A common TCN1 loss-of-function variant is associated with lower vitamin B12 concentration in African Americans

Yao Hu,1 Laura M. Raffield,2 Linda M. Polfus,3 Arden Moscati,4 Girish Nadkarni,5 Michael H. Preuss,4 Xue Zhong,6,7 Qiang Wei,6,8 Stephen S. Rich,9 Yun Li,10,11 James G. Wilson,12 Adolfo Correa,13 Ruth J. F. Loos,14,15 Bingshan Li,4,16 Paul L. Auer,17 Alex P. Reiner,1,18 and the NHLBI Trans-Omics for Precision Medicine Consortium

1Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA; 2Department of Genetics, University of North Carolina at Chapel Hill, Chapel Hill, NC; 3Center for Genetic Epidemiology, Department of Preventative Medicine, Keck School of Medicine, University of Southern California, Los Angeles, CA; 4Charles Bronfman Institute for Personalized Medicine and 5Department of Nephrology, Icahn School of Medicine at Mount Sinai, New York, NY; 6Vanderbilt Genetics Institute, Nashville, TN; 7Department of Medicine, Vanderbilt University Medical Center, Nashville, TN; 8Department of Molecular Physiology and Biophysics, Vanderbilt University, Nashville, TN; 9Center for Public Health Genomics, University of Virginia, Charlottesville, VA; 10Department of Genetics, 11Department of Biostatistics, and 12Department of Computer Science, University of North Carolina at Chapel Hill, Chapel Hill, NC; 13Department of Physiology and Biophysics and 14Department of Pediatrics and Medicine, University of Mississippi Medical Center, Jackson, MS; 15Genetics of Obesity and Related Metabolic Traits Program and 16Mindich Child Health and Development Institute, Icahn School of Medicine at Mount Sinai, New York, NY; 17Zilber School of Public Health, University of Wisconsin–Milwaukee, Milwaukee, WI; and 18Department of Epidemiology, University of Washington, Seattle, WA

Vitamin B12 (VB12), or cobalamin, is a water-soluble vitamin. It serves as an enzyme cofactor in the 1-carbon metabolism pathway, which plays a key role in a wide range of biological processes, including red blood cell (RBC) formation, DNA synthesis, and myelination of the central nervous system.1-3 VB12 deficiency is clinically associated with megaloblastic anemia and neurodegenerative disorders and is also linked to cardiovascular diseases, which is thought to be mediated via hyperhomocysteinemia.1,3 Uptake of VB12 from the diet in the gastrointestinal tract depends on intrinsic factor (encoded by GIF).3,4 VB12 in blood is bound to haptocorrin (HC; encoded by TCN1) and transcobalamin (encoded by TCN2) and circulates as holohaptocorrin (holoHC) and holotranscobalamin, respectively.3,5,6 Although VB12 deficiency often results from poor gastrointestinal absorption,7 genetic factors also contribute to phenotypic variation. Previous genome-wide association studies (GWASs), primarily focusing on populations of European and Asian ancestry, have identified 13 loci (FUT2, CUBN, TCN1, MUT, MS4A3, FUT6, PREUD2, CLYBL, CD320, TCN2, ABCD4, MMACA, and MMACHC) associated with VB12.8-15 GWASs in Chinese11 and Indians14 identified VB12-associated shared genetic variants across ancestry groups, as well as population-specific variants. VB12 and holoHC concentrations are higher in blacks than in whites,16 yet no GWAS has examined the genetic determinants of VB12 specifically in African Americans (AAs). In the current study, we used whole-genome sequencing (WGS) from the...
National Heart, Lung, and Blood Institute (NHLBI) Trans-Omics for Precision Medicine (TOPMed) Program to assess genetic variants associated with VB₁₂ in an unselected population-based sample of AAs from the Jackson Heart Study (JHS). The JHS is a population-based longitudinal study based in Jackson, Mississippi; additional information is reported in supplemental Methods (available on the Blood Web site). The JHS was approved by the Institutional Review Board of the NHLBI.

### Table 1. Association of TCN1-rs34530014 with VB₁₂ concentration

<table>
<thead>
<tr>
<th>Trait</th>
<th>Study</th>
<th>SNP</th>
<th>CHR:POS</th>
<th>N</th>
<th>EA/NEA</th>
<th>EAF</th>
<th>BETA (SE)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>VB₁₂</td>
<td>JHS</td>
<td>rs34530014</td>
<td>11:59631467</td>
<td>1280</td>
<td>A/AC</td>
<td>0.036</td>
<td>−0.817 (0.104)</td>
<td>6.48 × 10⁻¹⁵</td>
</tr>
<tr>
<td>VB₁₂</td>
<td>BioVu</td>
<td>rs11822978</td>
<td>11:59626896</td>
<td>725</td>
<td>T/C</td>
<td>0.034</td>
<td>−0.158 (0.038)</td>
<td>3.28 × 10⁻³</td>
</tr>
<tr>
<td>VB₁₂</td>
<td>BioMe</td>
<td>rs11822978</td>
<td>11:59626896</td>
<td>3199</td>
<td>T/C</td>
<td>0.032</td>
<td>−0.272 (0.037)</td>
<td>2.76 × 10⁻¹³</td>
</tr>
</tbody>
</table>

CHR, chromosome; EA, effect allele; EAF, effect allele frequency; NEA, noneffect allele; POS, position; SE, standard error; SNP, single nucleotide polymorphism.

*Genome-wide significance was predefined as \( P < 1.69 \times 10^{-8} \) or 0.05/29,665,030 variants tested.

---

![Figure 1. Locus-zoom plots.](image)

TCN1-rs34530014 (A) and FUT2-rs507766 (B). Genetic coordinates are displayed along the x-axis (Build 37/hg19), and genome-wide association significance level is plotted against the y-axis as \(-\log_{10}(P \text{ value})\). The purple diamond indicates the top hit. LD is generated using JHS WGS data and is indicated by the color scale in relationship to the top hit, with red for strong LD (\( r^2 > 0.8 \)) and navy blue for weak LD (\( r^2 < 0.2 \)).
University of Mississippi Medical Center, and participants provided written informed consent. At the baseline examination, VB₁₂ was measured in plasma in a subset of 1851 JHS participants using a homogenous enzyme immunoassay system and Hitachi 911 equipment (Roche Diagnostics, Indianapolis, IN).¹⁹ A total of 3406 JHS participants underwent 30× coverage WGS through the TOPMed project at the Northwest Genome Center at the University of Washington, and genotype calling was performed by the Informatics Resource Center at the University of Michigan, as previously described.²⁰ After quality control (supplemental Methods), a total of 29,665,030 variants (minor allele frequency > 0.001) and 1280 participants (20.6-91.6 years of age, 65.5% female, VB₁₂ = 639.9 ± 289.3 pg/mL) were included in the discovery analysis (phs000964.v2.p1 for sequencing data and phs000286.v5.p1 for VB₁₂ data on the Database of Genotypes and Phenotypes; https://www.ncbi.nlm.nih.gov/gap).

Association of each single variant with rank-based inverse-normal–transformed VB₁₂ concentration was tested in JHS participants adjusted for age, sex, and the first 10 principal components (PCs) of genetic ancestry using a linear mixed model approach to account for familial relationships, as implemented in EPACTS 3.2.6 on the University of Michigan ENCORE server (https://encore.sph.umich.edu). Genome-wide significance was predefined as P < 1.69 × 10⁻⁹, or 0.05/29,665,030 variants tested; 33 variants across 2 genomic regions (TCN1 and FUT2) reached genome-wide significance (P < 1.69 × 10⁻⁹) for VB₁₂ (supplemental Figure 1).

The index variant rs34530014 on chromosome 11 is a 1-bp deletion of TCN1 (minor allele frequency = 0.036; P = 6.48 × 10⁻¹⁵; Table 1; Figure 1A) associated with lower VB₁₂. It is a loss-of-function (LoF) frameshift mutation (p.Val58Cysfs) prevalent only among African ancestry populations, originally reported in 2 Afro-Caribbean pedigrees with HC deficiency.²¹ Replication of the novel LoF variant TCN1-rs34530014 was performed using genomic data from 2 AA electronic medical record–linked biobanks: the Biobank of Vanderbilt University (BioVU)²² and BioMe of Mount Sinai²³ (supplemental Methods). Because TCN1-rs34530014 was not directly genotyped or imputed in BioVU or BioMe, we used its linkage disequilibrium (LD) proxy rs11822978 (r² = 0.98 in JHS) and confirmed its association with lower VB₁₂ in 3924 additional AAs from BioVU and BioMe (Table 1). TCN1-rs34530014 is distinct from other VB₁₂-associated TCN1 variants (including 2 missense variants, rs34324219 and rs34528912) identified in Europeans and Indians.⁹,¹²,¹⁴ Of the TCN1 variants previously associated with lower VB₁₂, only rs34324219 was nominally associated with lower VB₁₂ in the JHS (P = .009; supplemental Table 1). Together, these results establish an ancestry-specific role for rs34530014 in lower VB₁₂ concentration in African ancestry populations and substantial allelic heterogeneity in the genetic architecture of VB₁₂ at the TCN1 locus.

The identification of this naturally occurring LoF mutation prevalent in AAs allowed us to further investigate additional hematologic and clinical consequences of mild HC deficiency, beyond the association with lower VB₁₂ concentration. The association of rs34530014 with additional quantitative traits, including RBC indices and homocysteine, was assessed in the JHS and the Women’s Health Initiative SNP Health Association Resource²⁴ (supplemental Methods). An elevated concentration of methylmalonate is a more sensitive and specific marker for VB₁₂ deficiency¹⁻³; unfortunately, it was not available in our data sets. In addition, a phenome-wide association study (PheWAS) of TCN1-rs11822978 was performed in BioVU and BioMe. A total of 340 traits was scanned for association using logistic regression adjusted for age, sex, and the first 10 PCs, including metabolic, neurological, and hematologic outcomes and disorders. Individual study association results were combined using fixed-effect inverse-variance–weighted meta-analysis, and P values were corrected for multiple testing. Although marginal associations (P < .05) were observed for mean corpuscular hemoglobin and mean corpuscular volume, as well as diagnosis codes Vitamin Deficiency and Other Deficiency Anemia, none of these reached the Bonferroni-corrected threshold (P > .006, or 0.05/8 traits for RBC indices, supplemental Table 2; and P > 1.47 × 10⁻⁹, or 0.05/340 traits for PheWAS, supplemental Table 3).

In contrast to mutations of TCN2, which result in transcobalamin II deficiency (OMIM #275350) with severe clinical manifestations,²⁵ the clinical impact of HC deficiency is poorly defined. The distinct consequences of TCN1 and TCN2 mutations are consistent with the fact that holotranscobalamin is the bioactive form of VB₁₂ that is taken up by all tissues, whereas the biological role of holoHC is unclear.⁶ Despite the relatively large overall sample, the small number of homozygotes (4 in JHS) limited our ability to accurately assess the recessive effect of the TCN1-rs34530014 on VB₁₂ and related traits and disorders. Therefore, further investigation, including very large phenotypic data sets of African ancestry individuals, will be needed to draw firm conclusions about the clinical impact of HC deficiency.

The index single nucleotide polymorphism at the other genomewide significant association peak in the JHS on chromosome 19 was rs507766 (located in the 3’ untranslated region of FUT2; P = 5.51 × 10⁻¹¹) (Figure 1B). This noncoding variant is in only moderate LD (r² = 0.55 in JHS) with the common secretor variant FUT2-rs601338 (P = 1.49 × 10⁻⁷ for association with VB₁₂ in JHS), which was previously identified in Europeans and Indians.⁸,⁹,¹⁴ Thus, we found evidence for 2 functional alleles involving FUT2: 1 with an additive genetic effect (rs507766) and 1 with a dominant effect (rs601338) on VB₁₂ (supplemental Table 4). We confirmed 4 previously identified loci (MUT, MMACHC, FUT6, and CD320; supplemental Table 1) at P < .05 with consistent association directions of effects.

We report a novel association between the African ancestry–specific LoF variant TCN1-rs34530014 and VB₁₂ concentration and an additional FUT2 variant rs507766 associated with VB₁₂ specific to AAs, highlighting the ancestry heterogeneity of genetic factors that influence VB₁₂. Another population-specific VB₁₂-associated LoF variant, CLYBL-rs41281112 (p.Arg259Ter), is found in ~3% of apparently healthy non-African individuals (but rare in Africans).¹¹ Further elucidation of the genetics and role of HC-bound VB₁₂ may lead to improved diagnosis and differentiation of true bioavailable VB₁₂ deficiency from total VB₁₂ deficiency.

Acknowledgments

The authors thank the staff and participants in the JHS. The contributions of the investigators of the NHLBI TOPMed Consortium (https://www.nhlbiwgs.org/topmed-banner-authorship) are gratefully acknowledged. The authors also gratefully acknowledge the
The views expressed in this article are those of the authors and do not
supported by NIH, National Institute of Diabetes and Digestive and
Philanthropies. Work in BioMe was also supported in part through the
Analysis of BioVU data was partially funded by NHGRI grant U01HG009086,
by NIH National Institute of General Medical Sciences/OD grant
supported by institutional funding and by NIH National Center for
obtained from the Vanderbilt University Medical Center, which was
HL129982. The BioVU data set used in the analyses described was

Contribution: A.P.R. and P.L.A. were responsible for the study concept
Authorship
17. Sempos CT, Bild DE, Manolio TA. Overview of the Jackson Heart Study:
Working Group*. D-Dimer in African Americans: whole genome sequence
analysis and relationship to cardiovascular disease risk in the Jackson Heart
18. Taylor HA, Jr., Wilson JG, Jones DW, et al. Toward resolution of car-
vascular health disparities in African Americans: design and methods of the
Suppression of homocysteine levels by vitamin B12 and folates: age and
20. Raffield LM, Zakai NA, Duan Q, et al; NHLBI Trans-Omics for Precision
Medicine (TOPMed) Consortium, Hematology & Hemostasis TOPMed
Working Group*. D-Dimer in African Americans: whole genome sequence
analysis and relationship to cardiovascular disease risk in the Jackson Heart
21. Carmel R, Parker J, Kelm Z. Genomic mutations associated with mild and
severe deficiencies of transcobalamin I (haptocorrin) that cause mildly and
22. Roden DM, Pulley JM, Basford MA, et al. Development of a large-scale de-
identified DNA biobank to enable personalized medicine. Clin Pharmacol

REFERENCES
A complete list of the members of the NHLBI Trans-Omics for Precision Medicine Consortium appears in the online appendix.

Footnote
The online version of this article contains a data supplement.
The recent Blood article by Schroeder et al demonstrates that plerixafor mobilizes a unique hematopoietic stem and progenitor cell (HSPC) product that is enriched in plasmacytoid dendritic cell (pDC) precursors (pre-pDCs). This study further reports that enrichment of these cells in plerixafor-mobilized allografts is associated with lower cumulative incidence of acute graft-versus-host disease (aGVHD) and chronic graft-versus-host disease (cGVHD). In an earlier study, Waller et al reported a protective advantage against aGVHD of pDCs derived from bone marrow (BM) but not granulocyte colony-stimulating factor (G-CSF)-mobilized peripheral blood (PB) graft. Studies have shown that allogeneic transplantation with a BM allograft results in lower rates of aGVHD and cGVHD when compared with G-CSF-mobilized PB graft. In a commentary to the Schroeder study, Waller proposes that the relatively rapid onset of mobilization by plerixafor (hours vs days by G-CSF) generates a novel PB graft that immunologically and phenotypically resembles cells harvested from bone marrow. He hypothesizes that this unique allograft contains immune subsets, including pre-pDCs and pDCs, which favorably modulate alloreactivity post-transplantation thus resulting in lower GVHD rates.

Recently, the Canadian Blood and Marrow Transplant Group (CBMTG) conducted a phase 3 randomized trial and compared the impact of G-CSF–mobilized PB to BM. In this trial, G-CSF-treated BM donors had a significantly lower frequency of cGVHD, similar to that seen in the Schroeder study. A further comprehensive investigation of the donor graft composition found that the lower rate of cGVHD in G-BM correlated most closely with a higher proportion of CD56bright regulatory NK cells (NKreg) represented as the percentage of CD56bright NKreg cells. Additional evidence of the importance of this immune-regulatory population is our recent observation of a co-relation of low numbers of CXCR3+CD56bright NKreg cells with the onset of cGVHD in adults. Based on these observations, we hypothesized that an alternate donor cell population, with a selective increase in NKreg cells by plerixafor, may contribute to the lower rate of cGVHD seen in the recent Schroeder study.

To address this possible mechanism, we recruited 9 healthy adult volunteers after full consent. This study was approved by the Dalhousie University and University of British Columbia (UBC) research ethical boards. All subjects were between 18 and 60 years of age and were enrolled at the Dalhousie University. All biological analyses were performed at the UBC-affiliated BC Children’s Hospital Research Institute. Five subjects received 1 dose of plerixafor at 240 μg/kg per day subcutaneously and PB and BM samples were harvested prior to administration and at 4 and 24 hours after plerixafor administration. The subsequent 4 participants each received 4 daily doses of G-CSF at 5 μg/kg per day for 4 days, followed by a dose of plerixafor on day 5. To minimize the impact of circadian rhythm, PB and BM samples were collected between 9 AM and noon, prior to G-CSF administration, after G-CSF completion, and at 4 and 24 hours after plerixafor administration. We performed a focused analysis on CD56bright NKreg cells in these samples using multiparametric flow cytometry. Nucleated cells isolated from peripheral blood and bone marrow samples were stained with CD3, CD8, perforin, granzyme B, CD56 antibodies conjugated to fluorescein isothiocyanate, phycoerythrin, PB, Flow-Check 770 fluorospheres, and allophycocyanin, respectively. Stained cells were acquired by LSR II cytometer (BD) and the data were analyzed by FlowJo v10. The immunophenotype of NKreg cells is CD3+, CD56bright, perforin, and granzyme-B+. Plerixafor significantly mobilized nucleated cells to PB after 4 hours of treatment, whereas no significant difference was observed after 24 hours of treatment (Figure 1A). Furthermore, longer treatment time resulted in a significantly lower cell number indicating that plerixafor’s action peaked at 4 hours after administration. The magnitude of mobilization observed 4 hours after plerixafor administration was similar to that seen in the previous phase II clinical study. Interestingly, plerixafor did not alter the nucleated cell number in the bone marrow (Figure 1A). Four daily injections of G-CSF followed by plerixafor administration significantly mobilized more nucleated cells to PB than either treatment alone (Figure 1B). However, the two agents mobilized similar number of nucleated cells to PB separately. Therefore, plerixafor mobilized nucleated cells to peripheral blood more rapidly than G-CSF.

TO THE EDITOR:

Plerixafor effectively mobilizes CD56bright NK cells in blood, providing an allograft predicted to protect against GVHD

Peggy P. C. Wong,1,2,* Amina Kariminia,3,* David Jones,4 Connie J. Eaves,5,7 Ronan Foley,6,9 Sabine Ivison,3 Stephen Couban,10 and Kirk R. Schultz1-3

1Division of Pediatric Hematology/Oncology/Blood and Marrow Transplant, BC Children’s Hospital, Vancouver, BC, Canada; 2Department of Pediatrics, University of British Columbia, Vancouver, BC, Canada; 3Michael Cuccione Childhood Cancer Research Program, BC Children’s Hospital Research Institute, Vancouver, BC, Canada; 4Department of Medicine and 5Department of Medical Genetics, University of British Columbia, Vancouver, BC, Canada; 6Department of Medicine and 7Department of Medical Genetics, University of British Columbia, Vancouver, BC, Canada; 8Hamilton Health Sciences Centre, Hamilton, ON, Canada; 9Department of Medicine, McMaster University, Hamilton, ON, Canada; and 10Department of Medicine, Dalhousie University, Halifax, NS, Canada
A common TCN1 loss-of-function variant is associated with lower vitamin B12 concentration in African Americans

Yao Hu, Laura M. Raffield, Linda M. Polfus, Arden Moscati, Girish Nadkarni, Michael H. Preuss, Xue Zhong, Qiang Wei, Stephen S. Rich, Yun Li, James G. Wilson, Adolfo Correa, Ruth J. F. Loos, Bingshan Li, Paul L. Auer, Alex P. Reiner and the NHLBI Trans-Omics for Precision Medicine Consortium