

GENETICS

Loss-of-function variants influence the human serum metabolome

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The metabolome is a collection of small molecules resulting from multiple cellular and biological processes that can act as biomarkers of disease, and African-Americans exhibit high levels of genetic diversity. Exome sequencing of a sample of deeply phenotyped African-Americans allowed us to analyze the effects of annotated loss-of-function (LoF) mutations on 308 serum metabolites measured by untargeted liquid and gas chromatography coupled with mass spectrometry. In an independent sample, we identified and replicated four genes harboring six LoF mutations that significantly affected five metabolites. These sites were related to a 19 to 45% difference in geometric mean metabolite levels, with an average effect size of 25%. We show that some of the affected metabolites are risk predictors or diagnostic biomarkers of disease and, using the principle of Mendelian randomization, are in the causal pathway of disease. For example, LoF mutations in *SLCO1B1* elevate the levels of hexadecanedioate, a fatty acid significantly associated with increased blood pressure levels and risk of incident heart failure in both African-Americans and an independent sample of European-Americans. We show that *SLCO1B1* LoF mutations significantly increase the risk of incident heart failure, thus implicating the metabolite in the causal pathway of disease. These results reveal new avenues into gene function and the understanding of disease etiology by integrating -omic technologies into a deeply phenotyped population study.

INTRODUCTION

Defining the genetic architecture of health and diseases is a key goal of contemporary human genetics. The human metabolome, a complete set of small molecules reflecting multiple metabolic and physiological processes, holds promise to bridge gene action to disease end points via intermediate phenotypes (1). Annotated loss-of-function (LoF) variants, which are expected to signal nonsense-mediated decay (2), are likely to have large effects on phenotypes and occur more often in genomes of African descent than in genomes of European descent (3). LoF variants that lower risk factor levels and disease risk have been proven to be good predictors of drug efficacy (4, 5). Given the biological role of LoF variants and the metabolome, we leveraged these two -omic technologies in a deeply phenotyped population of African-Americans to systematically investigate the effects of LoF sites on the human metabolome and further influences on disease risk.

RESULTS

We sequenced the exomes and measured the metabolomes of 1361 African-American (described in table S1) participants from the Atherosclerosis Risk in Communities (ARIC) Study. We defined LoF variation as sequence changes caused by single-nucleotide variants (SNVs) or small insertions and deletions (indels), which are predicted to result in a nonviable transcript or a greatly truncated protein product. A total of 7038 genes harboring 12,522 LoF variant sites (5060 stopgains, 2599 splice sites, and 4863 frameshift indels) were identified with an average of 111.7 heterozygous and 14.5 homozygous LoF sites per person (fig.

S1). We quantified metabolomic profiles in serum using liquid and gas chromatography followed by mass spectrometry (LC/GC-MS). After applying stringent quality control standards for metabolite levels, we analyzed 308 known serum metabolites consisting of 83 amino acids, 16 carbohydrates, 9 cofactors and vitamins, 7 energy metabolites, 136 lipids, 12 nucleotides, 25 peptides, and 20 xenobiotics (table S2).

To increase statistical power and reduce the false-positive rate, we limited the analyses to 324 LoF sites with a minor allele frequency (MAF) $\geq 5\%$ and 1285 genes with a cumulative minor allele count (cMAC) ≥ 7 , using single-variant and gene-based burden tests, respectively. We identified nine genes harboring 18 LoF sites and affecting 10 metabolite levels (Table 1; $P < 5.0 \times 10^{-7}$, single-variant test; $P < 1.3 \times 10^{-7}$, burden test). Detailed results are shown in table S3, and quantile-quantile (QQ) plots are shown in fig. S2. These sites were related to a 19 to 45% difference in geometric mean metabolite levels, with an average effect size of 31%. Genotypes of all significantly associated sites were validated using an orthogonal laboratory technology (that is, Array-based genotyping, Sequenom genotyping, or Sanger sequencing). As a positive control, we observed that LoF sites in *PCSK9* had lower cholesterol levels compared to the noncarriers ($P = 5.4 \times 10^{-9}$). Except for *PCSK9* and *HAL*, the remaining LoF sites in seven genes were novel findings (*C6orf25*, *CD36*, *FAM198B*, *LRRRC46*, *LRRRC69*, *SLCO1B1*, and *TEX15*; Table 1). To validate our findings, we sequenced the exomes of an additional 559 African-Americans and quantified their metabolomic profiles using LC/GC-MS. In this replication sample, 5 of 10 significant gene-metabolite relationships were reproduced ($P < 0.05$; Table 1). Four genes did not have enough LoF carriers to be analyzed, and one gene-metabolite association did not reach nominal statistical significance, although the direction of the effect was consistent.

Homozygous LoF genotypes are rare in the population at each site, uncommon within each individual across the genome, and more likely

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Table 1. Ten significant gene-metabolite associations identified among African-Americans in ARIC. Decanoylcarnitine and octanoylcarnitine were identified using the single-variant test, and the remains were identified using the gene-based burden test. Gene-related human pleiotropy was obtained through OMIM (Online Mendelian Inheritance in Man) (www.ncbi.nlm.nih.gov/omim) and the NHGRI GWAS catalog (www.genome.gov/gwastudies). NA, not applicable; LDL, low-density lipoprotein; MI, myocardial infarction; 5-HETE, 5-hydroxyicosatetraenoic acid; CHD, coronary heart disease; CVD, cardiovascular disease; MCAD, medium-chain acyl-CoA dehydrogenase.

Metabolite	Pathway	Gene	P	β (SE)	cMAC	Gene-related human pleiotropy	Metabolite-related human phenotypes	Replication P
Decanoylcarnitine	Lipid	<i>CD36</i>	2.7×10^{-7}	-0.19 (0.04)	221	Platelet glycoprotein IV deficiency, CHD	MCAD deficiency (7)	0.03
Octanoylcarnitine	Lipid	<i>CD36</i>	3.9×10^{-8}	-0.20 (0.04)	221	Platelet glycoprotein IV deficiency, CHD	MCAD deficiency (7)	0.03
Histidine	Amino acid	<i>HAL</i>	2.3×10^{-13}	0.23 (0.03)	26	Histidinemia	Rheumatoid arthritis (23), CHD (24)	0.05
Methionine sulfoxide	Amino acid	<i>C6orf25</i>	1.3×10^{-8}	-0.45 (0.08)	9	—	Aging (25)	NA
Mannose	Carbohydrate	<i>TEX15</i>	7.9×10^{-9}	-0.70 (0.12)	10	—	—	NA
Cholesterol	Lipid	<i>PCSK9</i>	5.4×10^{-9}	-0.21 (0.04)	30	LDL, CHD, MI, statin response, familial hypercholesterolemia	Atherosclerosis (26), CVD (27)	0.0002
Deoxycarnitine	Lipid	<i>LRRC69</i>	8.5×10^{-16}	-0.42 (0.05)	17	—	—	0.6
Hexadecanedioate	Lipid	<i>SLCO1B1</i>	2.2×10^{-9}	0.38 (0.06)	67	Hexadecanedioate, tetradecanedioate, octadecanedioate, bilirubin, hyperbilirubinemia, statin-induced myopathy, statin response	—	0.0001
5-HETE	Lipid	<i>FAM198B</i>	4.5×10^{-9}	-0.38 (0.07)	14	—	—	NA
Urate	Nucleotide	<i>LRRC46</i>	1.1×10^{-7}	-0.44 (0.08)	10	—	Gout (28), type 2 diabetes (29), CVD (30) mortality (31)	NA

to lead to extreme phenotypes. Here, we observed three genes (*CD36*, *SLCO1B1*, and *LRRC69*), each of which had homozygous stopgain mutations influencing four metabolite levels (Fig. 1). Each additional LoF allele in *CD36* (c.975T>G) had a lowering effect on octanoylcarnitine and decanoylcarnitine levels, and each additional LoF allele in *SLCO1B1* (c.481+1G>T) demonstrated an increasing effect on hexadecanedioate levels. *LRRC69* (c.933+2T>A) homozygous LoF status appeared to have a marked effect on deoxycarnitine levels ($P = 6.8 \times 10^{-35}$). We next genotyped these three variants in an independent sample of 508 ARIC African-Americans and replicated our findings with *CD36* and *SLCO1B1* ($P < 0.017$, Bonferroni correction); no homozygote was observed in the replication genotype samples for *LRRC69*.

CD36 is known as a fatty acid translocase that enhances cellular fatty acid uptake, which is a key step in energy metabolism (6). We discovered that LoF mutation in *CD36* influences serum octanoylcarnitine and decanoylcarnitine levels—two acylcarnitine biomarkers of medium-chain acyl-coenzyme A dehydrogenase (MCAD) deficiency (7)—and replicated this mutation. MCAD deficiency [MIM (Mendelian Inheritance in Man): 201450] is a rare metabolic disorder caused by homozygous or compound heterozygous mutations in the *ACADM* gene, which prevents the body from converting certain fatty acids to energy, especially under fasting conditions. Our results suggest an additional role of *CD36* in regulating acylcarnitine levels in addition to *ACADM*.

In genome-wide association studies (GWAS), common non-functional variants tagging *SLCO1B1* have been reported to be associated with fatty acid levels, including hexadecanedioate (8). Hexadecanedioic acid is a long-chain dicarboxylic acid, generated from fatty acid ω -oxidation and thereafter metabolized by β -oxidation in peroxisomes. *SLCO1B1* encodes a protein that mediates the cellular uptake of numerous endogenous compounds and is involved in the metabolism and clearance of multiple drug compounds, including (the popular cholesterol-lowering drug) statins (9). Here, we show that LoF variants in *SLCO1B1* have a profound effect on serum hexadecanedioate levels ($P = 2.2 \times 10^{-9}$). We next genotyped the LoF site in *SLCO1B1* (c.481+1G>T) among the entire ARIC participants (10,263 European-Americans and 3543 African-Americans) and demonstrated that one copy of mutated T allele was associated with 29% increased risk for heart failure (HF) [hazard ratio (HR), 1.29; $P = 0.048$], indicating a direct moderate effect of *SLCO1B1* on HF. One other disease relationship cascade, *TEX15* LoF variants with mannose levels and mannose levels with diabetes and HF (fig. S3), was unsurprising because of the correlation between mannose and glucose.

To determine whether this fatty acid is involved in the development of HF in a general population, we examined its association with incident HF among ARIC African-Americans ($n = 1792$), who had a median follow-up time of 22 years. We show that high levels of hexadecanedioate

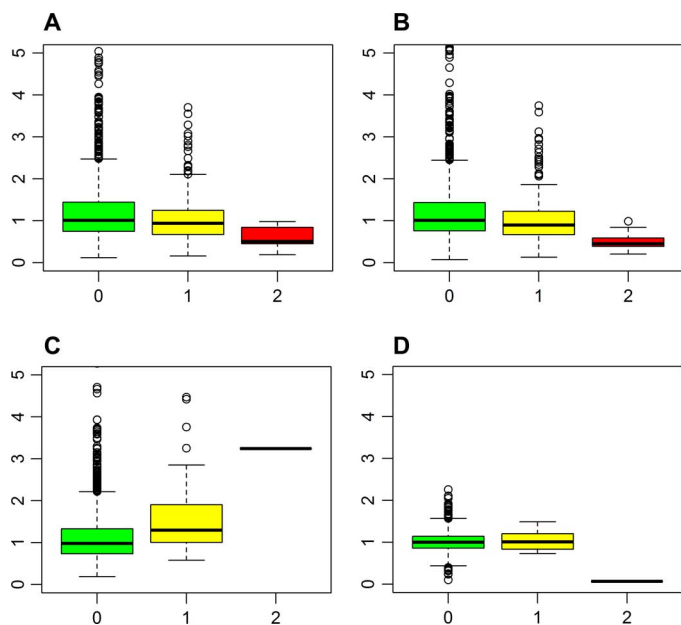


Fig. 1. Distribution of metabolite levels among LoF mutation carriers in ARIC. The x axis indicates the number of LoF allele carried, and the y axis indicates the metabolite levels. **(A)** Octanoylcarnitine levels among *CD36* (c.975T>G) LoF mutation carriers. **(B)** Decanoylcarnitine levels among *CD36* (c.975T>G) LoF mutation carriers. **(C)** Hexadecanedioate levels among *SLC01B1* (c.481+1G>T) LoF mutation carriers. **(D)** Deoxycarnitine levels among *LRRC69* (c.933+2T>A) LoF mutation carriers.

are associated with increased risk of incident HF beyond the effect of traditional risk factors (HR, 1.22; $P = 3.0 \times 10^{-7}$). To generalize its predictability of HF, we further measured this metabolite in 1421 ARIC European-Americans with 23.5 years of median follow-up time. Again, hexadecanedioate was positively and significantly related to incident HF risk in European-Americans (HR, 1.09; $P = 0.005$). The relationship between hexadecanedioate levels and HF in both ancestries remained significant even in those without a history of previous myocardial infarction. In addition, in both European-Americans and African-Americans, high hexadecanedioate levels were related to high systolic blood pressure and diastolic blood pressure levels, which are important risk factors for HF (all $P < 0.004$; table S4) (10). These observational data in humans are consistent with recent feeding studies in rats, showing that adding hexadecanedioate to the diet increased blood pressure levels (11). Vascular reactivity to noradrenaline was significantly increased in mesenteric resistance arteries among hexadecanedioate-treated rats (11), highlighting a possible vascular mechanism that underlies hexadecanedioate and blood pressure association.

DISCUSSION

The transition from GWAS to exome sequencing-based rare variant studies has proven difficult, requiring large sample sizes and often leading to novel variants in known genes rather than the discovery of novel genes (12). Our study focused on the human metabolome, an intermediate phenotype that bridges gene effects to clinical end points, to promote novel gene discoveries. Because the samples originated from a large longitudinal cohort study, we were able to explore

the predictive relationships of the observed findings on the onset of disease and the maintenance of health. Because of their increased genetic diversity (13) and undue burden of disease, this study focused on African-Americans. Future studies are encouraged to include other ethnic groups. Our findings illuminate the value of using -omic studies in a deeply phenotyped population to generate new hypotheses and enhance our understanding of gene function and disease etiology.

MATERIALS AND METHODS

Study population and metabolome measurements

The ARIC Study is a prospective epidemiological study designed to investigate the etiology and predictors of cardiovascular disease (CVD). The ARIC Study enrolled 15,792 individuals aged 45 to 64 years from four U.S. communities (Forsyth County, NC; Jackson, MS; suburbs of Minneapolis, MN; and Washington County, MD) in 1987–1989 (baseline) who were followed up for four completed visits in 1990–1992, 1993–1995, 1996–1998, and 2011–2013. A detailed description of the ARIC study design and methods is published elsewhere (14). Basic CVD risk factors were measured at each visit, and CVD end points, including HF, were ascertained annually using telephone interviews and hospital medical record review. In ARIC, incident HF was defined as the first hospitalization or death from HF for those without a prior HF hospitalization. The diagnosis of HF was based on *International Classification of Diseases, Ninth Revision* (ICD-9) code 428.3. Individuals were followed up for events from baseline to 31 December 2011, and those who were lost to follow-up were censored at the date of last contact. Incident type 2 diabetes was defined in diabetes-free participants at baseline as having any of the following during a follow-up visit until visit 4: (i) a fasting glucose level ≥ 7.0 mM, (ii) a nonfasting glucose level ≥ 11.1 mM, (iii) use of a diabetes medication, or (iv) a self-reported physician diagnosis.

Metabolite profiling was measured using fasting serum samples collected at the baseline examination in 1987–1989 among ARIC European-Americans and African-Americans. For the discovery African-American samples, a total of 602 metabolites were detected and semiquantified by Metabolon Inc. using an untargeted LC/GC-MS-based metabolomic quantification protocol (15, 16). Metabolites were excluded if (i) more than 50% of the samples had values below the detection limit or (ii) they had unknown chemical structures. After this assessment, a total of 308 named metabolites were included in the present study. For the replication samples, we focused on metabolites that were significantly identified in the discovery samples.

Whole exome sequencing and variant validation

The annotated exome was captured by NimbleGen's VCRome2.1 (Roche NimbleGen), and the captured exons were sequenced using Illumina HiSeq 2000. The Burrows-Wheeler Aligner was used to align sequences to the hg19 reference genome (17). Allele calling and variant call file construction were performed using the Atlas2 suite (18) (Atlas-SNP and Atlas-Indel). SNVs were excluded if they had a posterior probability < 0.95 , a total depth of coverage $< 6\times$, an allelic fraction < 0.1 , 99% of reads in a single direction, and homozygous reference alleles with $< 6\times$ coverage. Low-quality indels were excluded if they had a minimum total depth < 30 , an allelic fraction < 0.2 for heterozygous variants and < 0.8 for homozygous variants, and variant reads $< 10\times$.

Variants were annotated using ANNOVAR (19) and dbNSFP v2.0 (20) according to the reference genome GRCh37 and National Center for Biotechnology Information Reference Sequence. LoF variants included in this study were defined as premature stop codons occurring in the exon, essential splice site disrupting, and indels predicted to disrupt the downstream reading frame.

Following statistical analysis, all significantly associated variants were validated using an orthogonal laboratory technology (that is, Array-based genotyping, Sequenom genotyping, or Sanger sequencing). All reported results were validated with 100% accuracy, indicating identical genotypes in applied genotyping or sequencing methods.

For the purpose of replication, three LoF sites—*CD36* (c.975T>G), *SLCO1B1* (c.481+1G>T), and *LRRC69* (c.933+2T>A), having both homozygous and heterozygous genotypes in the study sample and which were significantly related to a clinical phenotype—were genotyped in an independent sample of 508 ARIC African-Americans. The calling and quality control methods were described elsewhere (18).

Statistical analyses

Metabolite levels below the detectable limit of the assay were imputed with the lowest detected value for that metabolite in all samples, and all metabolite values were natural log-transformed before the analyses. Single-variant analyses on sites with MAF $\geq 5\%$ and burden T5 tests (21) that evaluate the joint effects of rare alleles (MAF $< 5\%$) in a gene were conducted on each metabolite after adjusting for age, gender, estimate glomerular filtration rate calibrated (eGFR) (22), and population structure. Statistical significance was defined as $P < 5.0 \times 10^{-7}$ for single-variant tests (Bonferroni correction of 99,792 tests: 324 variants \times 308 metabolites) and $P < 1.3 \times 10^{-7}$ for the T5 tests (Bonferroni correction of 395,780 tests: 1285 genes \times 308 metabolites).

All available African-American samples with metabolomic data were used to estimate the association between metabolite levels and the longitudinal onset of four clinical end points, including coronary heart disease (CHD), HF, chronic kidney disease, and type 2 diabetes. Metabolite levels were standardized before the analysis. Cox proportional hazard models adjusting for age, gender, body mass index, hypertension, anti-hypertensive medication use, diabetes, high-density lipoprotein, total cholesterol, current smoking, eGFR, and prevalent CHD were generally applied for incident disease analyses. Prevalent cases were excluded for the corresponding incident disease analyses. The proportional hazard assumption was examined and not rejected. Statistical significance was defined as $P < 4.5 \times 10^{-5}$ (Bonferroni correction of 1232 tests: 4 diseases \times 308 metabolites).

Cox proportional hazard models were separately applied in ARIC European-Americans and African-Americans to evaluate whether the LoF variant in *SLCO1B1* was associated with incident HF adjusting for age, gender, and population structure. Inverse variance fixed-effect meta-analyses were used to combine the results across the races to obtain an overall disease risk estimate, SE, and P value.

Three LoF sites—*CD36* (c.975T>G), *SLCO1B1* (c.481+1G>T), and *LRRC69* (c.933+2T>A), having both homozygous and heterozygous genotypes in the study sample and which were significantly related to a clinical phenotype—were replicated in an independent sample of 508 ARIC African-Americans. Metabolite levels were natural log-transformed before the replication analyses along with adjustment for age, gender, eGFR, and population structure. Statistical significance for the replication study was defined as $P < 0.017$ (Bonferroni correction of three tests). All the analyses were performed using R (www.r-project.org).

SUPPLEMENTARY MATERIALS

Supplementary material for this article is available at <http://advances.sciencemag.org/cgi/content/full/2/8/e1600800/DC1>

table S1. Baseline characteristics of African-Americans in ARIC having metabolomic and exome sequence data.

table S2. List of 308 named metabolites measured in ARIC.

table S3. Eighteen significant LoF sites with metabolite associations identified among African-Americans in ARIC.

table S4. Relationship between hexadecanedioate and blood pressure levels among European-Americans and African-Americans in ARIC.

fig. S1. Distribution of the number of LoF sites per individual among ARIC African-Americans.

fig. S2. QQ plots of the expected and observed $-\log P$ values for 10 identified metabolites.

fig. S3. Pathways among genes, metabolites, and diseases identified among ARIC African-Americans.

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