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Newly identified loci that influence lipid concentrations and risk of coronary artery disease

Cristen J Willer[1,18], Serena Sanna[1,2,18], Anne U Jackson[1], Angelo Scuteri[3,4], Lori L Bonnycastle[5], Robert Clarke[6], Simon C Heath[7], Nicholas J Timpson[8], Samer S Najjar[3], Heather M Stringham[1], James Strait[3], William L Duren[1], Andrea Maschio[2], Fabio Busonero[2], Antonella Mulas[2], Giuseppe Albai[2], Amy J Swift[5], Mario A Morken[5], Narisu Narisu[5], Derrick Bennett[6], Sarah Parish[6], Haiqing Shen[9], Pilar Galan[10], Pierre Meneton[11], Serge Hercberg[11], Diana Zelenika[7], Wei-Min Chen[1], Yun Li[1], Laura J Scott[1], Paul A Scheet[1], Jouko Sundvall[12], Richard M Watanabe[13,14], Ramaiah Nagaraja[3], Shah Ebrahim[15], Debbie A Lawlor[8], Yoav Ben-Shlomo[8], George Davey-Smith[8], Alan R Shuldiner[9], Rory Collins[6], Richard N Bergman[13], Manuela Uda[2], Jaakko Tuomilehto[16], Antonio Cao[2], Francis S Collins[5], Edward Lakatta[3], G Mark Lathrop[7], Michael Boehnke[1], David Schlessinger[3], Karen L Mohlke[17], and Gonçalo R Abecasis[1]

[1]Center for Statistical Genetics, Department of Biostatistics, University of Michigan, 1420 Washington Heights, Ann Arbor, Michigan 48109, USA [2]Istituto di Neurogenetica e Neurofarmacologia (INN), Consiglio Nazionale delle Ricerche, c/o Cittadella Universitaria di Monserrato, Monserrato, Cagliari, Italy 09042 [3]Gerontology Research Center, National Institute on Aging, 5600 Nathan Shock Drive, Baltimore, Maryland 21224, USA [4]Unitá Operativa Geriatria, Istituto per la Patologia Endocrina e Metabolica, Rome, Italy [5]Genome Technology Branch, National Human Genome Research Institute, Bethesda, Maryland 20892, USA [6]Clinical Trial Service Unit, University of Oxford, Richard Doll Building, Old Road Campus, Roosevelt Drive, Oxford OX3 7LF, UK [7]Centre National de Génotypage, Institut Génomique, Commissariat à l'Énergie Atomique, 2 rue Gaston Crémieux, CP 5721, 91057 Evry Cedex, France [8]Department of Social Medicine, University of Bristol, Canynge Hall, Whiteladies Road, Bristol BS8 2PR, UK [9]Division of Endocrinology, Diabetes and Nutrition, University of Maryland School of Medicine, Baltimore, Maryland 21201, USA [10]U872 Institut National de la Santé et de la Recherche Médicale (INSERM) and Département de Santé Publique et d'Informatique Médicale, Faculté de Médecine René Descartes, 15 rue de l'Ecole de Médecine, 75270 Paris, France [11]U557 INSERM; U1125 Institut National de la Recherche Agronomique (INRA); Cnam; Paris 13 University; Centre de Recherche en Nutrition Humaine (CRNH) IdF, 74 rue Marcel Cachin, 93017 Bobigny Cedex, France [12]Laboratory of Analytical Biochemistry, Department of Health and Functional Capacity, National Public Health Institute, 00300 Helsinki, Finland [13]Department of Physiology and Biophysics, Keck School of Medicine, University of Southern California, Los Angeles, California 90033, USA [14]Department of Preventive Medicine, Keck School of Medicine, University of

Correspondence should be addressed to G.R.A. (goncalo@umich.edu) or K.L.M. (mohlke@med.unc.edu).

[18]These authors contributed equally to the work

URLs. Association data, http://www.sph.umich.edu/csg/abecasis/public/lipids/; Markov Chain Haplotyping Package, http://www.sph.umich.edu/csg/abecasis/MaCH.

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Southern California, Los Angeles, California 90089, USA [15]Department of Epidemiology and Population Health, London School of Hygiene & Tropical Medicine, Keppel St. London WC1E 7HT, UK [16]Diabetes Unit, Department of Health Promotion and Chronic Disease Prevention, National Public Health Institute, 00300 Helsinki, Finland and Department of Public Health, University of Helsinki, 00014 Helsinki, Finland [17]Department of Genetics, University of North Carolina, Chapel Hill, North Carolina 27599, USA

Abstract

To identify genetic variants influencing plasma lipid concentrations, we first used genotype imputation and meta-analysis to combine three genome-wide scans totaling 8,816 individuals and comprising 6,068 individuals specific to our study (1,874 individuals from the FUSION study of type 2 diabetes and 4,184 individuals from the SardiNIA study of aging-associated variables) and 2,758 individuals from the Diabetes Genetics Initiative, reported in a companion study in this issue. We subsequently examined promising signals in 11,569 additional individuals. Overall, we identify strongly associated variants in eleven loci previously implicated in lipid metabolism (*ABCA1*, the *APOA5-APOA4-APOC3-APOA1* and *APOE-APOC* clusters, *APOB, CETP, GCKR, LDLR, LPL, LIPC, LIPG* and *PCSK9*) and also in several newly identified loci (near *MVK-MMAB* and *GALNT2*, with variants primarily associated with high-density lipoprotein (HDL) cholesterol; near *SORT1*, with variants primarily associated with low-density lipoprotein (LDL) cholesterol; near *TRIB1*, *MLXIPL* and *ANGPTL3*, with variants primarily associated with triglycerides; and a locus encompassing several genes near *NCAN*, with variants strongly associated with both triglycerides and LDL cholesterol). Notably, the 11 independent variants associated with increased LDL cholesterol concentrations in our study also showed increased frequency in a sample of coronary artery disease cases versus controls.

Coronary artery disease (CAD) and stroke are the leading causes of morbidity, mortality and disability in industrialized countries, and the prevalence of these diseases is increasing rapidly in developing countries[1]. A main underlying pathology is atherosclerosis, a process of cumulative deposition of LDL cholesterol in the arteries supplying blood to the heart and brain that eventually leads to impaired or absent blood supply and myocardial infarction or stroke[1]. Consistent and compelling evidence has demonstrated association between lipoprotein-associated lipid concentrations and cardiovascular disease incidence worldwide[2–4]. Whereas high concentrations of LDL cholesterol are associated with increased risk of CAD, high concentrations of HDL cholesterol are associated with decreased risk of CAD. Specifically, it has been estimated that each 1% decrease in LDL cholesterol concentrations reduces the risk of coronary heart disease by ~1% (ref. 5), and each 1% increase in HDL cholesterol concentrations reduces the risk of coronary heart disease by ~2% (ref. 6). A recent meta-analysis of data on 150,000 individuals, including 3,000 with CAD-related deaths, shows that the two factors are independently associated with CAD risk[7]. There is evidence that a high concentration of triglycerides is an additional, independent risk factor for cardiovascular disease[8,9], although whether this association is causal is still under debate.

Smoking, diet and physical activity all have a role in determining individual lipid profiles. Still, family studies suggest that in many populations, about half of the variation in these traits is genetically determined[10,11], and it is clear that LDL cholesterol, HDL cholesterol and triglyceride concentrations are strongly influenced by the genetic constitution of each individual. Furthermore, genetic variants that increase LDL cholesterol concentrations—such as rare variants in the LDL receptor (*LDLR*) and apolipoprotein B (*APOB*) genes and common variants in the apolipoprotein E (*APOE*) gene—have also been associated with increased susceptibility to coronary heart disease[12]. Thus, the available evidence demonstrates not only that genetic variants account for a substantial fraction of individual variation in lipid concentrations, but also that lipid concentrations are associated with the risk of CAD.

Although several genes and genetic variants have been found that associate with individual variation in lipid concentrations, additional variants influencing these traits remain to be identified. As with other complex traits, identification of genes influencing lipid concentrations is likely to be much enhanced by large sample sizes. Thus, we decided to combine genome-wide association scan data from two of our studies, including 1,874 individuals from the FUSION study of type 2 diabetes[13] and 4,184 individuals from the SardiNIA study of aging-associated variables[10,14], with data on 2,758 individuals from the Diabetes Genetics Initiative[15,16]. Here, we describe results of a combined analysis of the three genome-wide association scans involving a total of 8,816 individuals and our follow-up assessments of up to 11,569 individuals, which were done in order to verify common genetic variants associated with plasma concentrations of LDL cholesterol, HDL cholesterol and triglycerides. Our results identify >25 independent common variants associated with individual variation in lipid concentrations (each with $P < 5 \times 10^{-8}$). Some are located in previously implicated loci, indicating that our approach was valid, and others are found in loci where genetic variants have not been previously implicated in lipid metabolism. Our results also provide promising, albeit not definitive, evidence of association between several other common variants and lipid concentrations. In a companion manuscript, Kathiresan and colleagues from the Diabetes Genetics Initiative report results of their own follow-up genotyping of SNPs selected on the basis of our combined analysis of the three scans, their original analyses, and previously published reports. Their independent follow-up samples and genotyping further support the newly identified loci reported here.

RESULTS

Genome-wide association scans

To survey the genome for common variants associated with plasma concentrations of HDL cholesterol, LDL cholesterol and triglyceride concentrations, we conducted genome-wide association scans on two different populations. In one scan, after we excluded markers on the basis of quality-control filters (see Methods), we examined 304,581 SNPs with minor allele frequency (MAF) >1% from the Illumina HumanHap300 BeadChip and a GoldenGate panel designed to improve coverage around type 2 diabetes (T2D) candidate genes in 1,874 Finnish individuals from the Finland–United States Investigation of NIDDM Genetics (FUSION) study[13]. In a second scan, after quality-control filtering, we examined 356,539

SNPs (MAF > 5%) from the Affymetrix 500K Mapping Array Set in 4,184 individuals from the SardiNIA Study of Aging[10,14]. The Sardinian sample is organized into a number of small-to medium-sized pedigrees. We took advantage of this relatedness to reduce genotyping costs: we genotyped 1,412 individuals with the Affymetrix 500K Mapping Array Set (organized into groups of 2–3 individuals per nuclear family) and then propagated their genotypes to the remaining individuals, who were genotyped using only the Affymetrix 10K Mapping Array[14,17,18] (see Methods). To increase statistical power, we also contacted the authors of a previously published study[15] to obtain results for 347,010 SNPs (MAF > 5%) genotyped in 2,758 Finnish and Swedish individuals from the Diabetes Genetics Initiative (DGI) using the Affymetrix 500K Mapping Array Set. Further details of the DGI study and independent follow-up analyses are provided in a companion manuscript[16]. All three initial scans excluded individuals taking lipid lowering therapies, for a total of 8,816 phenotyped individuals (Table 1). Informed consent was obtained from all study participants and ethics approval was obtained from the participating institutions.

Because the three studies used different marker sets with an overlap of only 44,998 SNPs across studies, we used information on patterns of haplotype variation in the HapMap CEU samples (release 21)[19] to infer missing genotypes *in silico* and to facilitate comparison between the studies[13]. Imputation analyses were carried out with Markov Chain Haplotyping software (MaCH; see URLs section in Methods). For our analyses, we only considered SNPs that were either genotyped or could be imputed with relatively high confidence; that is, SNPs for which patterns of haplotype sharing between sampled individuals and those genotyped by the HapMap consistently indicated a specific allele. Comparison of imputed and experimentally derived genotypes in our samples yielded estimated error rates of 1.46% (for imputation based on Illumina genotypes) to 2.14% (imputation based on Affymetrix genotypes) per allele, consistent with expectations from HapMap data. For additional details of quality-control and imputation procedures, see Methods and Supplementary Table 1 online.

We then conducted a series of association analyses to relate the ~2,261,000 genotyped and/or imputed SNPs with plasma concentrations of HDL cholesterol, LDL cholesterol and triglyceride concentrations. For each SNP, lipid concentrations were regressed onto allele counts in a regression model that also included gender, age and age^2 as covariates. For the FUSION sample, we analyzed T2D cases and controls separately, and added additional covariates accounting for birth province and study subset. For the DGI sample, we analyzed cases and controls together using an additional covariate to indicate diabetes status. For SNPs genotyped in the lab, allele counts were discrete (0, 1 or 2), whereas for SNPs genotyped *in silico*, allele counts were fractional (between 0.0 and 2.0, depending on the imputed number of copies of the allele for each individual; see Methods). To allow for relatedness in the FUSION and SardiNIA samples, we estimated regression coefficients in the context of a variance component model that modeled background polygenic effects[17]. As usual[20,21], modeling polygenic effects is important in the context of an association study such as this one, because ignoring relatedness among sampled individuals can lead to misleading *P* values and inflated false-positive rates.

Figure 1 shows the results of a meta-analysis of the initial scans from all three studies, comprising a total of 8,816 participants. The genomic control[22] parameters for this meta-analysis were 1.04, 1.02 and 1.01 (for HDL cholesterol, LDL cholesterol and triglycerides, respectively), suggesting that population stratification and unmodeled relatedness had negligible impact on our association results. Stage 1 results indicate strong association with lipids for 18 loci where at least one SNP exceeds the arbitrary threshold of $P < 5 \times 10^{-7}$ (Table 2). Several loci previously implicated in lipid metabolism show strong evidence for association, including regions near *CETP* (strongest association at rs3764261, $P < 10^{-18}$, HDL cholesterol concentration increase of 2.42 mg/dl per A allele), *LPL* (rs12678919, $P < 10^{-10}$, 2.44 mg/dl increase per G allele), *LIPC* (rs10468017, $P < 10^{-10}$, 1.76 mg/dl increase per T allele), *ABCA1* (rs4149274, P ~7.4×10^{-8}, 1.51 mg/dl increase per G allele) and *LIPG* (rs4939883, P ~1.4×10^{-7}, 1.87 mg/dl increase per C allele) associated with HDL cholesterol concentrations; the *APOE-APOC1-APOC4-APOC2* cluster (rs4420638, $P < 10^{-20}$, 8.02 mg/dl increase per G allele), *APOB* (rs515135, $P < 10^{-13}$, 6.08 mg/dl increase per C allele) and *LDLR* (rs6511720, $P < 10^{-9}$, 8.03 mg/dl increase per C allele) associated with LDL cholesterol concentrations; and near the *APOA5-APOA4-APOC3-APOA1* cluster (rs964184, $P < 10^{-15}$, 18.12 mg/dl increase per G allele), *GCKR* (rs1260326, $P < 10^{-14}$, 10.25 mg/dl increase per T allele) and *LPL* (rs6993414, $P < 10^{-12}$, 14.20 mg/dl increase per A allele) associated with triglyceride concentrations. At several of these loci, the SNP showing strongest association was in linkage disequilibrium (LD) with previously identified variants ($r^2 > 0.80$) or had itself been previously reported to show association. However, at other loci—in particular, the regions near *LIPC, LIPG, LDLR* and *APOB*—strongly associated SNPs were in only weak LD with previously identified variants ($r^2 < 0.30$) and thus were likely to represent new signals (Supplementary Table 2 online). At the *GCKR* locus, the strongest observed association was with a coding SNP, consistent with the results of a recent detailed analysis of the region (S. Kathiresan and M. Orho-Melander, personal communication). In addition to SNPs in these known loci, several other SNPs showed strong association in our initial genome-wide analysis. For example, SNPs near the *GRIN3A*, *GALNT2*, *CELSR2-PSRC1-SORT1*, *NCAN-SF4* and *TRIB1* genes all had *P* values $<5 \times 10^{-7}$ for at least one of the three lipid traits in our initial analysis (Table 2). We observed association with distinct gene sets for each of the three traits, consistent with the modest degree of correlation between the traits (the correlation between HDL and LDL cholesterol was essentially zero in our samples, the correlation between HDL cholesterol and triglycerides was approximately −0.4 and the correlation between LDL cholesterol and triglycerides was 0.3 in the SardiNIA sample and 0.1 in FUSION).

Follow-up of initial findings

To further evaluate these and other promising findings from our initial scan, we examined a subset of SNPs in six additional cohorts of European ancestry, totaling 11,569 individuals (Table 1). These follow-up analyses were conducted in several stages. In a first round of follow-up analysis, SNPs included on the Affymetrix arrays (genotyped in SardiNIA and DGI) and imputed or genotyped in FUSION were selected for follow-up on the basis of a preliminary meta-analysis. We selected a total of 100 SNPs in this manner for examination in the ISIS[23,24], HAPI[25,26] and SUVIMAX[27,28] samples, and 67 SNPs for examination in FUSION stage 2 samples. Once imputation of HapMap SNPs was completed for SardiNIA

and DGI samples and an additional meta-analysis carried out, we examined nine additional SNPs in loci not selected for initial follow-up in the FUSION stage 2 and SUVIMAX samples. Finally, we genotyped a single SNP in each of the 21 loci showing promising evidence for replication in the initial stage 2 samples in the Caerphilly[29,30] and BWHHS[31] samples (Supplementary Fig. 1 and Supplementary Methods online).

Table 3 provides a summary of the stage 2 results and a combined analysis of the data from both stage 1 and stage 2. The table includes the SNP with the strongest association signal at each locus and a selection of additional SNPs that also show strong association but only weak LD with the most strongly associated SNP ($r^2 < 0.30$). All loci with a P value $<5 \times 10^{-7}$ in our initial analysis were confirmed except for the association signal near *GRIN3A*. Supplementary Table 3 online provides stage 2 results for all SNPs, and Supplementary Table 4 online provides more detailed results for the SNPs highlighted in Table 3.

Overall, we observed the strongest evidence for association ($P < 10^{-20}$) between HDL cholesterol and SNPs in CETP (rs3764261, rs1864163 and rs9989419; the three are in weak LD with each other), *LIPC* (rs4775041) and *LPL* (rs10503669); between LDL cholesterol and SNPs in the *APOE-APOC* cluster (rs4420638), near the *CELSR2-PSRC1-SORT1* (rs599839), *LDLR* (rs6511720) and *APOB* (rs562338) genes; and between triglycerides and SNPs near the *GCKR* (rs780094), APOA5-APOA4-APOC3-APOA1 (rs12286037) and *LPL* (rs10503669) genes (P values and effect sizes are shown in Table 3). In each case, we observed strong evidence for association in both stages of genotyping ($P < 5 \times 10^{-7}$). The association of LDL cholesterol concentrations with the *CELSR2-PSRC1-SORT1* locus is particularly notable, because variants in the region have not been previously implicated in lipid metabolism (Supplementary Fig. 2c online). There is no obvious connection between the genes closest to the association signal, *CELSR2* and *PSRC1*, and lipid metabolism. One possibility is that rs599839 or an associated variant influences expression of *SORT1*, a nearby gene that mediates endocytosis and degradation of lipoprotein lipase[32]. In our sample, allele A at rs599839 was associated with an increase of 5.48 mg/dl in LDL cholesterol concentrations. Notably, the same rs599839 allele has recently been associated with an increased risk of CAD in an independent study[33], suggesting that the association to CAD risk might be mediated by the effect on LDL cholesterol concentrations.

Another tier of loci also remains significant after adjustment for 1,000,000 independent tests. This tier includes additional SNPs for loci within the previous tier and also SNPs near *ABCA1*, *LIPC*, *LIPG* and *PCSK9* (Table 3). Of note, although polymorphisms in all of these genes have a well-established role in lipid metabolism, some of the signals we identified do not overlap with established associations and likely point to new risk alleles (Supplementary Table 2). For example, in *PCSK9*, variants previously associated with LDL cholesterol concentrations have $r^2 < 0.10$ with the variants identified here (Supplementary Table 2). Other examples of newly identified risk alleles include *LIPG* (rs2156552), *LIPC* (rs4775041) and *LDLR* (rs6511720).

This tier also includes six loci where genetic variants have not previously been implicated in lipid metabolism. We found association between HDL cholesterol and SNPs near *GALNT2* and near *MVK* and *MMAB* (Supplementary Fig. 2a,b); between LDL cholesterol and

triglycerides and SNPs in an extended region near *NCAN* and *CILP2* (Supplementary Fig. 2d,h); and between triglycerides and SNPs near *TRIB1*, *MLXIPL* and *ANGPTL3* (Supplementary Fig. 2e–g). Among genes in these six regions, we observed the clearest connections to cholesterol and lipoprotein metabolism for *MLXIPL*, which encodes a protein that binds and activates specific motifs in the promoters of triglyceride synthesis genes, and for *ANGPTL3*, whose protein homolog is a major regulator of lipid metabolism in mice[34]. Rare variants in a related gene, *ANGPTL4*, have been associated with HDL and triglyceride concentrations in humans[35]. A connection to lipid metabolism has also been observed for *MVK* and *MMAB*, two neighboring genes that are regulated by SREBP2 and that share a common promoter[36]. *MVK* encodes mevalonate kinase, which catalyzes an early step in cholesterol biosynthesis, and *MMAB* encodes a protein that participates in a metabolic pathway that degrades cholesterol.

In the other three loci, we did not find any established connections to cholesterol metabolism. The signals near *GALNT2* and *TRIB1* each overlap a single gene. *GALNT2* encodes a widely expressed glycosyltransferase that could potentially modify a lipoprotein or receptor. *TRIB1* encodes a G-protein–coupled receptor-induced protein involved in the regulation of mitogen-activated protein kinases[37] and may regulate lipid metabolism through this pathway. In contrast, the association signal near *NCAN* extends for over 500 kb and encompasses 20 genes. In our combined data, rs16996148 (an Affymetrix array SNP near *CILP2*) was selected for follow-up and showed strong association with both LDL cholesterol ($P \sim 2.7 \times 10^{-9}$) and triglycerides ($P \sim 2.5 \times 10^{-9}$). The allele that is associated with increased LDL cholesterol concentrations is also associated with increased triglyceride concentrations, consistent with the modest positive correlation between the two traits but in contrast to other SNPs associated with both LDL cholesterol and triglycerides that showed association with only one of the traits in our sample. Notably, in the analysis of our three genome-wide association scans and imputed HapMap SNPs, a nonsynonymous coding SNP in the *NCAN* gene (rs2228603, Pro92Ser) showed the strongest evidence for association ($P \sim 1.8 \times 10^{-7}$). This SNP was not included in our initial follow-up analysis, which considered only SNPs on the Affymetrix arrays, but it was in strong LD with rs16996148 ($r^2 = 0.89$). NCAN is a nervous system-specific proteoglycan involved in neuronal pattern formation, remodeling of neuronal networks and regulation of synaptic plasticity[38], with no obvious relation to LDL cholesterol or triglyceride concentrations.

A final tier of genes has one or more SNPs with a *P* value $<10^{-5}$ when stage 1 and stage 2 data are considered together (Table 3). Among these genes is *LCAT*, which encodes a protein with a well-established role in lipid metabolism, and for which well-characterized, but rare, genetic variants have been shown to considerably affect lipid concentrations[39]. Our signal supports a single unconfirmed report of a common variant influencing HDL concentrations[40]. Two other association signals of note are located near the *B3GALT4* and *B4GALT4* genes. Similarly to *GALNT2*, these genes encode glycosyltransferases, and thus our results may implicate glycosyltransferases as having a previously unrecognized influence on variation in lipid concentrations: it is possible that they affect lipid concentrations by modifying lipoprotein receptors[41].

A summary of evidence for association between HDL cholesterol, LDL cholesterol and triglycerides and all markers genotyped or imputed in our initial survey of the genome is available online (see URLs section in Methods). This should enable other investigators to combine our results with their own data or to select SNPs for followup in other samples. As an example of the utility of this resource, in a companion report, Kathiresan and colleagues[16] used the DGI data and the meta-analysis resource to select a set of SNPs for examination in a sample of >18,000 individuals. They report convincing statistical evidence for six newly identified loci at $P < 5 \times 10^{-8}$, all of which overlap with those in our study.

Association with coronary artery disease

In view of the well-established associations between lipid concentrations and CAD, we examined whether the alleles associated with lipid concentrations in the present study were also associated with CAD in the Wellcome Trust Case Control Consortium (WTCCC) sample of ~2,000 CAD cases and an expanded reference panel of ~13,000 British individuals[42] (including ~3,000 random controls and ~2,000 cases for each of five common diseases). Given the relatively modest changes in LDL cholesterol concentrations associated with the alleles we identified (changes of ~2–9 mg/dl per allele), we expected that a subset of SNPs might also be associated with a small increase in susceptibility to CAD. Notably, the results show that all of the alleles that were associated with increased LDL cholesterol concentrations in our sample were more common among CAD cases than in the expanded reference panel (Table 4). Among eleven independent alleles ($r^2 < 0.30$ between nearby alleles) associated with increased LDL cholesterol concentrations in our sample (all with $P < 10^{-6}$ in our sample), all eleven showed increased frequency among CAD cases ($P = 2^{-11} = 0.0005$). The increase was significant ($P < 0.05$) for eight of the SNPs, and nearly so ($P < 0.06$) for another two (Table 4, penultimate column). Although the associated risk estimates are small (relative risk increases of 1.04–1.29 per allele, see Table 4), it is extremely unlikely ($P < 10^{-11}$) that 10 of the 11 SNPs would show suggestive association with CAD at $P < 0.06$ by chance, making the connection between LDL and associated SNPs and CAD particularly worthy of note. Overall, although we observed a correlation between the strength of the observed association with CAD and the impact of each allele on LDL cholesterol concentrations (Spearman correlation coefficient $r = 0.71$, $P = 0.015$), we also found some alleles that had a strong association with LDL cholesterol but no significant association with CAD (for example, rs562338 in the *APOB* locus). We did not find a similar pattern of association for alleles associated with the other lipid traits (Supplementary Table 5 online), although alleles associated with increased triglyceride concentrations near *TRIB1* (for example, at rs17321515) were also associated with increased risk of CAD ($P = 0.0008$). Although the data suggest that nearly all alleles associated with increased LDL cholesterol concentrations will be associated with increased risk of CAD (given a large sample size), the converse is not true, as expected. Alleles at the chromosome 9 locus that show strong association with CAD, coronary heart disease and myocardial infarction[33,42–44] do not seem to influence lipid concentrations in our sample ($P = 0.31$ for association between LDL cholesterol and the SNP most strongly associated with CAD, rs1333049, in our stage 1, and $P > 0.50$ for HDL cholesterol and triglycerides). Additional studies will show whether these variants are also associated with longevity[45], stroke[46] and the other health outcomes associated with LDL cholesterol concentrations.

DISCUSSION

Genes at the loci implicated in our study affect the entire cycle of formation, activity and turnover of lipoproteins and triglycerides. Thus, they encode many of the apolipoproteins themselves (APOE, APOB and APOA5), but they also encode a transcription factor activating triglyceride synthesis (MLXIPL), an enzyme involved in cholesterol biosynthesis (MVK), transporters of cholesterol (ABCA1) and cholesterol ester (CETP), a lipoprotein receptor (LDLR), potential receptor-modifying glycosyltransferases (B4GALT4, B3GALT4 and GALNT2), lipases (LPL, LIPC and LIPG) and a protein involved in cholesterol degradation (MMAB), an inhibitor of lipase (ANGPTL3) and a possible endocytic receptor for LPL (SORT1). Notably, some of the loci we identify (near *TRIB1* and in the large region surrounding *NCAN*, for example) include no obvious functional candidates, and further studies to pinpoint the genes and mechanisms involved could lead to important new insights about lipid metabolism.

In multiple regression models, the variants identified here together accounted for only about 5–8% of the variation in the three lipid traits in the populations studied, leaving much of the heritability of these traits unexplained. The missing genetic factors might be accounted for by a much longer list of loci with common variants of small effect, by rare variants of large effect that have been missed by the association approach, or by interactions between these and other genetic and environmental factors. To clarify the overall role of the loci reported here, it will be critical to resequence the exons and conserved regions in a large number of individuals, in order to identify and evaluate all potential variants within each gene or cluster of genes. This resequencing effort will help identify the functional variants involved in each region. In addition, resequencing may identify nonsense, nonsynonymous or other changes that are associated with variability in lipid concentrations, clarifying the identity of the genes involved in regions with multiple candidates. Resequencing of certain candidate genes has shown that such rare variants can sometimes be identified in individuals at the extremes of lipid concentration distributions[47]; thus, focused studies of the regions identified here in individuals with dyslipidaemia could be particularly informative.

Several of the loci newly identified in this report are potentially attractive drug targets. Furthermore, the ability to stratify individuals on the basis of specific genetic profiles may provide future benefits for optimization of therapy, given that lipid lowering drugs are already widely prescribed to help manage individual lipid profiles and reduce the risk of cardiovascular events[2]. For monogenic forms of diseases that lead to dysregulation of HDL cholesterol, LDL cholesterol or triglyceride concentrations, it is clear that individuals with different mutations require different therapeutic regimens[48,49]. Thus, it is our hope that common variants at the loci identified here will lead to development of novel therapeutics and influence optimal treatment profiles for each individual, resulting in improved management of blood lipid concentrations and reduction of cardiovascular disease risk.

METHODS

Genome-wide association scans

We used standard protocols to genotype the Illumina 317K HumanHap 300 BeadChip and Affymetrix 500K and 10K Mapping Array Sets in the FUSION and SardiNIA samples, respectively. We collaborated with the authors of a previously published study[15] to integrate their results into our analysis. To facilitate comparison of results among the three studies, and to better assess the effects of unmeasured variants, we first identified stretches of haplotype shared between individuals in our sample and those in the HapMap CEU sample and then used these shared stretches to impute missing genotypes. This resulted in a total of ~2,261,000 SNPs that were either genotyped or imputed with high confidence in all three samples.

Association analysis

We first analyzed each study independently. For each marker, we identified a reference allele and calculated statistics summarizing its evidence for association with HDL cholesterol, LDL cholesterol and triglycerides. Association models include gender, age and age^2 as covariates, and additional covariates appropriate to each study. These statistics were then combined across studies taking into account both the number of phenotyped individuals in each study and the direction and magnitude of the estimated effect.

Follow-up

SNPs from the loci showing the strongest evidence for association in the genome-wide scans were selected for analysis in follow-up samples. In our initial round of follow-up, we favored SNPs that were successfully genotyped in both the DGI and SardiNIA studies. As in the analysis of the initial scans, we first conducted analyses within each sample separately and then combined the resulting summary statistics by meta-analysis.

Coronary artery disease analysis

Individual genotype data for this analysis were obtained from the WTCCC website. We first imputed all relevant untyped SNPs using the HapMap CEU as a reference population and carried out tests for association with a likelihood-ratio test.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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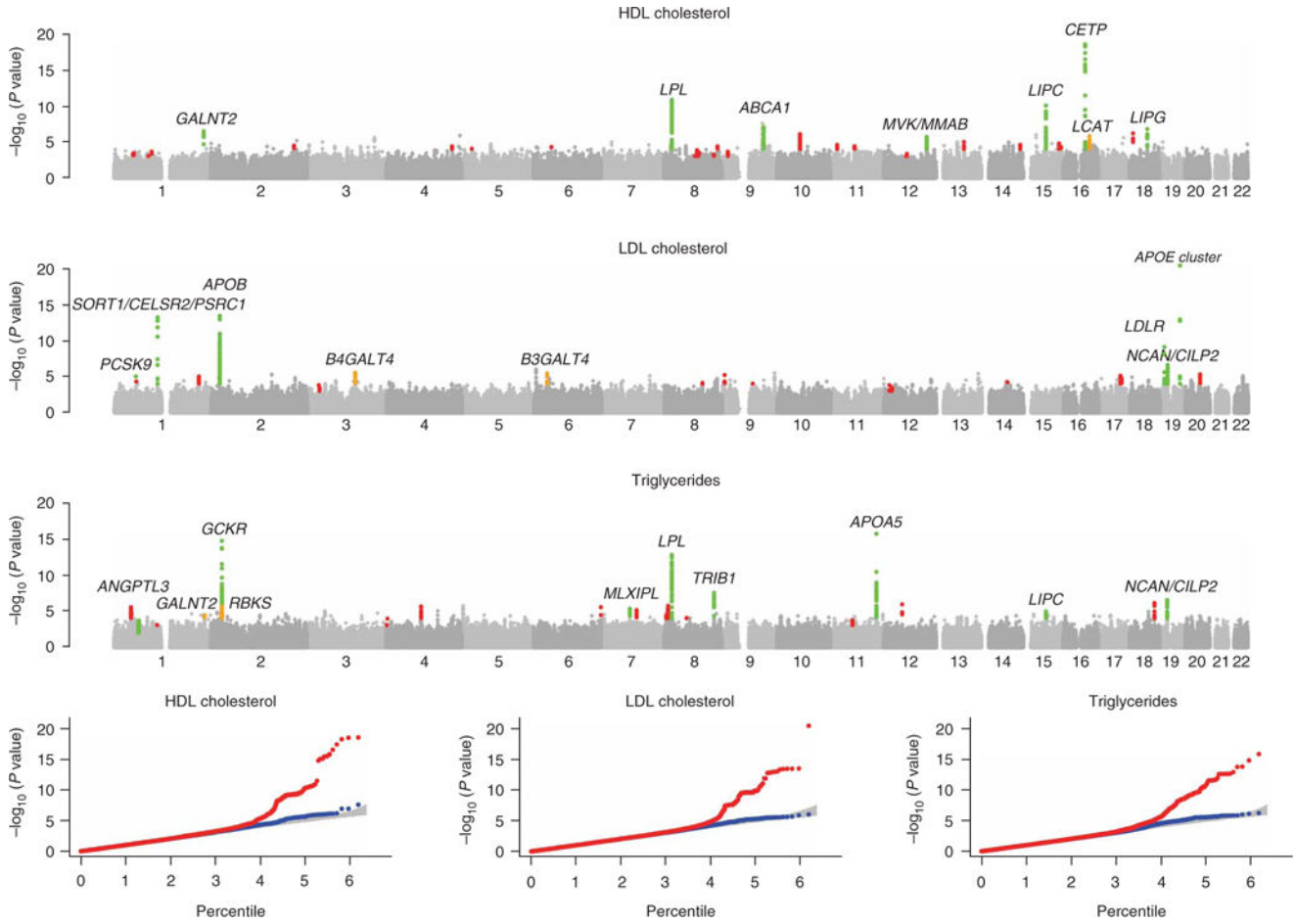

Figure 1.

Summary of genome-wide association scans. The figure summarizes combined genome-wide association scan results in the top 3 panels (plotted as $-\log_{10} P$ value for HDL cholesterol, LDL cholesterol and triglycerides). Loci that were not followed up are in gray. Loci that were followed-up are in green (combined dataset yielded convincing evidence of association, $P < 5 \times 10^{-8}$), orange (combined dataset yielded promising evidence of association, $P < 10^{-5}$), or red (combined dataset did not suggest association, $P > 10^{-5}$). The three panels in the bottom row display quantile-quantile plots for test statistics. The red line corresponds to all test statistics, the blue line corresponds to results after excluding statistics at replicated loci (in green, top panel), and the gray area corresponds to the 90% confidence region from a null distribution of P values (generated from 100 simulations).

Table 1

Characteristics of samples used in genome-wide and follow-up analyses

Samples	Phenotyped individuals[a] (% female)	Demographics			Median trait concentrations (quartile ranges)		
		Geographic origin	Median age (quartile range)	Median BMI (quartile range)	HDL-C (mg/dl)	LDL-C (mg/dl)	Triglycerides (mg/dl)
Genome-wide analyses (*n* = 8,816)							
FUSION							
Type 2 diabetics	773 (41%)	Finland	63.0 (11.1)	29.8 (6.1)	44.9 (15.9)	135.6 (44.5)	150.6 (106.3)
Controls	1,101 (48%)	Finland	62.0 (14.5)	26.6 (5.0)	54.6 (21.7)	141.1 (44.9)	103.7 (60.2)
SardiNIA	4,184 (57%)	Sardinia (in Italy)	42.4 (28.0)	24.9 (6.4)	62.7 (18.6)	124.6 (47.6)	70.0 (54.0)
DGI	2,758 (51%)	Finland, Sweden	62.8 (15.5)	27.3 (5.4)	46.2 (15.9)	148.3 (51.8)	121.7 (81.9)
Follow-up samples (*n* = 11,569)							
FUSION							
Type 2 diabetics	970 (41%)	Finland	60.0 (11.0)	30.2 (6.5)	49.1 (17.0)	123.5 (51.6)	139.1 (90.4)
Controls	1,249 (39%)	Finland	59.0 (10.5)	26.4 (4.9)	56.1 (21.3)	138.4 (46.1)	103.2 (55.8)
ISIS							
Myocardial infarction survivors	1,254 (28%)	United Kingdom	52.0 (14.0)	26.0 (6.0)	40.6 (12.4)	144.0 (48.4)	n/a
Controls	1,252 (35%)	United Kingdom	48.0 (14.0)	24.0 (5.0)	49.9 (16.3)	124.2 (41.4)	132.0 (102.8)
HAPI	861 (46%)	United States	43.0 (22.0)	25.9 (5.9)	55.8 (18.0)	139.1 (56.0)	68.5 (38.0)
SUVIMAX	1,551 (62%)	France	50.0 (9.0)	23.3 (4.1)	61.9 (21.9)	135.8 (41.4)	80.0 (41.6)
BWHHS	3,358 (100%)	United Kingdom	69.0 (9.0)	26.9 (6.1)	61.9 (23.2)	158.3 (54.2)	141.8 (90.4)
Caerphilly	1,074 (0%)	United Kingdom	57.0 (8.0)	26.1 (4.1)	51.5 (17.0)	142.3 (54.3)	132.9 (102.8)

[a]Individuals known to be on lipid lowering therapies were excluded; see Methods.

Nat Genet. Author manuscript; available in PMC 2017 January 03.

Table 2

Summary of GWAS meta-analysis stage 1 results (includes all signals with $P < 5 \times 10^{-7}$)

Locus			Association signal				Corroborating signals ($P < 10^{-6}$)		Nearby genes
SNP	**Chr**	**Position (Mb)**	**Allele(+/−)**	**Freq (+)**	**Effect (mg/dl)**	***P* value**	**SNPs**	**LD groups ($r^2 < 0.2$)**	**(Relative position) (−upstream, +downstream)**
HDL cholesterol (*n* = 8,656)									
rs3764261	16	55.6	A/C	0.29	2.42	**2.8×10^{-19}**	14	2	*CETP* (−2.4 kb)
rs12678919	8	19.9	G/A	0.12	2.44	**1.3×10^{-11}**	84	2	*LPL* (+19.5 kb)
rs10468017	15	56.5	T/C	0.32	1.76	**8.6×10^{-11}**	18	2	*LIPC* (−45.7 kb)
rs1323432	9	101.4	A/G	0.87	1.93	**2.5×10^{-8}**	4	1	*GRIN3A* (Intron 6); *PPP3R2* (−5.7 kb)
rs4149274	9	104.7	G/A	0.69	1.51	7.4×10^{-8}	20	1	*ABCA1* (Intron 5)
rs4939883	18	45.4	C/T	0.86	1.87	1.4×10^{-7}	2	1	*LIPG* (+47.9 kb)
rs4846914	1	226.6	A/G	0.62	1.15	2.9×10^{-7}	4	1	*GALNT2* (Intron 1)
LDL cholesterol (*n* = 8,589)									
rs4420638	19	50.1	G/A	0.16	8.02	**3.2×10^{-21}**	2	1	*APOE/APOC* cluster
rs515135	2	21.2	C/T	0.83	6.08	**3.1×10^{-14}**	116	3	*APOB* (−19.1kb)
rs602633	1	109.5	G/T	0.80	6.09	**4.8×10^{-14}**	8	1	*CELSR2* (+3.1kb); *PSRC1* (+668 bp); *SORT1* (−30 kb)
rs6511720	19	11.1	C/A	0.91	8.03	**6.8×10^{-10}**	1	1	*LDLR* (Intron 1)
rs2228603	19	19.2	C/T	0.93	6.46	1.8×10^{-7}	3	1	*NCAN* (Pro92Ser)
Triglycerides (*n* = 8,684)									
rs964184	11	116.2	G/C	0.12	18.12	**1.5×10^{-16}**	29	2	*APOA5* (+11.2 kb)
rs1260326	2	27.6	T/C	0.40	10.25	**1.5×10^{-15}**	52	2	*GCKR* (Leu446Pro)
rs6993414	8	19.9	A/G	0.46	14.20	**1.4×10^{-13}**	85	2	*LPL* (+78.1 kb)
rs2954029	8	126.6	A/T	0.56	6.42	**2.8×10^{-8}**	15	1	*TRIB1* (+40.3 kb)
rs10401969	19	19.3	T/C	0.92	12.28	2.3×10^{-7}	5	1	*NCAN* (+44.7 kb); *SF4* (Intron 8)

The table summarizes association signals observed in the analysis of lipid concentrations in three GWAS scans. Chromosome assignments, position and gene annotations all refer to the March 2006 Genome Build (UCSC). Alleles are ordered such that the first allele (+) is associated with increased lipid levels. Effect sizes are measured as additive effects, which correspond to the average change in phenotype when one (−) allele is replaced with one (+) allele. Corroborating signals refer to the number of additional SNPs within 1 Mb with $P < 10^{-6}$. The number of LD groups ($r^2 < 0.2$) among these corroborating signals was calculated using LD information from the HapMap CEU sample. *P* values in bold exceed a threshold of 5×10^{-8}, which corresponds to a false-positive rate of 0.05 after adjustment for 1 million independent tests, comparable to the number of independent common SNPs in the Phase II CEU HapMap. For each locus, the most strongly associated SNP is indicated together with its position relative to nearby genes, with a focus on genes previously implicated in lipid metabolism. In the nearby gene column, positions are relative to the transcription start for the nearest gene.

Table 3

Summary of most significant stage 1 and stage 2 results

SNP	Chr	Pos(Mb)	Alleles (+/−)	Freq (+)	Effect (mg/dl)	Association *P* values			Sample sizes		Nearby genes
						Stage 1 (two-sided)	Stage 2 (one-sided)	Combined (two-sided)	Stage 1	Stage 2	
SNPs associated with HDL cholesterol											
rs3764261	**16**	**55.6**	**A/C**	**0.69**	**3.47**	**2.8×10^{-19}**	**6.4×10^{-43}**	**2.3×10^{-57}**	**8,656**	**8,072**	***CETP***
rs1864163	**16**	**55.6**	**G/A**	**0.80**	**4.12**	**3.0×10^{-17}**	**4.3×10^{-28}**	**6.9×10^{-39}**	**8,656**	**3,684**	***CETP***
rs9989419	**16**	**55.5**	**G/A**	**0.65**	**1.72**	**8.0×10^{-16}**	**1.8×10^{-17}**	**3.2×10^{-31}**	**8,656**	**6,981**	***CETP***
rs12596776	**16**	**55.5**	**G/C**	**0.13**	**1.26**	**3.7×10^{-5}**	**1.0×10^{-4}**	**2.8×10^{-8}**	**8,656**	**7,030**	***CETP***
rs1566439	**16**	**55.6**	**C/T**	**0.45**	**0.96**	**2.0×10^{-5}**	**2.1×10^{-4}**	**3.3×10^{-8}**	**8,656**	**4,881**	***CETP***
rs4775041	**15**	**56.5**	**C/G**	**0.67**	**1.38**	**2.8×10^{-9}**	**9.6×10^{-13}**	**3.2×10^{-20}**	**8,656**	**11,426**	***LIPC***
rs261332	**15**	**56.5**	**A/G**	**0.19**	**1.41**	**1.7×10^{-9}**	**1.3×10^{-7}**	**2.3×10^{-15}**	**8,656**	**6,956**	***LIPC***
rs10503669	**8**	**19.9**	**A/C**	**0.10**	**2.09**	**3.2×10^{-10}**	**9.4×10^{-11}**	**4.1×10^{-19}**	**8,656**	**11,431**	***LPL***
rs2197089	**8**	**19.9**	**A/G**	**0.42**	**1.38**	**3.4×10^{-8}**	**3.2×10^{-5}**	**1.0×10^{-11}**	**8,656**	**3,644**	***LPL***
rs6586891	**8**	**20**	**A/C**	**0.34**	**1.00**	**3.5×10^{-5}**	**9.7×10^{-6}**	**2.9×10^{-9}**	**8,656**	**7,017**	***LPL***
rs2144300	**1**	**226.6**	**T/C**	**0.40**	**1.11**	**6.6×10^{-7}**	**4.0×10^{-9}**	**2.6×10^{-14}**	**8,656**	**11,406**	***GALNT2***
rs2156552	**18**	**45.4**	**T/A**	**0.84**	**1.20**	**8.4×10^{-7}**	**7.1×10^{-7}**	**6.4×10^{-12}**	**8,656**	**11,437**	***LIPG***
rs4149268	**9**	**104.7**	**C/T**	**0.355**	**0.82**	**3.3×10^{-7}**	**2.2×10^{-5}**	**1.2×10^{-10}**	**8,656**	**11,327**	***ABCA1***
rs2338104	**12**	**108.4**	**G/C**	**0.45**	**0.48**	**1.9×10^{-6}**	**7.6×10^{-4}**	**3.4×10^{-8}**	**8,656**	**11,399**	***MVK/MMAB***
rs255052	16	66.6	A/G	0.17	0.74	1.5×10^{-6}	0.0087	1.2×10^{-7}	8,656	4,534	*LCAT*
rs1323432	9	101.4	A/G	0.88	−0.03	2.5×10^{-8}	0.82	7.7×10^{-4}	8,656	8,176	*GRIN3A*
SNPs associated with LDL cholesterol											
rs4420638	**19**	**50.1**	**G/A**	**0.82**	**6.61**	**3.2×10^{-21}**	**4.9×10^{-24}**	**3.0×10^{-43}**	**8,589**	**10,806**	***APOE/C1/C4***
rs10402271	**19**	**50**	**G/T**	**0.67**	**2.62**	**9.8×10^{-6}**	**1.5×10^{-5}**	**1.2×10^{-9}**	**8,589**	**6,519**	***APOE/C1/C4***
rs599839	**1**	**109.5**	**A/G**	**0.77**	**5.48**	**1.2×10^{-13}**	**2.7×10^{-21}**	**6.1×10^{-33}**	**8,589**	**10,783**	***CELSR2/PSRC1/SORT1***
rs6511720	**19**	**11.1**	**G/T**	**0.90**	**9.17**	**6.8×10^{-10}**	**3.3×10^{-19}**	**4.2×10^{-26}**	**8,589**	**7,442**	***LDLR***
rs562338	**2**	**21.2**	**G/A**	**0.18**	**4.89**	**1.2×10^{-11}**	**3.6×10^{-12}**	**5.6×10^{-22}**	**8,589**	**10,849**	***APOB***
rs754523	**2**	**21.2**	**G/A**	**0.28**	**2.78**	**7.0×10^{-7}**	**1.3×10^{-6}**	**8.3×10^{-12}**	**8,589**	**6,542**	***APOB***
rs693	**2**	**21.1**	**A/G**	**0.42**	**2.44**	**1.2×10^{-7}**	**0.0034**	**3.1×10^{-9}**	**8,589**	**3,222**	***APOB***
rs11206510	**1**	**55.2**	**T/C**	**0.81**	**3.04**	**7.5×10^{-6}**	**5.4×10^{-7}**	**3.5×10^{-11}**	**8,589**	**10,805**	***PCSK9***

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						Association *P* values			Sample sizes		
SNP	**Chr**	**Pos(Mb)**	**Alleles (+/−)**	**Freq (+)**	**Effect (mg/dl)**	**Stage 1 (two-sided)**	**Stage 2 (one-sided)**	**Combined (two-sided)**	**Stage 1**	**Stage 2**	**Nearby genes**
rs16996148	**19**	**19.5**	**G/T**	**0.89**	**3.32**	**2.4×10^{-6}**	**8.3×10^{-5}**	**2.7×10^{-9}**	**8,589**	**10,841**	***NCAN/CILP2***
rs2254287	6	33.3	G/C	0.38	1.91	2.9×10^{-6}	0.0015	5.1×10^{-8}	8,589	7,440	*B3GALT4*
rs12695382	3	120.4	A/G	0.90	2.23	4.9×10^{-6}	0.0067	1.0×10^{-6}	8,589	10,802	*B4GALT4*
SNPs associated with triglycerides											
rs780094	**2**	**27.7**	**T/C**	**0.39**	**8.59**	**1.7×10^{-14}**	**2.0×10^{-19}**	**6.1×10^{-32}**	**8,684**	**9,723**	***GCKR***
rs11127129	2	28.0	C/G	0.79	3.77	2.0×10^{-4}	3.2×10^{-4}	4.7×10^{-7}	8,684	9,700	*RBKS/GCKR*
rs12286037	**11**	**116.2**	**T/C**	**0.94**	**25.82**	**1.1×10^{-7}**	**1.6×10^{-22}**	**1.0×10^{-26}**	**8,684**	**9,738**	***APOA5/A4/C3/A1***
rs662799	**11**	**116.2**	**G/A**	**0.05**	**16.88**	**4.3×10^{-8}**	**2.7×10^{-10}**	**2.4×10^{-15}**	**8,684**	**3,248**	***APOA5/A4/C3/A1***
rs2000571	11	116.1	A/G	0.17	6.93	4.7×10^{-5}	8.7×10^{-5}	5.7×10^{-8}	8,684	3,209	*APOA5/A4/C3/A1*
rs486394	11	116.0	C/A	0.28	1.50	1.7×10^{-4}	0.0073	7.4×10^{-6}	8,684	3,597	*APOA5/A4/C3/A1*
rs10503669	**8**	**19.9**	**C/A**	**0.895**	**11.57**	**1.4×10^{-9}**	**1.6×10^{-14}**	**3.9×10^{-22}**	**8,684**	**9,711**	***LPL***
rs2197089	**8**	**19.9**	**G/A**	**0.58**	**3.38**	**3.1×10^{-11}**	**0.0029**	**1.1×10^{-12}**	**8,684**	**3,202**	***LPL***
rs6586891	8	20.0	C/A	0.66	4.60	2.4×10^{-4}	5.0×10^{-4}	1.1×10^{-6}	8,684	3,622	*LPL*
rs17321515	**8**	**126.6**	**A/G**	**0.56**	**6.42**	**6.8×10^{-8}**	**1.0×10^{-6}**	**7.0×10^{-13}**	**8,684**	**5,312**	***TRIB1***
rs17145738	**7**	**72.4**	**C/T**	**0.84**	**8.21**	**4.1×10^{-6}**	**5.0×10^{-8}**	**2.0×10^{-12}**	**8,684**	**9,741**	***MLXIPL***
rs1748195	**1**	**62.8**	**C/G**	**0.70**	**7.12**	**2.3×10^{-4}**	**5.4×10^{-8}**	**1.7×10^{-10}**	**8,684**	**9,559**	***ANGPTL3***
rs16996148	**19**	**19.5**	**G/T**	**0.92**	**6.10**	**6.3×10^{-7}**	**2.4×10^{-4}**	**2.5×10^{-9}**	**8,684**	**9,707**	***NCAN/CILP2***
rs4775041	**15**	**56.5**	**C/G**	**0.67**	**3.62**	**7.3×10^{-5}**	**2.9×10^{-5}**	**1.6×10^{-8}**	**8,684**	**8,462**	***LIPC***
rs2144300	1	226.6	C/T	0.60	4.25	4.9×10^{-4}	2.4×10^{-4}	7.9×10^{-7}	8,684	8,473	*GALNT2*

The table summarizes association signals after follow-up of the promising SNPs in stage 2 samples. Column 1 headings are as described for Table 2, with the addition of one-sided *P* values for the stage 2 samples, in which we tested for the same direction of effect as Stage 1—consistent with current best practice for replication of GWAS findings. The effect sizes shown were estimated from stage 2 samples only. SNPs with a combined (stage 1 + 2) *P* value $<10^{-5}$ were included, although we also show GRIN3A for completeness because it was significant in the initial scan. Rows corresponding to SNPs with a combined *P* value $< 5 \times 10^{-8}$ are in boldface. SNPs in this table may not match those in Table 2, which only displays the strongest signal in each locus. The discrepancy also reflects our bias towards genotyped Affymetrix 500K SNPs in the Stage 2 follow-up. Association *P* values for each of the six stage 2 samples are shown in Supplementary Table 4.

Table 4

Association between coronary artery disease and LDL cholesterol–associated SNPs

Locus			LDL-C association (current study)		Association with coronary artery disease (WTCCC)						
					Expanded reference set		CAD cases				
SNP	Chr	Position (Mb)	Alleles (+/−)	*P* value (two-sided)	*n*	Frequency of LDL+ allele	*n*	Frequency of LDL+ allele	*P* value (one sided)	OR (95% CI)	Nearby genes
rs4420638	19	50.1	G/A	**3.0×10^{-43}**	12,281	0.184	1,926	0.209	1.0×10^{-4}	1.17 (1.08–1.28)	***APOE/C1/C4***
rs10402271	19	50.0	G/T	**1.2×10^{-9}**	12,256	0.319	1,921	0.339	0.0068	1.10 (1.02–1.18)	***APOE/C1/C4***
rs599839	1	109.5	A/G	**6.1×10^{-33}**	12,292	0.778	1,923	0.808	1.3×10^{-5}	1.20 (1.10–1.31)	***PSRC1/SORT1***
rs6511720[a]	19	11.1	G/T	**4.2×10^{-26}**	12,301	0.890	1,926	0.902	6.7×10^{-4}	1.29 (1.10–1.52)	***LDLR***
rs562338	2	21.2	G/A	**5.6×10^{-22}**	12,288	0.824	1,924	0.830	0.18	1.04 (0.95–1.14)	***APOB***
rs754523	2	21.2	G/A	**8.3×10^{-12}**	12,292	0.332	1,926	0.353	0.0042	1.10 (1.03–1.18)	***APOB***
rs693	2	21.1	A/G	**3.1×10^{-9}**	12,292	0.520	1,924	0.536	0.028	1.07 (1.00–1.14)	***APOB***
rs11206510	1	55.2	T/C	**3.5×10^{-11}**	12,284	0.807	1,925	0.825	0.0042	1.13 (1.03–1.23)	***PCSK9***
rs16996148	19	19.5	G/T	**2.7×10^{-9}**	12,182	0.915	1,921	0.922	0.055	1.11 (0.98–1.26)	***NCAN/CILP2***
rs2254287[a]	6	33.3	G/C	5.1×10^{-8}	12,301	0.385	1,926	0.399	0.039	1.07 (0.99–1.14)	*B3GALT4*
rs12695382	3	120.4	A/G	1.0×10^{-6}	12,292	0.865	1,924	0.874	0.051	1.09 (0.98–1.20)	*B4GALT4*

The table summarizes association between coronary artery disease and the alleles associated with LDL-C concentrations in our study. Evidence for association was evaluated in the Wellcome Trust Case Control Consortium panel and was not adjusted for additional covariates, because these are not available for the bulk of study participants. Rows corresponding to SNPs that show association with LDL cholesterol with $P < 5 \times 10^{-8}$ in our sample are in boldface.

[a]Expected genotype counts for rs6511720 and rs2254287 were imputed in the WTCCC samples, averaged over cases and controls to estimate allele frequencies and then analyzed using logistic regression to estimate odds ratios. The approach results in unbiased estimates of the odds ratio but can result in estimates of case and control frequencies that are ‘shrunk’ towards the null.