrogations of genetic variants as they relate to human disease.

Several limitations should be acknowledged. The approach to annotating rare missense variants in \( LPL \) using prediction algorithms and the ClinVar database has been previously validated and is fully reproducible. However, because functional validation of each variant was not performed, this method may have led to misclassification in some cases. Second, because the effect of \( LPL \) activity on regulation of circulating triglyceride levels is most pronounced following a meal, the degree of triglyceride level elevation among mutation carriers would likely have been greater if postprandial triglyceride levels were available. Third, this study assessed the association of \( LPL \) mutations with susceptibility to early-onset CAD; effect estimates might differ among individuals with later onset of disease. Fourth, levels of both triglycerides and calculated remnant cholesterol, the primary lipid components of triglyceride-rich lipoproteins, were increased in individuals harboring an \( LPL \) mutation. Because the level of remnant cholesterol was estimated and not directly measured in the present analysis, additional research is needed to determine the relative contributions of these components to human CAD.

**Conclusions**

The presence of rare damaging mutations in \( LPL \) was significantly associated with higher triglyceride levels and presence of CAD. However, further research is needed to assess whether there are causal mechanisms by which heterozygous \( LPL \) deficiency could lead to CAD.

**ARTICLE INFORMATION**

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**Figure 2. Association of Damaging Lipoprotein Lipase Gene (LPL) Mutations With Coronary Artery Disease (CAD) Among 46 891 Individuals in 11 Studies**

<table>
<thead>
<tr>
<th>Myocardial Infarction Genetics Consortium</th>
<th>LPL Mutation Carriers/Total, No.</th>
<th>Odds Ratio for CAD (95% CI)</th>
<th>P Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>JHS8</td>
<td>0/18</td>
<td>0/693 NA</td>
<td>.06</td>
</tr>
<tr>
<td>PROCARDIS11</td>
<td>7/914</td>
<td>0/910 15.05 (0.86-263.89)</td>
<td>.32</td>
</tr>
<tr>
<td>REGICOR13</td>
<td>3/369</td>
<td>1/391 3.20 (0.33-30.87)</td>
<td>.05</td>
</tr>
<tr>
<td>OHS10</td>
<td>6/572</td>
<td>2/968 5.12 (1.01-25.45)</td>
<td>.17</td>
</tr>
<tr>
<td>North German15</td>
<td>6/858</td>
<td>2/878 3.08 (0.62-15.32)</td>
<td>.29</td>
</tr>
<tr>
<td>ATVB8</td>
<td>5/1791</td>
<td>2/1719 2.40 (0.47-12.40)</td>
<td>.32</td>
</tr>
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<td>Leicester14</td>
<td>5/1201</td>
<td>2/1090 2.27 (0.44-11.75)</td>
<td>.42</td>
</tr>
<tr>
<td>South German2</td>
<td>2/400</td>
<td>4/198 0.49 (0.09-2.72)</td>
<td>.29</td>
</tr>
<tr>
<td>ESP-WOMEN7</td>
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<td>7/1471 0.42 (0.09-2.04)</td>
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<tr>
<td>PROMIS12</td>
<td>24/3026</td>
<td>17/3877 1.82 (0.97-3.39)</td>
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<td>Combined</td>
<td>60/10138</td>
<td>37/12395 1.96 (1.30-2.96)</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Heterogeneity: I^2 = 21%, P = .26</td>
<td></td>
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<td>Geisinger Health System</td>
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<tr>
<td>DiscovEHR16</td>
<td>23/4107</td>
<td>68/20251 1.67 (1.04-2.69)</td>
<td>.03</td>
</tr>
<tr>
<td>Overall</td>
<td>83/14245</td>
<td>105/32464 1.84 (1.35-2.51)</td>
<td>&lt;.001</td>
</tr>
</tbody>
</table>

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**Heterogeneity:** I^2 = 21%, P = .26

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**Heterogeneity:** I^2 = 12%, P = .33

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**Heterogeneity:** I^2 = 21%, P = .33
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**Author Contributions:** Drs Khera and Kathiresan had full access to all of the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis. Drs Khera and Won contributed equally to this work.

**Concept and design:** Khera, Won, Lander, Ardissino, Abecasis, Kathiresan.

**Acquisition, analysis, or interpretation of data:** Khera, Won, Peloso, O’Dushlaine, Liu, Stitziel, Marrugat, Nomura, Emland, Gupta, Borecki, Asselta, Duga, Merlini, Correa, Kessler, Wilson, Bown, Hall, Braund, Carey, Murray, Kirchner, Leader, Lavage, Manus, Hartzel, Samani, Schunkert, Marrugat, Ellosa, McPherson, Farrall, Watkins, Rader, Danesh, Gabriel, Willer, Saleheen, Dewey.

**Drafting of the manuscript:** Khera, Won, Marrugat, Nomura, Gupta, Saleheen, Kathiresan.

**Critical revision of the manuscript for important intellectual content:** Khera, Won, Peloso, O’Dushlaine, Liu, Stitziel, Emland, Iweya, Asselta, Duga, Merlini, Correa, Kessler, Wilson, Bown, Hall, Braund, Carey, Murray, Kirchner, Leader, Lavage, Manus, Hartzel, Samani, Schunkert, Marrugat, Ellosa, McPherson, Farrall, Watkins, Lander, Rader, Danesh, Ardissino, Gabriel, Willer, Abecasis, Dewey, Kathiresan.


**Administrative, technical, or material support:** Gupta, Borecki, Correa, Kessler, Bown, Hall, Braund, Carey, Kirchner, Leader, Lavage, Manus, Hartzel, Marrugat, McPherson, Watkins, Danesh, Gabriel, Dewey, Kathiresan.

**Supervision:** Khera, Gupta, Peloso, Bown, Carey, Schunkert, Ellosa, McPherson, Ardissino, Willer, Dewey, Kathiresan.

**Conflict of Interest Disclosures:** All authors have completed and submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Dr Khera reported receiving consulting fees from Merck and Co and Amarin Pharmaceuticals. Dr Stitziel reported receiving a research grant from AstraZeneca and consulting fees from Regeneron and Aegerion Pharmaceuticals. Dr Murray reported serving on an advisory board for Invitae and as a consultant for Merck. Dr Farrall reported receiving personal fees from Gendagel SL. Dr Ellosa reported serving on a Data Safety Monitoring Board for Gendagel SL. Dr Rader reported receiving consulting fees from Aegerion Pharmaceuticals, Alnylam Pharmaceuticals, Eli Lilly and Co, Pfizer, Sanofi, and Novartis; being an inventor on a patent related to lomitapide that is owned by the University of Pennsylvania and licensed to Aegerion Pharmaceuticals; and being a co-founder of Vascular Strategies and Stater Biotechnology. Dr Danesh reported receiving personal fees and nonfinancial support from Merck Sharp & Dohme UK Atherosclerosis, Novartis Cardiovascular and Metabolic Advisory Board, Sanofi, Population Research Advisory Panel, and Sanofi Advisory Board; nonfinancial support from diaDexus; and grants from the British Heart Foundation, Bupa Foundation, diaDexus, European Research Council, European Union, Evelyn Trust, Fogarty International Center, GlaxoSmithKline, Merck, National Heart, Lung, and Blood Institute, National Institute for Health Research, National Institute of Neurological Disorders and Stroke, NHS Blood and Transplant, Novartis, Pfizer, UK Medical Research Council, Wellcome Trust, and UK Biobank. Dr Ardisino reported receiving speaker fees from AstraZeneca, Boehhringer Ingelheim, Johnson & Johnson, Bayer, Daiichi Sankyo, GlaxoSmithKline, Eli Lilly and Co, Boston Scientific, Bristol-Myers-Squibb, Scenarini Group, Novartis, and Sanofi-Aventis; and research grants from GlaxoSmithKline, Eli Lilly and Co, Pfizer, and Novartis. Dr Abecasis reported serving as a consultant to Regeneron Pharmaceuticals.

Dr Saleheen reported receiving grants from Pfizer and the National Institutes of Health. Dr Dewey reported receiving support from Aegerion Pharmaceuticals and Personalis. Dr Kathiresan reported receiving research grants from Bayer Healthcare, Aegerion Pharmaceuticals, and Regeneron Pharmaceuticals; serving on scientific advisory boards for Regeneron, Catabasis Pharmaceuticals, Merck, Celera, and Genomics PLC; serving as a consultant to Bayer, Merck, Novartis, Sanofi, AstraZeneca, Alnylam Pharmaceuticals, Eli Lilly and Co, Leerink Partners, Noble Insights, Ionis, Quest Diagnostics, and Genomics PLC; and holding equity in Catabasis Pharmaceuticals and San Therapeutics. No other disclosures were reported.

**Funding/Support:** Dr Khera was supported by an ACCF/Merck Cardiovascular Research Fellowship from the American College of Cardiology Foundation and Merck, a John S. Ladue Memorial Fellowship at Harvard Medical School, and KL2/Catalyst Medical Research Investigator Training Program T01OD00 from Harvard Catalyst funded by the National Institutes of Health. Dr Won was supported by grant 2016R1C1B2007920 from the National Research Foundation of Korea funded by the Ministry of Science, ICT and Future Planning. Dr Peloso was supported by grant K08HL125751 from the National Heart, Lung, and Blood Institute, and Dr Stitziel was supported by grants K08 HL116642 and R01 HL131961 from the National Institutes of Health. Drs Carey, Murray, and Kirchner and Messrs Leader, Lavage, Manus, and Hartzel were supported by the Regeneron Genetics Center. Dr McPherson was supported by grants from the Canadian Institutes of Health Research, the Heart and Stroke Foundation of Canada, and the Canada Foundation for Innovation. Dr Farrall was supported by core award 090532Z/07/9Z and the Institutional Strategic Support Fund from the Wellcome Trust and grant RE/13/1/30181 from the British Heart Foundation Centre of Research Excellence. Dr Lander was supported by grant 5U54HG003067 from the National Institutes of Health. Dr Danesh was supported by grants from the UK Medical Research Council, the British Heart Foundation, the UK National Institute for Health Research, and the European Commission Framework Programme. Dr Willer was supported by grants HL109946 and HL127564 from the National Heart, Lung, and Blood Institute. Dr Abecasis was supported by a grant from the National Institutes of Health. Dr Kathiresan was supported by a research scholar award from the Massachusetts General Hospital, the Donovan Family Foundation, and grant R01 HL127564 from the National Heart, Lung, and Blood Institute. Field work, genotyping, and standard clinical chemistry assays in the Pakistan Risk of Myocardial Infarction Study (PROMIS) were principally supported by grants awarded to the University of Cambridge from the British Heart Foundation, UK Medical Research Council, Wellcome Trust, EU Framework 6-funded Bloodomics Integrated Project, Pfizer, Novartis, and Merck. Additional support for PROMIS was provided by the UK Medical Research Council.
Association of Lipoprotein Lipase Gene Variation With Coronary Artery Disease

The Myocardial Infarction Genetics Consortium, DiscovEHR Study Group, CARDIoGRAM Exome Consortium, and Global Lipids Genetics Consortium members are listed in the eAppendix in the Supplement.

REFERENCES


6. Atherosclerosis, Thrombosis, and Vascular Biology Italian Study (ATVB) was supported by grant R01-HL-068879 from the National Heart, Lung, and Blood Institute. Exome sequencing was performed through grants R21 HL102925 (BroadGeno) and R22 HL102926 (SeattleGene) from the National Heart, Lung, and Blood Institute. Exome sequencing in ATVB, the Precocious Coronary Artery Disease study (PROCARDIS), the Ottawa Heart Health Research Unit (O2R), the South German Myocardial Infarction Study, and the Jackson Heart Study was supported by grant 5U54HG003067 from the National Institutes of Health (Drs Lander and Gabriel). The DiscovEHR study was supported in part by the Regenener Genetics Center.

Role of the Funder/Sponsor: For the analysis of the Myocardial Infarction Genetics Consortium, the Global Lipid Genetics Consortium, and the CARDIoGRAM Exome Consortium studies, the funders of the individual study cohorts had no role in the design and conduct of the study; collection, management, analysis, and interpretation of the data; preparation, review, or approval of the manuscript; and decision to submit the manuscript for publication. The DiscovEHR study was funded in part by the Regenener Genetics Center, and employees of Regenener Pharmaceuticals were involved in the design and conduct of the study; collection, management, analysis, and interpretation of the data; preparation, review, or approval of the manuscript; and decision to submit the manuscript for publication. Regenener Pharmaceuticals did not have the power to veto a decision to submit the study for publication. Investigators associated with each study had access to the data, and Drs Khera and Kathiresan were responsible for the final decision to submit the manuscript for publication.

Group Information: The Myocardial Infarction Genetics Consortium, DiscovEHR Study Group, CARDIoGRAM Exome Consortium, and Global Lipids Genetics Consortium members are listed in the eAppendix in the Supplement.

Disclaimer: The views expressed in this article are those of the authors and do not necessarily represent the views of the National Heart, Lung, and Blood Institute, the National Institutes of Health, the Harvard Catalyst, or the US Department of Health and Human Services.

Additional Contributions: We thank the MyCode Community Health Initiative participants for their permission to use their health and genomics information in the DiscovEHR collaboration.

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