Genome-wide analysis of mitochondrial DNA copy number reveals multiple loci implicated in nucleotide metabolism, platelet activation, and megakaryocyte proliferation

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Abstract

Blood-derived mitochondrial DNA copy number (mtDNA-CN) is a minimally invasive proxy measure of mitochondrial function that exhibits both inter-individual and intercellular variation. While mtDNA-CN has been previously associated with various aging-related diseases, little is known about the genetic factors that may modulate this phenotype. We performed a genome-wide association study (GWAS) in 465,809 individuals of White (European) ancestry from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium and the UK Biobank (UKB). We identified 129 SNPs with statistically significant, independent effects associated with mtDNA-CN across 96 loci. A combination of fine-mapping, variant annotation, co-localization, and gene set enrichment analyses were used to prioritize genes within each of the 129 independent sites. Putative causal genes were enriched for known mitochondrial DNA depletion syndromes ($p = 3.09 \times 10^{-15}$) and the gene ontology (GO) terms for mtDNA metabolism ($p = 1.43 \times 10^{-8}$) and mtDNA replication ($p = 1.2 \times 10^{-7}$). A clustering approach leveraged pleiotropy between mtDNA-CN associated SNPs and 42 mtDNA-CN associated phenotypes to identify functional domains, revealing five distinct groups, including platelet activation, megakaryocyte proliferation, and mtDNA metabolism. In conclusion, in a GWAS of mtDNA-CN conducted in >450,000 individuals, we identified SNPs within loci that implicate novel pathways that provide a framework for defining the underlying mechanisms involved in genetic control of mtDNA-CN.

Introduction

Mitochondria are the cellular organelles primarily responsible for producing the chemical energy required for metabolism, as well as signaling the apoptotic process, maintaining homeostasis, and synthesizing several macromolecules such as lipids, heme and iron-sulfur clusters[1,2].

Mitochondria possess their own genome (mtDNA); a circular, intron-free, double-stranded, haploid, ~ 16.6 kb maternally inherited molecule encoding 37 genes vital for proper mitochondrial function. Due to the integral role of mitochondria in cellular metabolism, mitochondrial dysfunction is known to play a critical role in the underlying etiology of several aging-related diseases[3–5].

Unlike the nuclear genome, a large amount of variation exists in the number of copies of mtDNA present within cells, tissues, and individuals. The relative copy number of mtDNA (mtDNA-CN) has been shown to be positively correlated with oxidative stress[6], energy reserves, and mitochondrial membrane potential[7]. As a minimally invasive proxy measure of mitochondrial dysfunction[8], decreased blood-derived mtDNA-CN has been previously associated with aging-related disease states including frailty[9], cardiovascular disease[10–12], chronic kidney disease[13], neurodegeneration[14,15], and cancer[16].

Although mtDNA-CN measured from whole blood presents itself as an easily accessible and minimally invasive biomarker, cell type composition has been shown to be an important confounder, complicating analyses[17,18]. For example, while platelets generally have fewer mtDNA molecules than leukocytes, the lack of a platelet nuclear genome drastically skews mtDNA-CN estimates. As a result, not only is controlling for cell composition extremely vital for accurate mtDNA-CN estimation, but interpreting the results in relation to the impact of cell composition becomes a necessity[18–20].

Although the comprehensive mechanism through which mtDNA-CN is modulated is largely unknown[21,22], twin studies have estimated broad-sense heritability ~0.65, consistent with moderate genetic control[23]. Several nuclear genes have been shown to directly modulate mtDNA-CN, specifically those within the mtDNA replication machinery such as the mitochondrial

polymerase, *POLG* and *POLG2*[24,25], as well as the mitochondrial DNA helicase, *TWNK*, and the mitochondrial single-stranded binding protein, *mtSSB*[26]. Furthermore, nuclear genes which maintain proper mitochondrial nucleotide supply including *DGUOK* and *TK2* have also been shown to regulate mtDNA-CN[27–29]. To further elucidate the genetic control over mtDNA-CN, several genome-wide association studies (GWAS) of mtDNA-CN have been published[30–33], including a study that was published while the current manuscript was in preparation, analyzing ~300,000 participants from the UK Biobank (UKB), and identifying 50 independent loci[33].

In the present study, we report mtDNA-CN GWAS results from 465,809 individuals across the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium[34] and the UK Biobank (UKB)[35]. Using multiple gene prioritization and functional annotation methods, we assign genes to loci that reach genome-wide significance. Finally, we perform gene expression analyses and gene-set enrichment through PHEWAS-based SNP-clustering to identify functional domains related to mtDNA-CN.

Subjects and Methods

Study Populations

470,579 individuals participated in this GWAS, 465,809 of whom self-identified as White. Participants were derived from 7 population-based cohorts representing the Cohorts for Heart and Aging Research in Genetic Epidemiology (CHARGE) consortium (Avon Longitudinal Study of Parents and Children [ALSPAC], Atherosclerosis Risk in Communities [ARIC], Cardiovascular Health Study [CHS], Multi-Ethnic Study of Atherosclerosis [MESA], Religious Orders Study and Memory and Aging Project [ROSMAP], Study of Health in Pomerania [SHIP]) and from the UK Biobank (UKB) (Supplemental Table 1). Detailed descriptions of each participating cohort, their quality control practices, study level analyses, and ethic statements are available in the

Supplemental Methods. All study participants provided written informed consent and all centers obtained approval from their institutional review boards.

Methods for Mitochondrial DNA Copy Number Estimation (CHARGE cohorts)

qPCR

mtDNA-CN was determined using a quantitative PCR assay as previously described[32,36]. Briefly, the cycle threshold (Ct) value of a nuclear-specific and mitochondrial-specific probe were measured in triplicate for each sample. In CHS, a multiplex assay using the mitochondrial *ND1* probe and nuclear *RPPH1* probe was used, whereas ALSPAC used a mitochondrial probe targeting the D-Loop and a nuclear probe targeting *B2M*. In CHS, we observed plate effects, as well as a linear increase in ΔCt due to the pipetting order of each replicate. These effects were corrected in the analysis using linear mixed model regression, with pipetting order included as a fixed effect and plate as a random effect to create a raw measure of mtDNA-CN. In ALSPAC, run-to-run variability was controlled using 3 calibrator samples added to every plate, to allow for adjustment by a per-plate calibration factor[32].

Microarray

Microarray probe intensities were used to estimate mtDNA-CN using the Genvisis software package[37] as previously described[10,36]. Briefly, Genvisis uses the median mitochondrial probe intensity across all homozygous mitochondrial SNPs as an initial estimate of mtDNA-CN. Technical artifacts such as DNA input quality, DNA input quantity, and hybridization efficiency were captured through either surrogate variable (SV) or principal component (PC) analyses. SVs or PCs were adjusted for through stepwise linear regression by adding successive components until each successive surrogate variable or principal component no longer significantly improved the model.

Whole Genome Sequencing (ARIC)

Whole genome sequencing read counts were used to estimate mtDNA-CN as previously described[36]. Briefly, the total number of reads in a sample were web scraped from the NCBI sequence read archive. Mitochondrial reads were downloaded directly from dbGaP through Samtools (1.3.1). There was no overlap between ARIC microarray and ARIC whole-genome sequencing samples. A ratio of mitochondrial reads to total aligned reads was used as a raw measure of mtDNA-CN.

Adjusting for Covariates

Each method described above represents a raw measure of mtDNA-CN, adjusted for technical artifacts; however, several potential confounding variables (e.g., age, sex, blood cell composition) have been identified previously[18]. Raw mtDNA-CN values were adjusted for white blood cell count in ARIC, SHIP and CHS (which also adjusted for platelet count), depending on available data. Standardized residuals (mean = 0, standard deviation = 1) of mtDNA-CN were used after adjusting for covariates (Supplemental Table 1.

Estimation of Mitochondrial DNA Copy Number (UKB)

Due to the availability of more detailed cell count data, as well as a different underlying biochemistry for the Affymetrix Axiom array compared to the genotyping arrays used in the CHARGE cohorts, mtDNA-CN in the UKB was estimated differently (Supplemental Methods). Briefly, mtDNA-CN estimates derived from whole exome sequencing data, available on ~50,000 individuals, were generated first using customized Perl scripts to aggregate the number of mapped sequencing reads and correct for covariates through both linear and spline regression models. Concurrently, mitochondrial probe intensities from the Affymetrix Axiom arrays, available on the full ~500,000 UKB cohort, were adjusted for technical artifacts through principal

components generated from nuclear probe intensities. Probe intensities were then regressed onto the whole exome sequencing mtDNA-CN metric, and beta estimates from that regression were used to estimate mtDNA-CN in the full UKB cohort. Finally, we used a 10-fold cross validation method to select the cell counts to include in the final model (Supplemental Table 2). The final UKB mtDNA-CN phenotype is the standardized residuals (mean = 0, standard deviation = 1) from a linear model adjusting for covariates (age, sex, cell counts) as described in the Supplemental Methods.

Genome-Wide Association Study

For each individual cohort, regression analysis was performed with residualized mtDNA-CN as the dependent variable adjusting for age, sex, and cohort-specific covariates (e.g., principal components, DNA collection site, family structure, cell composition). Cohorts with multiple mtDNA-CN estimation platforms were stratified into separate analyses. Ancestry-stratified meta-analyses were performed using Metasoft software using the Han and Eskin random effects model to control for unobserved heterogeneity due to differences in mtDNA-CN estimation method[38]. Effect size estimates for SNPs were calculated using a random effect meta-analysis from cohort summary statistics, as the Han and Eskin model relaxes the assumption under the null hypothesis without modifying the effect size estimates that occur under the alternative hypothesis[38]. In total, three complementary analyses were performed in self-identified White individuals, (1) a meta-analysis using all available studies, (2) a meta-analysis of studies with available data for cell count adjustments, and (3) an analysis of UKB-only data. As the vast majority of samples are derived from the UKB study, and given the difficulty in interpreting effect size estimates from a random effects model, further downstream analyses were all performed using effect size estimates from UKB-only data.

Identification of Independent GWAS Loci

To identify the initial genome-wide significant (lead) SNPs in each locus, the most significant SNP that passed genome-wide significance ($p < 5 \times 10^{-8}$) within a 1 Mb window was selected. To avoid Type I error, SNPs were only retained for further analyses if there were either (a) at least two genome-wide significant SNPs in the 1 Mb window or (b) if the lead SNP was directly genotyped. Conditional analyses were performed in UKB, where the lead SNPs from the original GWAS were used as additional covariates in order to identify additional independent associations.

Fine-mapping

The susieR package was used to identify all potential causal variants for each independent locus associated with mtDNA CN[39]. UKB imputed genotype data for unrelated White subjects were used and variants were extracted using a 500 kb window around the lead SNP for each locus with minor allele frequency (MAF) > 0.001. 95% credible sets (CS) of SNPs, containing a potential causal variant within a locus, were generated. The minimum absolute correlation within each CS is 0.5 and the scaled prior variance is 0.01. When the CS did not include the lead SNP identified from the GWAS, some of the parameters were slightly relaxed [minimum absolute correlation is 0.2, estimate prior variance is TRUE]. The SNP with the highest posterior inclusion probability (PIP) within each CS was also identified (Supplemental Table 3). With a few exceptions, final lead SNPs were selected by prioritizing initially identified SNPs unless the SNP with the highest PIP had a PIP greater than 0.2 and was 1.75 times larger than the SNP with the second highest PIP.

Functional Annotation and Gene Prioritization

Functional Annotation

ANNOVAR was used for functional annotation of variants identified in the fine-mapping step[40]. First, variants were converted to an ANNOVAR-ready format using the dbSNP version 150

database[41]. Then, variants were annotated with ANNOVAR using the RefSeq Gene database[42]. The annotation for each variant includes the associated gene and region (e.g., exonic, intronic, intergenic). For intergenic variants, ANNOVAR provides flanking genes and the distance to each gene. For exonic variants, annotations also include likely functional consequences (e.g., synonymous/nonsynonymous, insertion/deletion), the gene affected by the variant, and the amino acid sequence change (Supplemental Table 4).

Co-localization Analyses

Co-localization analyses were performed using the approximate Bayes factor method in the R package *coloc*[43]. Briefly, *coloc* utilizes eQTL data and GWAS summary statistics to evaluate the probability that gene expression and GWAS data share a single causal SNP (colocalize). *Coloc* returns multiple posterior probabilities; H0 (no causal variant), H1 (causal variant for gene expression only), H2 (causal variant for mtDNA-CN only), H3 (two distinct causal variants), and H4 (shared causal variant for gene expression and mtDNA-CN). In the event of high H4, we can assume that the gene is potentially causal for the GWAS phenotype of interest. eQTL summary statistics were obtained from the eQTLGen database[44]. Genes with significant associations with lead SNPs were tested for co-localization using variants within a 500 kb window of the sentinel SNP. Occasionally, some of the eQTLGen p-values for certain SNPs were identical due to R's (ver 4.0.3) limitation in handling small numbers. To account for this, if the absolute value for a SNP's z-score association with a gene was greater than 37.02, z-scores were rescaled so that the largest z-score would result in a p-value of 5×10^{-300}. Additionally, a few clearly co-localized genes did not result in high H4 PPs due to the strong effect for each phenotype of a single SNP (Supplemental Figure 1), possibly due to differences in linkage disequilibrium (LD) between the populations. To account for this, we summed mtDNA-CN GWAS p-values and eQTLGen p-values for each SNP and removed the SNP with the lowest combined p-value. Co-localization

analyses were then repeated without the lowest SNP. Genes with H4 greater than 50% were classified as genes with significant evidence of co-localization.

DEPICT

Gene prioritization was performed with Depict, an integrative tool that incorporates gene co-regulation and GWAS data to identify the most likely causal gene at a given locus[45]. Across GWAS SNPs which overlapped with the DEPICT database, we identified SNPs representing 119 independent loci with LD pruning defined as $p < 5 \times 10\text{-}8$, r2 < 0.05 and > 500 kb from other locus boundaries. Only genes with a nominal p-value of less than 0.05 were considered for downstream prioritization.

Gene Assignment

To prioritize genes for each identified locus, we utilized functional annotations, eQTL co-localization analyses, and DEPICT gene prioritization results (Supplemental Figure 2). First, genes with missense variants within *SusieR* fine-mapped credible sets were assigned to loci. If loci co-localized with a gene's expression with a posterior probability (PP) of greater than 0.50 and there were no other co-localized genes with a PP within 5%, the gene with the highest posterior probability was assigned. If there was still no assigned gene, the most significant DEPICT gene was assigned. If there was no co-localization or DEPICT evidence, the nearest gene was assigned.

Gene Set Enrichment Analyses

Using the finalized gene list from the prioritization pipeline, GO and KEGG pathway enrichment analyses were performed using the "goana" and "kegga" functions from the R package *limma*[46], treating all known genes as the background universe[47]. Only one gene per locus was used for "goana" and "kegga" gene set enrichment analysis, prioritizing genes assigned to primary independent hits. If there were multiple assigned genes, one gene was randomly selected to avoid biasing results through loci with multiple genes. To identify an appropriate p-value cutoff,

96 genes were randomly selected from the genome and run through the same enrichment analysis. This permutation was repeated 1000 times to generate a null distribution of the smallest p-values from each permutation. For cluster 5 gene set enrichment analyses, permutation testing used 47 random genes. To ensure robustness of results, gene set enrichment analysis was repeated 50 times with random selection of genes at loci with multiple assigned genes. GO and KEGG terms that passed permutation cutoffs at least 40/50 times were retained.

Gene-based Association Test

We used metaXcan, which employs gene expression prediction models to evaluate associations between phenotypes and gene expression[48]. We obtained pre-calculated expression prediction models and SNP covariance matrices, computed using whole blood from European ancestry individuals in version 7 of the Genotype-Tissue expression (GTEx) database[49]. Using prediction performance p-values of less than 0.05, a total of 6,285 genes were predicted. Of these genes, 74 passed Bonferroni correction of $p < 7.95 \times 10^{-6}$. Gene set enrichment analyses were performed on Bonferroni-significant genes as previously described. REVIGO[50] was used on the "medium" setting (allowed similarity = 0.7) to visualize significantly enriched GO terms.

We used a one-sided Fisher's exact test to test for enrichment of genes that have been previously identified as causal for mtDNA depletion syndromes[51–53].

PHEWAS-based SNP Clustering

mtDNA-CN Phenome-wide Association Study (PHEWAS)

We used the PHEnome Scan ANalysis Tool (PHESANT)[54] to identify mtDNA-CN associated quantitative traits in the UKB. Briefly, we tested for the association of mtDNA-CN with 869 quantitative traits (Supplemental Table 5), limiting analyses to 365,781 White, unrelated

individuals (used.in.pca.calculation=1), and excluding individuals with extreme cell count measurements (see Supplementary Methods). Analyses were adjusted for age, sex, and assessment center.

SNP Phenotype Associations

SNP genotypes were regressed on mtDNA-associated quantitative traits using linear regression, adjusted for sex, age with a natural spline (df=2), assessment center, genotyping array, and 40 principal components (provided as part of the UKB data download).

SNP Clustering

To identify distinct clusters of mtDNA-CN GWS SNPs based on phenotypic associations, beta estimates from the SNP phenotype associations were first divided by the beta estimate of the mtDNA-CN SNP-mtDNA-CN association, so that all SNP-phenotype associations are relative to the mtDNA-CN increasing allele and scaled to the effect of the SNP on mtDNA-CN. The adjusted beta estimates were subjected to a dimensionality reduction method, Uniform Manifold and Approximation Projection (UMAP), as implemented in the R package *umap*[55] (random_state=123, n_neighbors=10, n_components=2, n_epochs=5000). SNPs were assigned to clusters using Density Based Clustering of Applications with Noise (DBSCAN) as implemented in the R package *dbscan*[56] (minPts=3). Clusters represent groups of SNPs with similar phenotypic associations.

To identify reproducible sub-clusters within cluster 5, we ran *umap* 100 times, varying the initial random state (n_neighbors=4, n_epochs=5000, min_dist=0.05, n_components=3). For each *umap* run, sub-clusters were assigned using *dbscan* as described above. Final SNP sub-cluster assignments were determined by identifying SNPs that all mapped to the same cluster >50% of the time (i.e., all pairwise correlations for each SNP within the cluster against all other SNPs in

the cluster was >50%). The final umap run for plotting in 2 dimensions used the following parameters: random_state=123, n_neighbors=4, n_epochs=5000, min_dist=0.05.

Phenotype Enrichment and Permutation Testing

To test for enrichment of specific phenotypes within clusters, we compared the median mtDNA-CN scaled phenotype beta estimates within the cluster to the median beta estimates for all SNPs not in the cluster, with significance determined using 20,000 permutations in which cluster assignment was permuted. For multi-test correction of the overall cluster and sub-cluster analyses, we performed 300 permutations of the initial cluster assignment (separately for the cluster and sub-cluster analyses), followed by the comparison of median beta estimates as described above. We retained only the most significant result from across all phenotypes and clusters from each of the 300 permutations, and then selected the 15th most significant value as the study-wide threshold for multi-test corrected significance of $p < 0.05$.

All statistical analyses were performed using R version 4.0.3

Results

Sample Characteristics

The current study included 465,809 individuals of White (European) ancestry (53.9% female) with an average age of 56.6 yrs (sd = 8.2 yrs) (Supplemental Table 1). Follow-up validation analyses were performed in 4,770 Blacks (60.2% female) with an average age of 61.2 yrs (sd = 7.4 yrs). The majority of the data originated from the UKB (93%). The bulk of the DNA used for mtDNA-CN estimation was derived from buffy coat (95.5%) while the rest was derived from peripheral leukocytes (2.2%) or whole blood (2.3%). mtDNA-CN estimated from Affymetrix genotyping arrays consisted of 97.9% of the data while the remainder was derived from qPCR- (1.8%) and WGS (0.3%).

GWAS

Previous work has demonstrated that the method used to measure mtDNA-CN can impact the strength of association[36]. To account for potential differences across studies due to the different mtDNA-CN measurements used, as well the inclusion of blood cell counts in only a subset of the cohorts, we took two approaches. First, we used a random effects model to perform meta-analyses, allowing for different genetic effect size estimates across cohorts. Second, we performed three complementary analyses in individuals who self-identified as White: 1) meta-analysis of all available studies (n = 465,809); 2) meta-analysis of studies with available data for cell count adjustment (n = 456,151); and 3) GWAS of UKB only (n = 440,266). 77 loci were significant in all three meta-analyses, and we identified 93 independent loci, of which 92 were genome-wide significant in the UKB data alone (Supplemental Figure 3, Figure 1). Given that > 90% of the samples come from the UKB study, and the challenge of interpreting effect size estimates from a random effects model, downstream analyses all use effect size estimates from the UKB only (Supplemental Table 6).

The most significant SNP associated with mtDNA-CN was a missense mutation in *LONP1* ($p = 3.00 \times 10^{-141}$), a gene that encodes a mitochondrial protease that can directly bind mtDNA, and has been shown to regulate *TFAM*, a transcription factor involved in mtDNA replication and repair (for review see Gibellini *et al.*)[57].

Fine-mapping and Secondary Hits

To identify additional independent SNPs within novel loci whose effects were masked by the original significant SNP, as well as identify additional loci, we took two approaches. First, a conditional analysis adjusting for the top 93 SNPs from the initial (primary) GWAS run revealed 3 novel loci and 19 additional independent significant SNPs within existing loci. We also performed fine-mapping with SuSiE[39] and discovered an additional 14 independent SNPs within

existing loci. The majority of loci had only one 95% credible set of SNPs; further, twenty of the credible sets contained only one SNP. However, many of the credible sets contained greater than 50 SNPs after fine-mapping, and 12 of the 122 credible sets had a missense SNP as the SNP with the highest PIP in the set. Using these two methods, we identified in total 129 independent SNPs across 96 loci (Supplemental Figure 4).

Associations in African Ancestry (AA) Populations

Examining the 129 SNPs from the Whites-only analysis, 99 were available in the Blacks-only meta-analysis (n = 4770). After multiple testing correction, one of these SNPs was significant (rs73349121, $p = 0.0001$), 9 were nominally significant ($p < 0.05$, with 5 expected), and 58/99 had a direction of effect that was consistent with the White-only analyses (one-sided $p = 0.04$, Figure 2). Despite being under-powered, these results in the Black-only analyses provide evidence for similar genetic effects in a different ancestry.

Gene Prioritization and Enrichment of mtDNA Depletion Syndrome Genes

We integrated results from three different gene prioritization and functional annotation methods (ANNOVAR[40], COLOC[43] , and DEPICT[45]) so that loci with nonsynonymous variants in gene exons were prioritized first, with eQTL co-localization results considered second (Supplemental Table 7), and those from DEPICT (Supplemental Table 8) were considered last (Supplemental Figure 2). For 20 loci, multiple genes were assigned as analyses could not identify a single priority gene (Supplemental Table 9). We noted the identification of a number of mtDNA depletion syndrome genes in the priority list and tested for enrichment of these known causal genes using a one-sided Fisher's exact test. For this analysis, all genes for loci assigned to multiple genes were used, and genes for all primary and secondary loci were considered. Our gene prioritization approach identified 7 of 16 mtDNA depletion genes (Supplemental Table 10), consistent with a highly significant enrichment (one-sided $p = 3.09 \times 10^{-15}$).

Gene Set Enrichment Analyses

To avoid bias from a single locus with multiple functionally related genes contributing to a false-positive signal, only one gene per unique locus was used, prioritizing genes assigned to primary loci. One gene was randomly selected for loci with multiple assigned genes. To test for robustness of gene set enrichment results, random selection was repeated 50 times, and only gene sets that were significantly enriched for at least 40 iterations were retained. In all, a total of 96 genes were utilized for GO term and KEGG pathway enrichment analyses. Using a Bonferroni-corrected p-value cutoff, 15 gene sets were significantly enriched for all 50 iterations, including mitochondrial DNA metabolic process, mitochondrial DNA replication, coagulation, hemostasis, amyloid-beta clearance, and mitochondrial genome maintenance (Supplemental Table 11). No KEGG terms were significant across multiple iterations.

MetaXcan Gene Expression Analysis

As a complementary approach to single-SNP analyses, we explored the associations between mtDNA-CN and predicted gene expression using MetaXcan[48] MetaXcan incorporates multiple SNPs within a locus along with a reference eQTL dataset to generate predicted gene expression levels. As our study estimated mtDNA-CN derived from blood, we used whole blood gene expression eQTLs from the Gene-Tissue Expression (GTEx) consortium[58] to predict gene expression in the UKB dataset. We identified 6,285 genes that had a predicted performance p-value of less than 0.05 (i.e., they had sufficient data to generate robust gene expression levels) and were tested for association with mtDNA-CN. Of these genes, 74 were significantly associated with mtDNA-CN ($p < 7.95 \times 10^{-6}$, Figure 3), including 8 that were not identified through single-SNP analyses. Many of the significant genes have known mitochondrial functions, notably the mtDNA transcription factor *TFAM* ($p = 1.09 \times 10^{-29}$) and mitochondrial exonuclease *MGME1* ($p = 5.87 \times 10^{-23}$), genes known as causal for mtDNA depletion

syndromes[51,52]. Additionally, *LONP1*, *MRPL43*, and *BAK1*, are all genes with known mitochondrial functions[59–61]. Bonferroni significant MetaXcan genes were used for gene enrichment analysis, finding enrichment for "nucleobase metabolic process" ($p = 1.47 \times 10^{-4}$) and "mitochondrial fusion" ($p = 1.86 \times 10^{-4}$, Supplemental Figure 5).

PHEWAS-based SNP Clustering and Gene Set Enrichment

mtDNA-CN is associated with numerous quantitative and qualitative phenotypes, many of which are relevant to aging-related disease[3–5,9,10,13–16]. We hypothesized that this pleiotropy may reflect different underlying functional domains captured by mtDNA-CN that may be reflected in GWAS-identified SNPs and their likely causal genes. To test this hypothesis, we used the UKB data to identify quantitative traits associated with mtDNA-CN and selected 42 highly significant, non-redundant traits to test for association with the mtDNA-CN GWAS SNPs (Supplemental Table 5, in PHEWAS = 1). We clustered SNPs using the trait effect size (beta) divided by the mtDNA-CN effect size estimate, so that all effects are standardized to the effect of the mtDNA-CN increasing allele for each locus. We identified 5 clusters of SNPs (Figure 4A), with clusters 1, 2, and 3 containing SNPs in which the mtDNA-CN increasing allele is associated with decreased platelet count (PLT) (Figure 4B), increased mean platelet volume (MPV) (Figure 4C), and platelet distribution width (PDW) (Figure 4D), consistent with a role in platelet activation[62]. Cluster 4 is most strongly enriched for SNPs in which the mtDNA-CN increasing allele is associated with increased PLT, plateletcrit (PLTCRIT, a measure of total platelet mass), serum calcium (Figure 4E), serum phosphate, as well as decreased mean corpuscular volume (MCV) and mean spherical cellular volume (Figure 4F) (Supplemental Table 12). The cluster 4 phenotypes, and supported by the genes identified for this cluster, implicate megakaryocyte proliferation and proplatelet formation (*MYB*, *AK3*, *JAK2*)[63], and apoptosis and autophagy (*BAK1*, *BCL2, TYMP*)[64]. Cluster 5 did not yield any specific trait enrichment (all significant results reflected the strong enrichment observed in clusters 1-4); however, gene set enrichment

for this cluster identified multiple mtDNA-related gene ontology terms, including mitochondrial genome maintenance, regulation of phospholipid efflux, and amyloid-beta clearance (Supplemental Table 13). Cluster 5 contains a highly diverse set of SNP-trait associations. A secondary clustering only with SNPs mapped to this cluster identified 9 sub-clusters (Supplemental Figure 6A), 3 having clear evidence for enrichment of specific phenotypes. Cluster 6 is enriched for decreased MCV (Supplemental Figure 6B). Cluster 7 is enriched for decreased MPV (Supplemental Figure 6C), PDW, serum phosphate, serum calcium, and PLTCRT. Cluster 10 is enriched for decreased apoA, apoB, total cholesterol (Supplemental Figure 6D), LDL, and HDL, and increased vitamin D, pulse rate, and direct bilirubin. SNPs that were not assigned to a cluster were enriched for decreased fasting blood glucose and maximum workload from fitness testing (Supplemental Table 14).

Discussion

We conducted a GWAS for mtDNA-CN using 465,809 individuals from the CHARGE consortium and the UKB. In addition to replicating two previously reported loci, we discovered 94 novel loci and report multiple independent hits for 26 loci. Examining our GWS SNPs in a Black population, we observed a concordant signal, suggesting that the genetic etiology of mtDNA-CN may be broadly similar across populations. Using several functional follow-up methods, genes were assigned for each identified independent hit and significant enrichment was observed for genes involved in mitochondrial DNA metabolism, homeostasis, cell activation, and amyloid-beta clearance. In total, we assigned 124 unique genes to independent GWAS signals associated with mtDNA-CN. We also identified 8 additional genes whose predicted gene expression is associated with mtDNA-CN that could not be mapped back to GWS loci. Finally, using a clustering approach based on SNP associations with various mtDNA-CN associated phenotypes, we were able to functionally categorize SNPs, providing insight into biological pathways that impact mtDNA-CN. We note that during the preparation of this manuscript, a

GWAS including 295,150 unrelated individuals from the UK Biobank was published, which reported 50 genome-wide significant regions[33]. While many of our loci overlap with their findings, our study reports twice as many loci largely due to the increased power of our study.

We were able to identify a substantial proportion of the genes involved in mtDNA depletion syndromes (7/16, $p = 3.09 \times 10^{-15}$ for enrichment), including *TWNK*, *TFAM*, *DGUOK*, *MGME1*, *RRM2B, TYMP,* and *POLG*. mtDNA depletion syndromes can be broken down into 5 subtypes based on their constellation of phenotypes[65] , and with the exception of cardiomyopathic subtypes (associated with mutations in *AGK* and *SLC25A4*), we were able to identify at least 1 gene from the other 4 subtypes, suggesting that our mtDNA-CN measurement in blood-derived DNA can identify genes widely relevant to non-blood phenotypes. This finding is consistent with a large body of work showing that mtDNA-CN measured in blood is associated with numerous aging-related phenotypes for which the primary tissue of interest is not blood (e.g. chronic kidney disease[13], heart failure[11], and diabetes[66]). Also consistent with this finding is recent work demonstrating that mtDNA-CN measured in blood is associated with mtRNA expression across numerous non-blood tissues, suggesting a link between mitochondrial function measured in blood and other tissues[67].

In addition to identifying the mtDNA depletion syndrome genes directly linked to mitochondrial DNA metabolic processes, DNA replication, and genome maintenance, we also identify genes which play a role in mitochondrial function. The top GWAS hit is a missense mutation in *LONP1*, which encodes a mitochondrial protease that has been shown to cause mitochondrial cytopathy and reduced respiratory chain activity[68,69]. Interestingly, this missense mutation was recently found to be associated with mitochondrial tRNA methylation levels[70]. Additional genes known to impact mitochondrial function include *MFN1*, which encodes a mediator of mitochondrial fusion[71,72], *STMP1*, which plays a role in mitochondrial respiration[73], and *MRPS35*, which encodes a ribosomal protein involved in protein synthesis in the mitochondrion[74,75].

Using a combination of gene-based tests and gene prioritization using functional annotation, pathway analyses reveal enrichment for numerous mitochondrial related pathways, as well as those involved in regulation of cell activation ($p < 3.65 \times 10^{-5}$), homeostatic processes ($p < 1.82 \times 10^{-5}$), and regulation of immune system processes ($p < 2.75 \times 10^{-5}$) (Supplemental Table 11). These results provide additional evidence for the broad role played by mitochondria in numerous aspects of cellular function. Of particular interest, the GO term for amyloid beta is significantly enriched, reinforcing a link between mtDNA-CN and neurodegenerative disease[76–78]. Previous work from our lab using the UKB has shown that increased mtDNA-CN is associated with lower rates of prevalent neurodegenerative disease, as well as predictive for decreased risk of incident neurodegenerative disease[67]. mtDNA-CN is also known to be decreased in the frontal cortex of Alzheimer's disease (AD) patients[79]. Interestingly, the four GWAS-identified genes driving the enrichment for amyloid-beta clearance are all related to regulation of lipid levels, and lipid homeostasis within the brain is known to play an important role in Alzheimer's disease[80]. *APOE*, one of the most well-known risk genes for Alzheimer's disease, is a cholesterol carrier involved in lipid transport, and the ApoE-ε4 isoform involved in AD pathogenesis is associated with mitochondrial dysfunction and oxidative distress in the human brain[81]; *CD36* is a platelet glycoprotein which mediates the response to amyloid-beta accumulation[82]; *LDLR* is a low-density lipoprotein receptor associated with AD[83]; and *ABCA7* is a phospholipid transporter[84]. *ABCA7* loss of function variants are enriched in both AD and Parkinson's disease (PD) patients[85], suggesting a broad role across neurodegenerative diseases.

Given the integral role of mitochondria in cellular function, not just with ATP formation/energy production, but signaling through ROS, and its key role in apoptosis, there is a strong reason to *a priori* assume that genetic variants associated with mtDNA-CN are likely to be highly pleiotropic. Indeed, mtDNA-CN itself is associated with numerous phenotypes (Supplemental Table 5). Through our PHEWAS-based clustering approach using 42 mtDNA-CN

associated phenotypes, we uncovered phenotypic associations between five distinct clusters of GWS mtDNA-CN associated SNPs. Cluster 1-3 were characterized by increased MPV, PDW, and decreased PLT (note that measured MPV and PLT are generally inversely correlated to maintain hemostasis), which are the hallmarks of platelet activation[62]. The link between platelets and mtDNA-CN has typically revolved around platelet count, as platelets have functional mitochondria, but do not have a nucleus. Given that the mtDNA-CN measurement is the ratio between mtDNA and nuclear DNA, increased platelets, all else being equal, would directly equate with increased mtDNA-CN. We note that the mtDNA-CN metric used in this GWAS was adjusted for platelet count, likely increasing the ability to detect variants that impact mtDNA-CN through increased platelet activation. Examining the genes within this cluster suggests role for actin formation/regulation (*CARMIL1*, *TPM4*, *PACSIN2*)[86–88] and vesicular transport/endocytic trafficking (*DNM3*, *EHD3*)[89,90] in platelet activation.

Cluster 4 is most strongly enriched for SNPs in which the mtDNA-CN increasing allele is associated with increased PLT/PLTCRIT and serum calcium/phosphate. Examining the genes assigned to the cluster, we implicate megakaryocyte proliferation and proplatelet formation (*MYB*, *AK3*, *JAK2*)[63], and apoptosis and autophagy (*BAK1*, *BCL2, TYMP*)[64]. Megakaryocytes are used to form proplatelets, and the process includes an important role for both intra- and extracellular calcium levels[91]. A role for apoptosis, and specifically *BCL2*, in proplatelet formation and platelet release has been suggested[92,93], however work in mice has suggested that apoptosis does not play a direct role in these processes[94]. Nevertheless, apoptosis is important for platelet lifespan[95].

Cluster 5 was particularly challenging to interpret, given that no particular phenotype was enriched relative to the non-cluster 5 SNPs. We note that this cluster appeared to be enriched for the mtDNA depletion syndrome genes, containing 6/7 genes identified in the GWAS, and significantly enriched for GO Terms related mitochondrial DNA. Examining sub-clusters within cluster 5 identified MCV as an important phenotype (while only sub-cluster 6 was formally

associated, looking at Figure 3B suggests more widespread clustering based on MCV). MCV is a measure of the average volume of a red blood corpuscle, and the link between red blood volume and mtDNA-CN is unlikely to be direct, given that red blood cells contain neither nuclei nor mitochondria. Sub-cluster 7 is surprisingly enriched for variants associated with decreased MPV/PDW and serum phosphate/calcium, inverse of what we observe for cluster 4. Finally, sub-cluster 10 is strongly associated with lipids, and includes a number of genes known to be associated with lipid levels (*LIPC*, *CETP*, *LDLR*, *APOE*). While lipids play a role in both energy metabolism (largely through fatty acids) and cellular membrane formation, a link to mtDNA-CN and/or mitochondrial function is not well-established. One potentially interesting result is provided by Olkowicz and colleagues, who demonstrated that $ApoE^{-/-}/LDLR^{-/-}$ mice had increased cardiac mitochondrial oxidative metabolism, with proteomic analysis suggesting increased mitochondrial abundance in mouse hearts[96]. However, we note that our results show an association between decreased lipids and increased mtDNA-CN, rather than the reverse, shown in the Olkowicz study.

Although the question of causality is of great interest, this study was unable to determine the directionality of effect between mtDNA-CN and phenotypes of interest, as we are underpowered for Mendelian randomization (MR), with less than 1% of the variance in mtDNA-CN explained by GWS loci when predicted into ARIC. As an additional limitation, we note that despite the large sample size and numerous loci identified, we are likely missing a great deal of the true signal, as previous studies have estimated mtDNA-CN heritability to be 65%[23]. Finally, while we have adjusted our mtDNA-CN metric for a variety of confounders, it is important to note that mtDNA-CN can be influenced by a variety of environmental factors including smoking[97] and drugs, which have not been adjusted for in these analyses.

In summary, we performed the largest-to-date GWAS for mtDNA-CN, including almost 500,000 individuals. We identified distinct groups of SNPs associated with mtDNA-CN that are related to platelet activation, megakaryocyte formation and apoptotic processes, and showed

clear enrichment for genes involved in mtDNA depletion and nucleotide regulation. Given the role of mtDNA-CN in aging-related disease, this work begins to unravel the many varied underlying mechanisms for genetic control of mtDNA-CN.

Supplemental Data

Supplemental Data include six supplemental figures, fourteen supplemental tables, and supplemental methods.

Declaration of Interests

Psaty serves on the Steering Committee of the Yale Open Data Access Project funded by Johnson & Johnson. All other authors declare no competing interests.

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Web Resources

REVIGO was accessed at http://revigo.irb.hr/.

Data and Code Availability

All data used in this manuscript is available through either the UKBiobank and CHARGE consortiums. Code and scripts are available in a zipped file at https://www.arkinglab.org/resources/.

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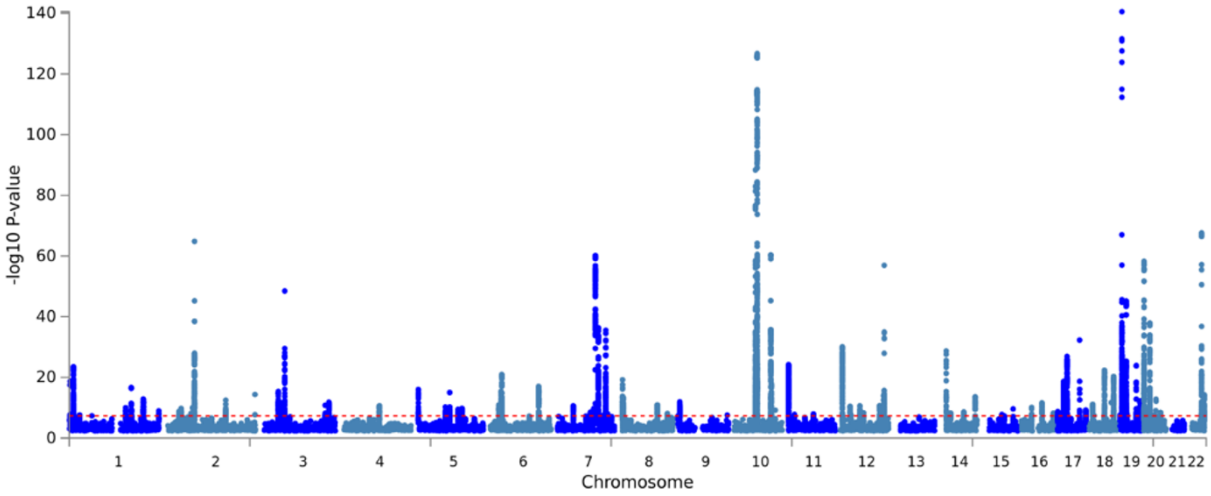
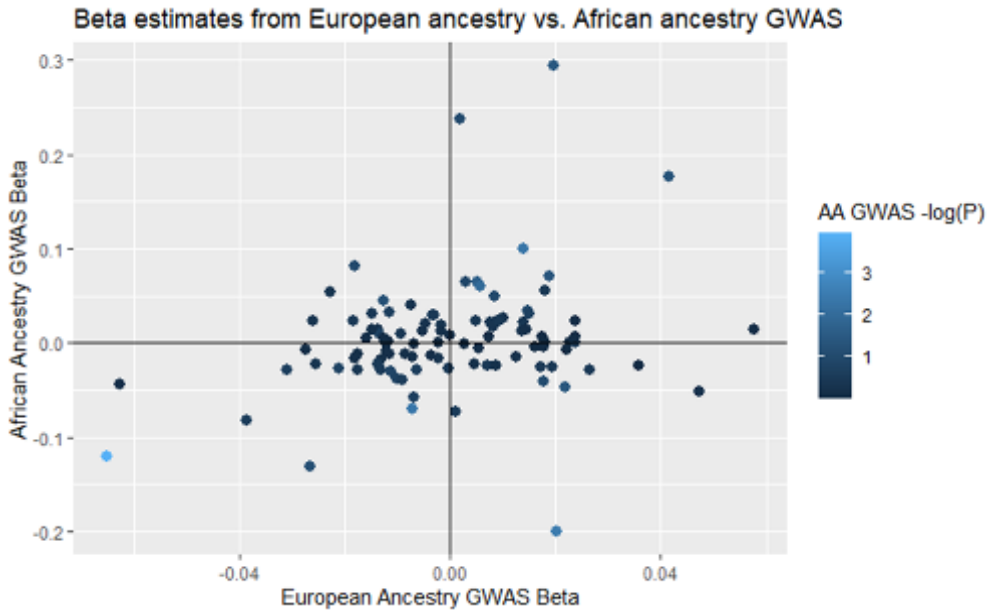
Figures

Figure 1. Manhattan plot of GWS loci from UKB-only analyses.



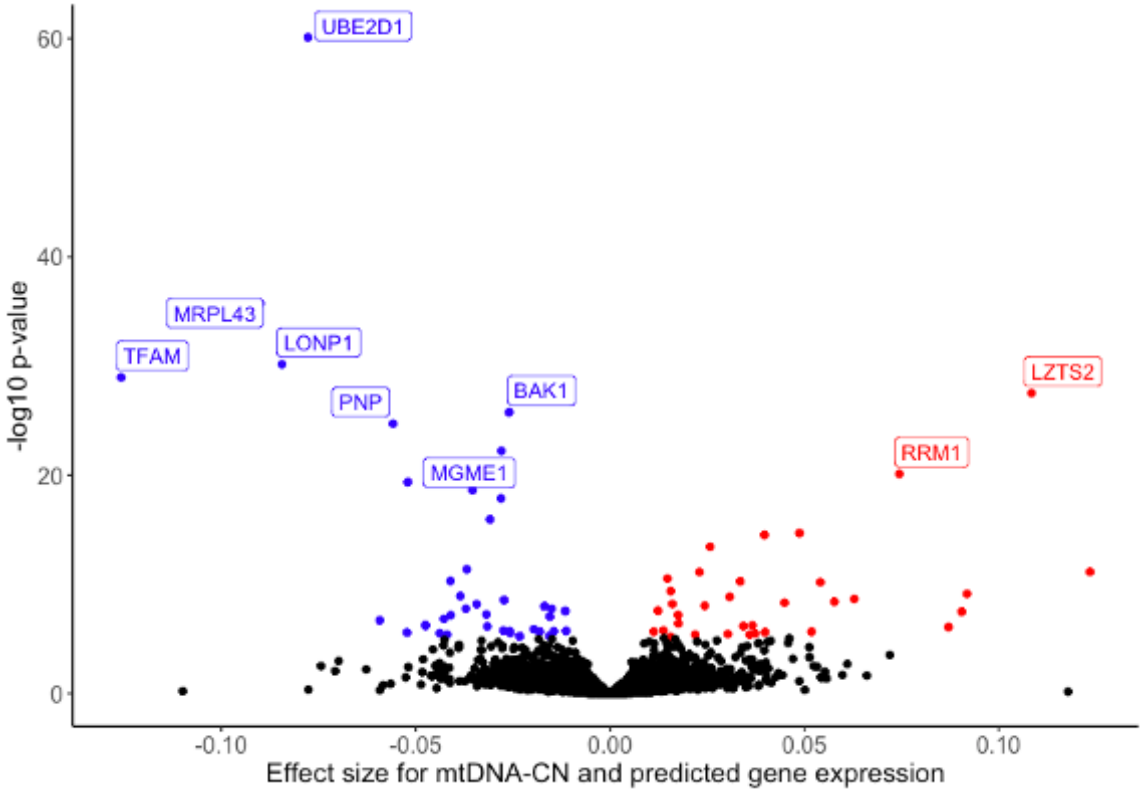
Manhattan plot showing genome-wide significant loci for the UK Biobank-only analyses.

Figure 2. Scatterplot displaying effect size estimates between Whites and Blacks GWAS results for the 129 loci identified in the Whites analyses.



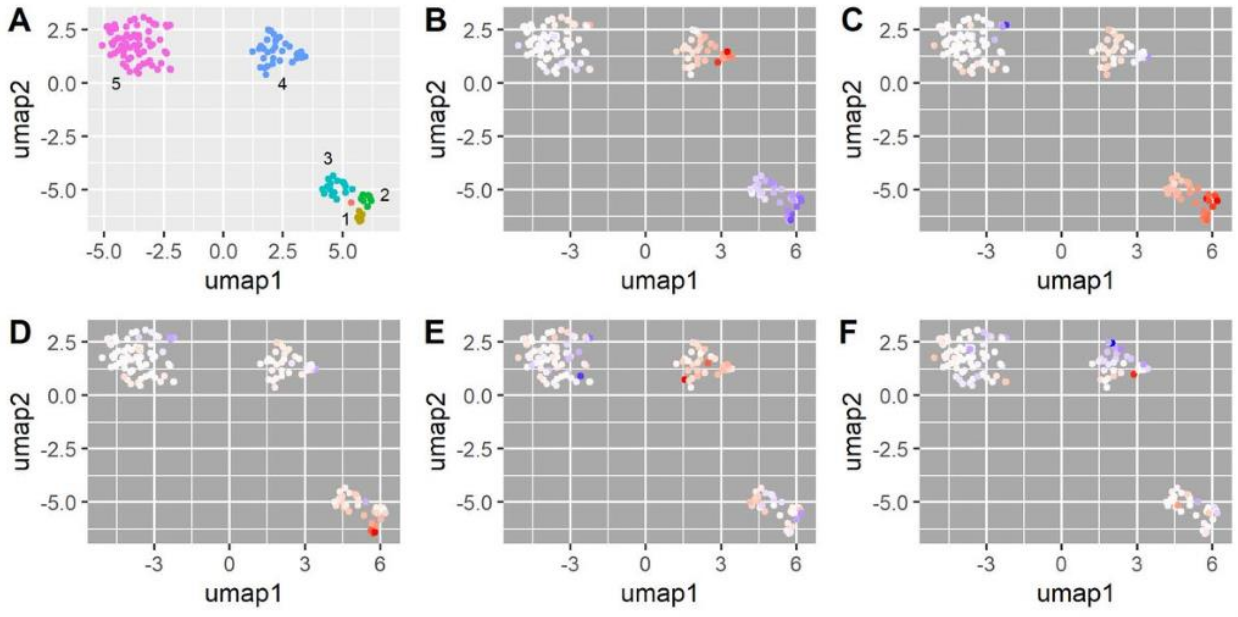
Scatterplot showing comparison between effect size estimates for White (European ancestry) and Black (African Ancestry) individuals. Color represents significance of effect for each locus in Blacks GWAS analyses.

Figure 3. Volcano plot of genes whose predicted gene expression is significantly associated with mtDNA-CN.



Volcano plot showing genes whose predicted gene expression is significantly associated with mtDNA-CN. Red indicates positive associations, blue indicates negative associations. Three genes (ARRDC1, EHMT1, PNPLA7) had extreme effect size estimates greater than 0.3 but were non-significant and removed from the plot for readability.

Figure 4. PHEWAS-based clustering of mtDNA-CN associated SNPs.



UMAP clusters created from PHEWAS associations for mtDNA-CN associated SNPs. (A) Five clusters were identified as labeled in the panel; orange indicates no cluster. (B-F) SNPs are colored based on their effect estimate size, standardized to the effect on mtDNA-CN (red = positive, blue = negative estimates), for (B) platelet count, (C) mean platelet volume, (D) platelet distribution width, (E) serum calcium levels, (F) mean spherical cellular volume.