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A Genome-Wide Screen for Interactions Reveals a New Locus on 4p15 Modifying the Effect of Waist-to-Hip Ratio on Total Cholesterol


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Abstract

Recent genome-wide association (GWA) studies described 95 loci controlling serum lipid levels. These common variants explain ~25% of the heritability of the phenotypes. To date, no unbiased screen for gene–environment interactions for circulating lipids has been reported. We screened for variants that modify the relationship between known epidemiological risk factors and circulating lipid levels in a meta-analysis of genome-wide association (GWA) data from 18 population-based cohorts with European ancestry (maximum N = 32,225). We collected 8 further cohorts (N = 17,102) for replication, and rs6448771 on 4p15 demonstrated genome-wide significant interaction with waist-to-hip-ratio (WHR) on total cholesterol (TC) with a combined P-value of 4.79 × 10^-5. There were two potential candidate genes in the region, PCDH7 and CCKAR, with differential expression levels for rs6448771 genotypes in adipose tissue. The effect of WHR on TC was strongest for individuals carrying two copies of G allele, for whom a one standard deviation (sd) difference in WHR corresponds to 0.19 sd difference in TC concentration, while for A allele homozygous the difference was 0.12 sd. Our findings may open up possibilities for targeted intervention strategies for people characterized by specific genomic profiles. However, more refined measures of both body-fat distribution and metabolic measures are needed to understand how their joint dynamics are modulated by the newly found locus.


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Introduction

Serum lipids are important determinants of cardiovascular disease and related morbidity [1]. The heritability of circulating lipid levels is estimated to be 40%–60% and recent genome-wide association (GWA) studies implicated a total of 95 loci associated with serum high-density lipoprotein cholesterol (HDL-C), low-density lipoprotein cholesterol (LDL-C), total cholesterol (TC), and triglyceride (TG) levels [2]. Currently identified common variants explain 10%–12% of the total variation in lipid levels, corresponding to ~25% of the trait heritability [2].

Epidemiological risk factors, such as alcohol consumption, smoking, physical activity, diet and body composition are known to affect lipid levels [3–5]. These risk factors also show moderate to high heritabilities, and over 120 loci with genome-wide significant association have been identified (http://www.genome.gov/26252384). To better understand the biological processes underlying lipid levels, several twin studies [6–8] and candidate gene studies [9–14] have tested for interactions between genes and epidemiological risk factors.

Interactions between genes and modifiable risk factors might help us develop new lifestyle interventions targeted to susceptible epidemiological factor combinations (http://www.genome.gov/18010428). To better understand the biological processes corresponding to triglyceride (TG) levels [2]. Currently identified common variants explain 10%–12% of the total variation in lipid levels, corresponding to ~25% of the trait heritability [2].

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Author Summary

Circulating serum lipids contribute greatly to the global health by affecting the risk for cardiovascular diseases. Serum lipid levels are partly inherited, and already 95 loci affecting high- and low-density lipoprotein cholesterol, total cholesterol, and triglycerides have been found. Serum lipids are also known to be affected by multiple epidemiological risk factors like body composition, lifestyle, and sex. It has been hypothesized that there are loci modifying the effects between risk factors and serum lipids, but to date only candidate gene studies for interactions have been reported. We conducted a genome-wide screen with meta-analysis approach to identify loci having interactions with epidemiological risk factors on serum lipids with over 30,000 population-based samples. When combining results from our initial datasets and 8 additional replication cohorts (maximum N = 17,102), we found a genome-wide significant locus in chromosome 4p15 with a joint P-value of 4.79 × 10^-9 modifying the effect of waist-to-hip ratio on total cholesterol. In the area surrounding this genetic variant, there were two genes having association between the genotypes and the gene expression in adipose tissue, and we also found enrichment of association in genes belonging to lipid metabolism related functions.

Additionally, using Ingenuity software (IPA), we conducted a pathway analysis for genes with eQTL P-value < 0.01 (both trans- and cis-eQTLs). Among other diverse IPA-defined biological functions, there was an eQTL association enrichment among genes belonging to the ‘degradation of phosphatidylcholine’ (3 genes out of 6, P = 6.64 × 10^-3, Benjamini-Hochberg corrected P = 0.0138) and ‘degradation of phosphatidic acid’ (4 genes out of 6, P = 4.71 × 10^-4, B-H corrected P = 0.0349) functions, which are members of broader defined IPA categories “Lipid Metabolism” and “Carbohydrate Metabolism”. These pathways were up-regulated in individuals carrying the G allele of rs6448771, possibly indicating a role for rs6448771 in lipid and carbohydrate metabolism.

The associated SNP also shows evidence for interactions with WHR on LDL-C (effect estimate for the interaction = 0.03, P = 0.0016) and HDL-C (effect estimate = 0.02, P = 0.029) in our stage 1 meta-analysis and after adjusting for TC no residual interaction effect on LDL-C and a little on HDL-C remains (P = 0.834 and P = 0.131 respectively) when testing in data subset. Therefore we tested the SNP – WHR interaction also on a range of lipoprotein subclasses measured using NMR metabolomics platform [16] available in two cohorts (NFBC1966, N = 4624 mean age = 31.0; YFS, N = 1889, mean age = 37.6). The results show that the SNP has a positive interaction effect on large HDL particle concentration (combined effect for the interaction = 0.338, P = 0.0186) and a negative effect on large very-low-density lipoprotein (VLDL) particles (combined effect = −0.466, P = 0.0291) and total triglycerides (combined effect = −0.454, P = 0.0343) (Figure 2).

Discussion

Our genome-wide scan for interactions between SNP markers and traditional epidemiological risk factors in population-based random samples found a genome-wide significant locus, rs6448771, modifying the relationship between WHR and TC. The effect of WHR is estimated to be 64% stronger for individuals carrying two copies of the G allele than for individuals carrying two A alleles. The interaction explains around half a percent of the TC variance that is in par with the main effects of the strongest previously identified TC SNPs individually. This SNP also shows similar interaction effects on a cascade of more detailed lipid fractions suggesting broad involvement in lipid metabolism, which was also suggested by our eQTL association enrichment analysis with adipose tissue expression data.

The eQTL analysis pointed towards two potential candidate genes in the region. The first one of these was protocadherin 7 (PCDH7) gene, which produces a protein that is thought to function in cell-cell recognition and adhesion. The other candidate gene, cholecystokinin A receptor (CCKAR) regulates satiety and release of beta-endorphin and dopamine in the central and peripheral nervous system. It has been previously shown that rats with no expressed CCKAR developed obesity, hyperglycemia and type 2 diabetes [17]. To test whether our eQTL finding was adipose tissue specific, we ran the eQTL analysis for PCDH7 and CCKAR in another dataset with genome wide expression data from blood leukocytes (N = 518) available. CCKAR could not be tested due to its negligible expression in blood leukocytes, and no association was found for the PCDH7 (P-value = 0.284) gene most likely indicating an adipose tissue specific eQTL for PCDH7 as a function of rs6448771.

One interesting aspect of this study, given our large sample size, is that only one signal achieved genome-wide significance, where previously published lipid GWA studies have found close to a hundred. Although power to detect interaction is typically lower than for main effects, especially for rare exposures and SNPs, several of the exposures considered here [such as WHR, BMI, and gender] were common and available for a large proportion of the study sample. This suggests that the contribution of two-way G×E interactions to lipid levels, at least for the risk factors we examined, is rather small, or that our current measures of risk factors may not be robust enough for identifying interactions. More specific measures of both phenotypes and interacting risk factors would give better statistical power in future screens of G×E interactions.

Our findings allow us to draw several conclusions. First, to our knowledge, this is the first time an interaction between a genetic loci and a risk factor has been identified in a genome-wide scan using a stringent statistical threshold for genome-wide significance. Second, in our samples, rs6448771 modified the relationship between WHR and TC, but was not associated with either WHR or TC alone. This observation suggests that genome-wide screens for interactions may be complementary to the current large-scale GWAS efforts for finding main effects. Third, in addition to careful harmonization of both risk factor data and phenotypes, large sample sizes are needed to identify interactions. In our study, 43,903 samples were combined to robustly identify the interaction. Our data, however, suggest that the contribution of G×E interaction using current phenotypes appears limited. Finally, from clinical point of view, the interaction may open up possibilities for targeted intervention strategies for people characterized by specific genomic profiles but more refined measures of both body-fat distribution and metabolic measures are needed to understand how their joint dynamics are modified by the newly found locus.

Materials and Methods

Participating studies

18 studies, with a combined sample size of over 30,000 individuals, participated in the discovery phase of this analysis; 8 studies were available for replication with over 14,000 individuals. In the discovery stage, only population-based cohorts not
ascertained on the basis of phenotype, with a wide variety of well-defined epidemiological measures available, were included. In the replication datasets, the NTR cohort was selected on the basis of low risk for depression and the Genmets samples were selected for metabolic syndrome. In further replication of rs6448771, the EPIC cases were ascertained by BMI. Descriptive statistics for

**Figure 1. Forest plot of main and WHR interaction effect sizes of rs6448771 on TC across the study cohorts.** The circles in the plot are positioned at the effect estimates, betas, and the size corresponds to the number of individuals. The whiskers correspond to the standard errors of betas.

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- Number of individuals
- Effect estimate
- Standard error
these populations are detailed in Table S1A (discovery), S1B (replication) and S1C (further replication). Brief descriptions of the cohorts are provided in the Text S1 section “Short descriptions of the cohorts”.

Phenotype determination

Individuals were excluded from analysis if they were not of European descent or were receiving lipid-lowering medication at the time of sampling. TC, HDL-C, and TG concentrations were measured from serum or plasma extracted from whole blood, typically using standard enzymatic methods. LDL-C was either directly measured or estimated using the Friedewald Equation (LDL-C = TC – HDL-C – 0.45 \* TG for individuals with TG \# 4.52 mmol/l, samples with TG level higher than 4.52 were discarded in the calculation of LDL-C) [18].

Covariates and epidemiological risk factors were ascertained at the same time that blood was drawn for lipid measurements. BMI was defined as weight in kilograms divided by the square of height in meters. Waist circumference was measured at the mid-point between the lower border of the ribs and the iliac crest; hip circumference was measured at the widest point over the buttocks. Waist-to-hip ratio was defined as the ratio of waist and hip circumferences. Alcohol consumption and smoking habits were determined via interviews and/or questionnaires. Both behaviors were coded as dichotomous (abbreviations: ALC for drinker/abstainer and SMO for current smoker/current non-smoker) and semi-quantitative traits. Semi-quantitative alcohol usage (ALCq) was based on daily consumption in grams (0: 0 g/day; 1: >0 and \# 10 g/day; 2: >10 and \# 20 g/day; 3: >20 and \# 40 g/day; 4: >40 g/day). Semi-quantitative smoking (SMOq) was assessed based on the number of cigarettes per day (0: 0 cigarettes/day; 1: >0 and \# 10 cigarettes/day; 2: >10 and \# 20 cigarettes/day; 3: >20 and \# 30 cigarettes/day; 4: >30 cigarettes/day).

Genotyping and imputations

Affymetrix, Illumina or Perlegen arrays were used for genotyping in the discovery cohorts. Each study filtered both individuals and SNPs to ensure robustness for genetic analysis. After quality control, these data were used to impute genotypes for approximately 2.5 million autosomal SNPs based on the LD patterns observed in the HapMap 2 CEU samples. Imputed genotypes were coded as dosages, fractional values between 0 and 2 reflecting the estimated number of copies of a given allele for a given SNP for each individual. Cohort specific details concerning quality control filters, imputation reference sets and imputation software are described in Table S4.

In silico replication

Replication cohorts utilized genome-wide imputed data, as described above, where available. Details on the genotyping methods implemented in the replication samples are described in Table S4.

Serum NMR metabonomics, lipoprotein subclasses

Proton NMR spectroscopy was used to measure lipid, lipoprotein subclass and particle concentrations in native serum samples. NMR methods have been previously described in detail [16,19]. Serum concentrations of total triglycerides (TG), total cholesterol (TC) together with LDL-C and HDL-C were determined. In addition, total lipid and particle concentrations in 14 lipoprotein subclasses were measured. The measurements of these subclasses have been validated against high-performance liquid chromatography [20]. The subclasses were as follows: chylomicrons and largest VLDL particles (particle diameters from approx 75 nm upwards), five different VLDL subclasses: very large VLDL (average particle diameter 64.0 nm), large VLDL (53.6 nm), medium-size VLDL (44.5 nm), small VLDL (32.0 nm), HDL: High-density lipoprotein; IDL: Intermediate-density lipoprotein; LDL: Low-density lipoprotein; HDL: High-density lipoprotein; TG: Triglycerides; TC: Total cholesterol.

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Figure 2. Lipoprotein subclass particle and key serum lipid concentration correlations with WHR for different genotypes of rs6448771. The height of the bar is the meta-correlation between the lipoprotein particle concentration and waist-to-hip ratio, and the whiskers correspond to standard error of the meta-correlation. The P-values have been taken from the interaction meta-analysis and only P-values<0.01 are shown in the figure. The two cohorts in which the lipid particle concentrations were measured with NMR metabonomics platform were YFS and NFBC1966 with combined number of samples of 6,500. XXL, VLDL: Chylomicrons and extremely large very low-density lipoprotein particles; XL: Very large, L: Large, M: Medium, S: Small, XS: Very small; VLDL: very low-density lipoprotein; IDL: Intermediate-density lipoprotein; LDL: Low-density lipoprotein; HDL: High-density lipoprotein; TG: Triglycerides; TC: Total cholesterol.

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Normal transformed residuals resulting from the regression of the other analyses, the phenotypes were defined as the inverse of 

\[ z = \frac{x - \mu}{\sigma} \]

where \( x \) is the original phenotype, \( \mu \) is the mean, and \( \sigma \) is the standard deviation. For analyses where the variable of interest was the phenotypic variance, the residuals were calculated as the inverse-normal transformation of ranks. For analyses where sex was the epidemiological variable of interest, the phenotypes were defined as the inverse-normal transformed residuals resulting from the regression of the lipid measurement on age and age squared. For the other analyses, the phenotypes were defined as the inverse-normal transformed residuals resulting from the regression of the lipid measurement on age, age squared, and sex.

Associations between the transformed residuals and epidemiological risk factors/SNPs were tested using linear regression models under the assumption of an additive (allelic trend) model of genotypic effect. The models regressed phenotypes on epidemiological factor, SNP, and epidemiological factor x SNP terms

\[ \text{Transform}(\text{residuals}) = E + \text{SNP} + E \times \text{SNP} \]

and tested if the effect for E x SNP was 0 using 1 df Wald tests. In family-based cohorts, linear mixed modeling was implemented to control for relatedness among samples [21]. Analysis software used by the individual cohorts is described in Table S1A and S1B.

The interaction terms from the regression analyses were meta-analyzed using inverse variance weighted fixed-effects models [22]. Prior to meta-analysis, genomic control correction factors (\( \lambda \text{GC} \)) [23], calculated from all imputed SNPs, were applied on a per-study basis to correct for residual bias possibly caused by population sub-structure. Meta-analyses were performed by two independent analysts using METAL (http://www.sph.umich.edu/csg/abecasis/Metal/index.html) and the R [24] package MetaABEL (part of the GenABEL suite, http://www.genabel.org/). All results were concordant, reflecting a robust analysis. Results were selected for in silico replication if the meta-analysis P-value was less than 10^{-6}. Results passing the threshold of suggestive genome-wide association (\( P \text{-value} \leq 5 \times 10^{-7} \)) were selected for further replication by direct genotyping.

The commonly accepted genome wide level of significance (5 \times 10^{-8}) reflects the estimated testing burden of one million independent SNPs in samples of European ancestry [25]. To address the multiple testing arising from testing interactions with multiple risk factors, we set the genome wide significance threshold to 5 \times 10^{-6} as 1.67 \times 10^{-8} corresponding to three principal components explaining 97.8% of the total variation of the risk factors (Table S3).

Pathway analysis. The functional analyses were generated through the use of Ingenuity Pathways Analysis (Ingenuity Systems, www.ingenuity.com). The Functional Analysis identified the biological functions and/or diseases that were most significant to the data set. Molecules which met the P-value cutoff of 0.01 for the rs6448771 – expression association in dataset of 54 Finnish individuals with both genotype and adipose tissue expression data, and were associated with biological functions and/or diseases in Ingenuity’s Knowledge Base were considered for the analysis. Right-tailed Fisher’s exact test was used to calculate a P-value determining the probability that each biological function and/or disease assigned to that data set is due to chance alone and Benjamini-Hochberg multiple test correction [26] was applied.

Supporting Information

Figure S1 Effect of waist-to-hip ratio on total cholesterol as a function of rs6448771 genotypes. The bars in the plot are the effect estimates from three meta-analyzed linear models where total cholesterol (TC) has been explained using waist-to-hip ratio (WHR). The analyses were ran in three strata based on the rs6448771 genotypes. The whiskers in the plot correspond to the confidence intervals of the effect estimates.

Table S1 Cohort characteristics. The number of study subjects with available phenotype and genotype (lower line) and summary statistics (upper line) for each cohort and trait. For continuous traits mean (standard deviation) is presented. For dichotomous traits number of individuals with phenotype present (%) is presented. TC: total cholesterol (mmol/l); HDL-C: high-density lipoprotein cholesterol (mmol/l); LDL-C: low-density lipoprotein cholesterol (mmol/l); TG: triglycerides (mmol/l); BMI: body mass index; WHR: waist-to-hip ratio; NA: not available.

Table S2 Loci having \( P \text{-value} < 1 \times 10^{-6} \) in Stage 1 analyses and replication of the SNPs. Best SNP per locus having \( P \text{-value} < 1 \times 10^{-6} \) in the Stage 1 analysis combining 19 cohorts. The bolded number is the genome-wide significant \( P \text{-value} \). \( N \): number of individuals; \( SE \): standard error of the effect estimate, Beta; LDL-C: low-density lipoprotein cholesterol; TC: total cholesterol; TG: triglycerides; HDL-C: high-density lipoprotein cholesterol; ALC: alcohol usage (drinker/abstainer); WHR: waist-to-hip ratio; BMI: body mass index; SMO: smoking (current/not); SMOQ: semi-quantitative smoking (0: 0 cigarettes/day; 1: 10 cigarettes/day; 2: >10 and \( \leq 20 \) cigarettes/day; 3: >20 and \( \leq 30 \) cigarettes/day; 4: >30 cigarettes/day); ALCQ: semi-quantitative alcohol (0: 0 g/day; 1: >0 and \( \leq 10 \) g/day; 2: >10 and \( \leq 20 \) g/day; 3: >20 and \( \leq 40 \) g/day; 4: >40 g/day).

Table S3 Effect of rs6448771 on total cholesterol (TC) by waist-to-hip ratio (WHR) tertiles and effect of WHR on TC by SNP genotype classes. Section A shows the combined effect of waist-to-hip ratio (WHR) on total cholesterol (TC) stratified by the rs6448771 genotype class from five Finnish cohorts (FINRISK, NFBC1966, YFS, Gennets and HBBCs, combined number of individuals is 12,782) and section B shows the combined effect of the SNP on TC stratified by WHR tertiles from the same cohorts. The limit values for the waist-to-hip ratio (WHR) tertiles have been calculated using WHR values from all five datasets. Both analyses were ran using untransformed and standardized scales and were adjusted with age, age squared, and sex. Beta: effect estimate; CI: confidence interval.

Table S4 Details of GWA data in discovery and replication cohorts. QC: quality control; MAF: minor allele frequency; HWE: Hardy-Weinberg equilibrium.

Table S5 Proportions of variance explained by principal components. Principal components analysis (PCA) was run for the seven risk factors used in the screening. PC: Principal Component.
Text S1  Short descriptions of the cohorts and a full list of acknowledgements.

References


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Author Contributions

Conceived and designed the experiments: LP CMD YSA SR. Performed the experiments: IS AI LCK. Analyzed the data: IS AI LCK PPL RPSM ET JSR CL MM WI JIH VI PH IML TE ZK NW MV APS AKJ. Contributed reagents/materials/analysis tools: JSV MP TR AKP PS AJ NS AC H TP IP AT FK AD FR GWM JBW MK TL NBF GW EJ CG AP MSS DW AM MS AGU AJ GN CW BHRW MRJ MAK JR KOK DIB NLP UG JFW IR HC PPP TDS JCMW JGE VS BAO OTR HEW CG MRJ NGM AH. Wrote the paper: IS AI MIM CMD YSA SR.