Mitochondrial DNA Haplogroups and Neurocognitive Impairment During HIV Infection

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Background. Neurocognitive impairment (NCI) remains an important complication in persons infected with human immunodeficiency virus (HIV). Ancestry-related mitochondrial DNA (mtDNA) haplogroups have been associated with outcomes of HIV infection and combination antiretroviral therapy (CART), and with neurodegenerative diseases. We hypothesize that mtDNA haplogroups are associated with NCI in HIV-infected adults and performed a genetic association study in the CNS HIV Antiretroviral Therapy Effects Research (CHARTER) cohort.

Methods. CHARTER is an observational study of ambulatory HIV-infected adults. Haplogroups were assigned using mtDNA sequence, and principal components were derived from ancestry-informative nuclear DNA variants. Outcomes were cross-sectional global deficit score (GDS) as a continuous measure, GDS impairment (GDS ≥ 0.50), and HIV-associated neurocognitive disorder (HAND) using international criteria. Multivariable models were adjusted for comorbidity status (incidental vs contributing), current CART, plasma HIV RNA, reading ability, and CD4 cell nadir.

Results. Haplogroups were available from 1027 persons; median age 43 years, median CD4 nadir 178 cells/mm³, 72% on CART, and 46% with HAND. The 102 (9.9%) persons of genetically determined admixed Hispanic ancestry had more impairment by GDS or HAND than persons of European or African ancestry (P < .001 for all). In multivariate models including persons of admixed Hispanic ancestry, those with haplogroup B had lower GDS (β = −0.34; P = .008) and less GDS impairment (odds ratio = 0.16; 95% confidence interval, .04, .63; P = .009) than other haplogroups. There were no significant haplogroup associations among persons of European or African ancestry.

Conclusions. In these mostly CART-treated persons, mtDNA haplogroup B was associated with less NCI among persons of genetically determined Hispanic ancestry. mtDNA variation may represent an ancestry-specific factor influencing NCI in HIV-infected persons.

Keywords. HIV; AIDS; cognitive disorders; DNA, mitochondrial.
comorbidity [4]. Given the potential impact of these untreatable disorders in aging CART-treated populations, understanding, predicting, and preventing them is important. Although host factors have been associated with HAND [4,5], genetic predictors of HAND should be more thoroughly characterized.

Early studies of HAND genetics examined HIV-associated dementia (HAD), AIDS dementia complex, or HIV-associated encephalitis, phenotypes that are uncommon in the CART era, and identified associations with chemokine coreceptor 5 (CCR5) [6] and apolipoprotein E (ApoE) [7] gene variants. Recent analyses have included milder NCI phenotypes and have continued to primarily examine the ApoE ε4 allele, with inconsistent results [8,9]. Reviews on this topic provide additional background and highlight the limitations of relatively small sample sizes and heterogeneous phenotypes [10]. One genome-wide association study (GWAS) of HAND has been reported in a sample of 1287 adults of predominantly European ancestry enrolled in the Multicenter AIDS Cohort Study [11]. This analysis did not find associations meeting GWAS-level significance (P < 5 x 10^{-8}) but did identify associations between processing speed and 2 single-nucleotide polymorphisms (SNPs) in ion channel transporters (SLC8A1 and NALCN) that approached statistical significance.

The critical and complex roles of mitochondria in energy production, reactive oxygen species (ROS) homeostasis, and apoptotic regulation make them vulnerable targets and key mediators of cellular damage in response to environmental stresses. Given high-energy demands of the central nervous system (CNS), mitochondrial function is critically important in neuronal function and neurodegenerative diseases. Mitochondrial DNA (mtDNA) is maternally inherited and encodes 13 electron transport chain polypeptides. Patterns of mtDNA variants—haplogroups—define maternal ancestry, may influence successful aging, and have been associated with human diseases [12]. The potential importance of mtDNA variation in NCI is supported by the prominence of neurologic phenotypes in inherited mtDNA diseases and associations between mtDNA haplogroups and neurodegenerative diseases [13]. Several studies have reported associations between mtDNA haplogroups and HIV- or CART-associated outcomes, including peripheral neuropathy and neuroretinal disease [14]. Furthermore, haplogroup-defining mtDNA variants have recently been linked to altered expression of inflammation, complement, and apoptosis genes, raising the possibility that mitochondrial-nuclear interactions play a role in immune regulation [15].

We hypothesized that genetic variation in mtDNA modulates susceptibility to or severity of NCI in HIV infection, perhaps through neuroinflammation. There are data in HIV-uninfected populations supporting a link between mitochondrial dysfunction and neuroinflammation in neurodegenerative processes [16], and associations with these diseases and mtDNA variation cited above provide indirect evidence for this hypothesis. This link is yet to be established in HAND. Characterizing associations between mtDNA haplogroups and NCI in this population may facilitate risk stratification of patients and identify targets for prevention or therapy. Because studies of the role of mtDNA haplogroups in HAND have not been published, we used stored DNA and cross-sectional data from the CHARTER study to address this question, and present the first report of a genetic association.

METHODS

Where appropriate, methods followed recommendations from the STrengthening the Reporting of Genetic Association Studies Statement (Supplementary Table 1) [17].

Study Design and Participants

CHARTER is a prospective, observational study conducted at 6 US locations: Baltimore, Maryland; New York, New York; San Diego, California; Galveston, Texas; Seattle, Washington; and St Louis, Missouri. Institutional review boards at each site approved this research, and each participant provided written informed consent. Data were collected between 2003 and 2007 according to a protocol of comprehensive neuromedical, neurobehavioral, and laboratory assessments that were standardized across sites [4]. The data reported herein are a cross-sectional genetic association analysis of a subgroup of CHARTER participants.

Assessments of Neurocognitive Impairment

Participants were English-speaking and underwent a comprehensive test battery that included seven neurocognitive domains affected by HIV-associated CNS dysfunction [4]. Composite global deficit score (GDS) was derived from standard T-scores using best available normative standards to correct for learning, age, education, sex, and ethnicity, as appropriate. For self-reported Hispanics, 3 of 15 measures were corrected for English-speaking Hispanic normative standards; the remainder was adjusted for Caucasian normative standards [18,19]. The GDS as a continuous variable reflects the number and severity of neurocognitive deficits across the battery; it is the average of the deficit scores on each test, where T ≥ 40 = 0 (no deficit), 35–39 = 1(mild deficit), 30–34 = 2 (mild to moderate deficit); 25–29 = 3 (moderate deficit), 20–24 = 4 (moderate to severe deficit), and <20 = 5 (severe deficit). An established cutoff of GDS ≥ 0.50 defines NCI [20]. To further classify presence and severity of HAND, we applied a published objective algorithm that has been shown to yield excellent inter-rater reliability in previous multisite studies [21]. This algorithm conforms to the Frascati criteria for diagnosing HAND [22], requiring at least mild impairment in ≥2 of seven domains, and includes functional
Mitochondrial DNA Sequencing and Haplogroup Determination
Isolation of DNA from whole blood samples was performed using PUREGENE (Gentra Systems Inc, Minneapolis, Minnesota). Full mtDNA sequencing was performed using the GeneChip Human Mitochondrial Resequencing Array v2.0 (Affymetrix, Inc, Santa Clara, California).

Array intensity data were processed using the MitoChip Filtering Protocol [23], and variants were called relative to the Revised Cambridge Reference Sequence [24]. Haplogroups were assigned using HaploGrep (http://haplogrep.uibk.ac.at/) [25].

Most participants also underwent nuclear DNA genotyping using the Affymetrix Genome-Wide Human SNP Array 6.0 (Affymetrix, Inc, Santa Clara, California). Ancestry-informative markers were analyzed using EIGENSTRAT software [26] to generate principal components (PC) (Supplementary Figure 1). Model-based clustering on the top 3 PCs, using the mclust R package, was used to assign individuals to genetic ancestry clusters using an ellipsoidal model [27]. Genetic ancestry clusters showed 97.4% agreement with self-reported race and ethnicity (Supplementary Table 2). All analyses used PC-ancestry based stratifications (European, African, or admixed Hispanic).

Statistical Analyses
Three outcomes were analyzed: (1) Continuous GDS; (2) dichotomous NCI (defined as GDS ≥ 0.50) vs no impairment (GDS < 0.50); and (3) HAND (any HAND category vs normal) [22]. Prior research has shown strong agreement between the latter 2 methods of classifying NCI, such that NCI by GDS criteria virtually guarantees the presence of HAND, but a minority of HAND cases are classified as within normal limits by the GDS [20]. Primary analyses were stratified by PC-derived genetic ancestry. Univariate analyses included nonparametric Wilcoxon tests for continuous variables and Fisher exact tests for dichotomous variables. Multivariable regression of associations between mtDNA haplogroups and GDS and HAND were adjusted for: comorbidity status (incidental vs contributing); current CART use (yes vs no); plasma HIV RNA; reading ability (by Wide-Range Achievement Test-III [WRAT] Reading subtest score); and self-reported nadir CD4+ T-cell count. Adjustments for multiple comparisons were not performed given the exploratory nature of these analyses, the limited number of exposure (genetic) variables within stratified groups, and the relatively limited number of outcomes assessed. Statistical analyses were conducted using R (version 2.15.1) and Stata Statistical Software, Release 13 (College Station, Texas: StataCorp LP).

RESULTS
Participant Characteristics
Haplogroups were available from 1068 participants. Of these, 1027 (96%) had nuclear DNA genotypes that allowed for PC assessment of genetic ancestry (Supplementary Figure 2). The median age for the analysis group (Table 1) was 43 years, median CD4+ T-cell nadir was 178 cells/mm³, 736 (72%) were on CART at initial assessment, 474 (46%) had HAND, and the median (interquartile range [IQR]) GDS was 0.32 (0.11–0.63). Haplogroup frequencies within each ancestry category were consistent with US population based data [28] (Supplementary Table 3) and did not differ across CHARTER sites (data not shown).

Univariate Analyses of Global Deficit Score and HIV-associated Neurocognitive Disorders
Persons of admixed Hispanic ancestry had a higher median (IQR) GDS (0.53; 0.21–0.94) than persons of African (0.26; 0.11–0.53; P < .0001) or European (0.37; 0.16–0.68; P = .003) ancestry (Supplementary Figure 3A). Persons of admixed Hispanic ancestry also had a greater likelihood of either impaired GDS (52% vs 29% African [P < .0001] and 37% European [P = .009]; Supplementary Figure 3B) or HAND diagnosis (64% vs 40% African [P < .0001] and 48% European [P = .003]; Supplementary Figure 3C and 3D).

Median GDS did not differ significantly by mtDNA haplogroup in participants of African or European ancestry (Figure 1A and 1B). Among the 102 persons of admixed Hispanic ancestry, WRAT-III, GDS, and percentage with GDS impairment or HAND differed significantly across haplogroups in univariate analyses (Table 1). Persons belonging to haplogroup...
### Table 1. Subject Characteristics at CNS HIV Antiretroviral Therapy Effects Research Entry, Overall, Among Those of European, African, and Admixed Hispanic Ancestry, and by Major Hispanic Mitochondrial DNA Haplogroups

<table>
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<tbody>
<tr>
<td>Age, median (range)</td>
<td>43 (18–69)</td>
<td>44 (19–68)</td>
<td>44 (18–69)</td>
<td>40 (21–61)</td>
<td>43 (30–54)</td>
<td>39 (22–61)</td>
<td>42 (32–52)</td>
<td>40 (21–53)</td>
<td>.31</td>
</tr>
<tr>
<td>Female sex</td>
<td>235 (23%)</td>
<td>52 (12%)</td>
<td>161 (33%)</td>
<td>22 (22%)</td>
<td>9 (26%)</td>
<td>2 (10%)</td>
<td>4 (29%)</td>
<td>7 (21%)</td>
<td>.50</td>
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<td></td>
<td></td>
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<td></td>
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<td></td>
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<tr>
<td>European</td>
<td>440 (43%)</td>
<td>440 (100%)</td>
<td></td>
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<tr>
<td>Admixed Hispanic</td>
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<tr>
<td>Plasma HIV RNA, log₁₀ copies/mL</td>
<td>2.3 (1.7–4.0)</td>
<td>2.1 (1.7–4.0)</td>
<td>2.5 (1.7–4.0)</td>
<td>2.0 (1.7–3.6)</td>
<td>1.7 (1.7–3.5)</td>
<td>1.8 (1.7–2.1)</td>
<td>2.5 (1.7–4.2)</td>
<td></td>
<td>.49</td>
</tr>
<tr>
<td>Estimated duration of HIV infection, months</td>
<td>120 (55–184)</td>
<td>120 (47–190)</td>
<td>125 (71–180)</td>
<td>108 (37–164)</td>
<td>124 (58–177)</td>
<td>105 (34–125)</td>
<td>152 (95–178)</td>
<td>49 (17–135)</td>
<td>.10</td>
</tr>
<tr>
<td>On CART</td>
<td>736 (72%)</td>
<td>308 (70%)</td>
<td>350 (72%)</td>
<td>78 (76%)</td>
<td>26 (74%)</td>
<td>16 (80%)</td>
<td>12 (86%)</td>
<td>24 (73%)</td>
<td>.83</td>
</tr>
<tr>
<td>Estimated time on CART, months</td>
<td>48 (9–88)</td>
<td>53 (8–98)</td>
<td>45 (10–79)</td>
<td>45 (5–95)</td>
<td>65 (32–100)</td>
<td>73 (15–103)</td>
<td>60 (3–138)</td>
<td>17 (1–73)</td>
<td>.05</td>
</tr>
<tr>
<td>Comorbidity</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>.25</td>
</tr>
<tr>
<td>Incidental</td>
<td>660 (64%)</td>
<td>304 (69%)</td>
<td>296 (61%)</td>
<td>60 (59%)</td>
<td>18 (51%)</td>
<td>14 (70%)</td>
<td>6 (43%)</td>
<td>22 (67%)</td>
<td></td>
</tr>
<tr>
<td>Contributing</td>
<td>367 (36%)</td>
<td>136 (31%)</td>
<td>189 (39%)</td>
<td>42 (41%)</td>
<td>17 (49%)</td>
<td>6 (30%)</td>
<td>8 (57%)</td>
<td>11 (33%)</td>
<td></td>
</tr>
<tr>
<td>WRAT-III</td>
<td>96 (83–105)</td>
<td>102 (96–109)</td>
<td>87 (76–96)</td>
<td>96 (83–102)</td>
<td>93 (79–105)</td>
<td>100 (96–109)</td>
<td>88 (83–96)</td>
<td>94 (87–100)</td>
<td>.04</td>
</tr>
<tr>
<td>HAND</td>
<td></td>
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<td></td>
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<tr>
<td>NCN</td>
<td>553 (54%)</td>
<td>228 (52%)</td>
<td>289 (60%)</td>
<td>36 (35%)</td>
<td>8 (23%)</td>
<td>12 (60%)</td>
<td>2 (14%)</td>
<td>14 (42%)</td>
<td>.01**</td>
</tr>
<tr>
<td>Any HAND</td>
<td>474 (46%)</td>
<td>212 (48%)</td>
<td>195 (40%)</td>
<td>66 (65%)</td>
<td>27 (77%)</td>
<td>8 (40%)</td>
<td>12 (86%)</td>
<td>19 (58%)</td>
<td></td>
</tr>
<tr>
<td>ANI</td>
<td>354 (34%)</td>
<td>150 (34%)</td>
<td>158 (33%)</td>
<td>46 (45%)</td>
<td>17 (49%)</td>
<td>6 (30%)</td>
<td>8 (57%)</td>
<td>15 (45%)</td>
<td>.06***</td>
</tr>
<tr>
<td>MND</td>
<td>88 (9%)</td>
<td>44 (10%)</td>
<td>30 (6%)</td>
<td>14 (14%)</td>
<td>6 (17%)</td>
<td>2 (10%)</td>
<td>2 (14%)</td>
<td>4 (12%)</td>
<td></td>
</tr>
<tr>
<td>HAD</td>
<td>31 (3%)</td>
<td>18 (4%)</td>
<td>7 (1%)</td>
<td>6 (6%)</td>
<td>4 (11%)</td>
<td>0 ( . . )</td>
<td>2 (14%)</td>
<td>0 ( . . )</td>
<td></td>
</tr>
<tr>
<td>GDS</td>
<td>0.32 (0.11–0.63)</td>
<td>0.37 (0.16–0.68)</td>
<td>0.26 (0.10–0.53)</td>
<td>0.53 (0.21–0.94)</td>
<td>0.68 (0.42–1.0)</td>
<td>0.21 (0.08–0.32)</td>
<td>0.58 (0.43–1.4)</td>
<td>0.53 (0.16–0.89)</td>
<td>.003</td>
</tr>
<tr>
<td>GDS impaired</td>
<td>359 (35)</td>
<td>164 (37%)</td>
<td>142 (29%)</td>
<td>53 (52)</td>
<td>24 (69)</td>
<td>4 (20)</td>
<td>8 (57)</td>
<td>17 (52)</td>
<td>.006</td>
</tr>
</tbody>
</table>

Values are N (%) or median (interquartile ranges), except where noted.

Abbreviations: ANI, asymptomatic neurocognitive impairment; CART, combination antiretroviral therapy; GDS, global deficit score; HAD, HIV-associated dementia; HAND, HIV-associated neurocognitive disorder; HIV, human immunodeficiency virus; MND, mild neurocognitive disorder; NCN, neurocognitively normal; WRAT, wide-range achievement test.

*Values by analysis of variance (ANOVA) or exact test comparisons across Admixed Hispanic Ancestry haplogroups except where noted.

** P for comparison of any HAND vs NCN.

*** P for ANOVA comparison across all HAND categories.
B (N = 20; 20%) had a lower median GDS (0.21 vs 0.63; \( P = .002 \); Figure 1C and Table 1), and lower likelihood of either GDS impairment (odds ratio [OR] 0.17; 95% confidence interval [CI], .05, .55; \( P = .001 \); Figure 2A and Supplementary Table 4) or HAND (OR 0.27; 95% CI, .10, .75; \( P = .013 \); Figure 2B and Supplementary Table 5) than Hispanic persons with other haplogroups. These relationships persisted in analyses of subgroups on CART, with detectable plasma HIV RNA, and with only incidental neurocognitive comorbidities (data not shown). Among persons of European or African ancestry, there were no statistically significant haplogroup associations with GDS, proportion with GDS impairment, or HAND (data not shown).

Figure 1. Box and dotplots of global deficit scores among participants of African (panel A), European (panel B), and Hispanic (panel C) ancestry, by major mtDNA haplogroups. Boxes denote median and interquartile range; whiskers denote 95th percentiles. \( P \)-value = .002 by univariate linear regression for haplogroup B vs other haplogroups among the admixed Hispanic population in Panel C. Abbreviation: mtDNA, mitochondrial DNA.

Figure 2. Bar graphs of percentage of participants with global deficit score (GDS) impairment (GDS ≥ 0.50; panel A) and HIV-associated neurocognitive disorder (HAND) of any severity (panel B), by ancestry and major mtDNA haplogroups. Error bars for frequency estimates were calculated as \( 2 \times \) Standard Error. \( P \)-values from univariate logistic regression models are shown. Abbreviations: HIV, human immunodeficiency virus; mtDNA, mitochondrial DNA; NS, not significant.
Multivariate Analyses of Global Deficit Score and HIV-associated Neurocognitive Disorders

In adjusted models of persons of admixed Hispanic ancestry, haplogroup B was associated with a lower GDS (β = −0.34; −0.59, −0.09; P = .008; Table 2) compared with non-B haplogroups, and a lower likelihood of GDS impairment (adjusted OR 0.16; 0.04, 0.63; P = .009; Supplementary Table 4), independent of comorbidity status, WRAT-III score, CART status, nadir CD4 T-cell count, and plasma HIV RNA level. Although persons with haplogroup B were less likely to have HAND of any severity in univariate analyses, this association was not statistically significant in adjusted analyses (adjusted OR 0.36; 0.11, 1.14; P = .08; Supplementary Table 5).

DISCUSSION

In this analysis of chronically HIV-infected, mostly CART-treated CHARTER participants, persons of Hispanic ancestry had more NCI overall, but a common mtDNA haplogroup within the population was associated with significantly lower prevalence of NCI. Specifically, among the almost 20% of persons of admixed Hispanic ancestry having mtDNA haplogroup B, median GDS and the proportion with impaired GDS were significantly lower than in persons with other haplogroups after adjustment for potential confounders. Mitochondrial DNA variants, including haplogroups, have been studied in relation to neurodegenerative diseases in HIV-negative populations. Several studies have explored host genetic risks for HIV-associated NCI [10] and associations between mtDNA haplogroups and non-CNS HIV-related outcomes [14]. This is the first analysis to our knowledge of mtDNA variation and NCI in an HIV-infected population.

Haplogroup B is a major haplogroup seen in persons of East Asian, Native American, and admixed Hispanic ancestry [29, 30], is part of the R superhaplogroup, and includes variations common to the related European haplogroups J and T [31] (Supplementary Figure 4). Haplogroup B has been associated with nonneurocognitive phenotypes in recent studies [32, 33]. The B haplogroup was also recently associated with changes in epidermal nerve fiber density (ENFD, a measure of small fiber neuropathy) in lower extremity skin biopsies from HIV-infected persons starting CART as part of a clinical trial in Thailand [34]. In that study, persons with the B haplogroup had an increase in ENFD and plasma 8-oxo-deoxyguanosine (a marker of oxidative DNA damage also associated with HAND and mtDNA damage in brain tissue [35]) on CART. Our data cannot address apparently discrepant associations between haplogroup B and what may be an adverse peripheral nerve phenotype in HIV-infected Thais and less NCI in US Hispanics. A recent publication reported an association between subhaplogroup B5a and increased risk for Alzheimer’s disease in Han Chinese [36]. Lymphoblastoid and HeLa cells harboring haplogroup B5a and a nonsynonymous SNP (m.8584G > A) found in B5a, respectively, demonstrated adverse mitochondrial phenotypes compared to control cells. Importantly, although B5 was the predominant subhaplogroup in this Han Chinese population and the study of HIV-infected Thais [34], B5 is not represented in our population of admixed Hispanics from the United States. We speculate that this population-specific subhaplogroup could determine whether the B haplogroup is associated with neurodegeneration or neuroprotection.

Potential mechanisms by which mtDNA variation could alter susceptibility to NCI would be similar to those posited for other neurodegenerative processes in aging populations, including differences in ROS production, oxidative stress, inflammation, and apoptotic regulation. In chronic HIV infection, systemic or CNS inflammation or both may contribute to NCI. Given the role of mitochondria in inflammatory processes [37], mtDNA variation could be an additional susceptibility factor. A potential confounder in this population is exposure to older mitochondria-toxic CART drugs, particularly “d-drug” NRTIs zalcitabine, didanosine, or stavudine. Among these CHARTER participants, 13% were taking 1 or more of these at enrollment; 39% had a history of exposure.

### Table 2. Linear Regression of Global Deficit Score in Persons of Admixed Hispanic Ancestry

<table>
<thead>
<tr>
<th>Variable</th>
<th>Unadjusted Coefficient (95% CI)</th>
<th>P Value</th>
<th>Adjusted Coefficient (95% CI)</th>
<th>P Value</th>
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</thead>
<tbody>
<tr>
<td>Haplogroup B (vs all others)</td>
<td>−0.37 (−0.61, −0.13)</td>
<td>.002</td>
<td>−0.34 (−0.59, −0.09)</td>
<td>.008</td>
</tr>
<tr>
<td>Comorbidity (incidental vs contributing)</td>
<td>−0.26 (−0.46, −0.07)</td>
<td>.008</td>
<td>−0.16 (−0.36, .04)</td>
<td>.12</td>
</tr>
<tr>
<td>WRAT-III score</td>
<td>−0.008 (−0.016, −0.001)</td>
<td>.022</td>
<td>−0.003 (−0.01, .0004)</td>
<td>.40</td>
</tr>
<tr>
<td>On CART (yes vs no)</td>
<td>0.24 (.009, .464)</td>
<td>.041</td>
<td>−0.02 (−0.36, .33)</td>
<td>.92</td>
</tr>
<tr>
<td>Nadir CD4 (per cell/mm³)</td>
<td>−0.0006 (−0.0011, −.00009)</td>
<td>.020</td>
<td>−0.0004 (−0.001, −.0002)</td>
<td>.16</td>
</tr>
<tr>
<td>Plasma HIV RNA (per log₁₀ copies/mL)</td>
<td>−0.09 (−.17, −.01)</td>
<td>.023</td>
<td>−0.06 (−.17, .04)</td>
<td>.23</td>
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</table>

N = 96. Model P-value = .001, R² = 0.16.

Abbreviations: CART, combination antiretroviral therapy; CI, confidence interval; HIV, human immunodeficiency virus; WRAT, wide-range achievement test.
multivariate models, neither d-drug exposure at enrollment nor past exposure were associated with NCI in the admixed Hispanic population, and associations between mtDNA haplogroup B did not change substantially (data not shown). There tended to be variability in the duration of CART exposure by haplogroup among the admixed Hispanic population (Table 1). We therefore also performed a secondary model adjusting for CART duration, and did not observe substantial differences in the haplogroup B results (data not shown).

A strength of our study is the well-characterized and racially and geographically diverse population with NCI and HAND diagnoses and confounders identified in a standardized fashion. Limitations include those inherent to cross-sectional analyses and the lack of an HIV-uninfected control population. Longitudinal approaches to NCI in CHARTER have recently been published [2, 3], and genetic analyses of longitudinal changes in NCI are needed. Although this analysis includes an overall large sample, numbers of persons from minority genetic ancestry groups and within individual mtDNA haplogroups are relatively small. The small sample size of adults of admixed Hispanic ancestry suggests that although the effect sizes identified were large enough to reach statistical significance, the findings may not generalize to other populations of HIV-infected adults of Hispanic ancestry. We did not observe statistically significant associations between mtDNA haplogroup and NCI or HAND in persons of European or African genetic ancestry in CHARTER. Despite relatively large sample sizes, our analyses may be underpowered to detect small but potentially clinically relevant differences, or that subhaplogroups or mtDNA variants not specifically included in our analysis are associated with NCI. The relevance of ANI, the most common HAND category in this population, has been questioned [38]. Recent data, however, have demonstrated that persons with ANI are at risk for symptomatic decline, supporting its clinical and prognostic value [3].

We performed sensitivity analyses of the HAND outcome in admixed Hispanic participants excluding those with ANI (ie, comparing neurocognitively normal vs MND or HAD). With this smaller population (N = 54), the adjusted OR for the B haplogroup was of a similar direction and magnitude (0.22), with an increase of P-value from .08 to .14.

Utility of standardized NCI measures in persons of non-European ancestry is less well established, an important consideration given that we observed both greater prevalence of and haplogroup associations with NCI only in the admixed Hispanic ancestry population. Because specific Hispanic neurocognitive norms exist for only 3 of the tests in the CHARTER battery, use of Caucasian norms for the other tests may have contributed to higher rates of impairment among Hispanics. The choice of norms was based upon evidence that performance of US Hispanics on multiple neurocognitive tests is closer to that of Caucasian than African Americans [39].

In addition, recent longitudinal CHARTER analyses found self-reported Hispanic ethnicity to be a risk factor for decline in neurocognitive performance from baseline over a mean of 36 months of follow-up [2]; those analyses did not use cross-sectional neurocognitive norms and also found Hispanic ethnicity to be associated with NCI. Although self-identified Hispanic participants were drawn from CHARTER sites across the United States, haplogroup frequency did not differ significantly across sites, and the B haplogroup was associated with NCI independent of WRAT-III, a measure of premorbid intelligence and quality of educational background. In addition, birthplace (US or Canada vs other) and primary language (English vs other) did not differ significantly between B and other haplogroups among participants of admixed Hispanic ancestry (data not shown), but there may be other unmeasured or unknown biologic or sociodemographic confounders associated with both mtDNA haplogroup and NCI. Due to genetic diversity and admixture of persons of self-identified Hispanic-American ethnicity, genotype-phenotype associations are complex [40], and definitive conclusions must be drawn cautiously and only after replication.

Future analyses should examine associations between haplogroups and CSF neuroinflammation and non-haplogroup-defining SNPs and NCI, and interactions between mtDNA variants and SNPs in nuclear genes relevant for mitochondrial function and inflammation. Prospective studies may also explore targeted genetic testing for risk-stratification and personalized interventions. Should this association be validated, mtDNA variation may be a novel, ancestry-specific host factor influencing HAND in chronically HIV-infected persons and may provide pathogenic clues that will lead to a better understanding of this condition.

**Supplementary Data**

Supplementary materials are available at Clinical Infectious Diseases online (http://cid.oxfordjournals.org). Supplementary materials consist of data provided by the author that are published to benefit the reader. The posted materials are not copyedited. The contents of all supplementary data are the sole responsibility of the authors. Questions or messages regarding errors should be addressed to the author.

**Notes**

**Acknowledgments.** The authors thank the CNS HIV Antiretroviral Therapy Effects Research (CHARTER) participants for their selfless commitment and the staff and investigators at all CHARTER sites. The CHARTER group is affiliated with Johns Hopkins University; the Icahn School of Medicine at Mount Sinai; University of California, San Diego; University of Texas, Galveston; University of Washington, Seattle; Washington University, St. Louis; and is headquartered at the University of California, San Diego and includes: Director: Igor Grant, MD; Co-Directors: Scott L. Letendre, MD, Ronald J. Ellis, MD, PhD, Thomas D. Marcotte, PhD; Center Manager: Donald Franklin, Jr; Neuromedical Component: Ronald J. Ellis, MD, PhD (principal investigator [PI]), J. Allen McCutchan, MD; Laboratory and Virology Component: Scott Letendre, MD (Co-PI), Davey M. Smith, MD (Co-PI); Neurobehavioral Component: Robert
K. Heaton, PhD (PI), J. Hampton Atkinson, MD, Matthew Dawson; Imaging Component: Christine Fennema-Notestine, PhD (PI), Michael J Taylor, PhD, Rebecca Theilmann, PhD; Data Management Component: Anthony C. Gamst, PhD (PI), Clint Cushman; Statistics Component: Ian Abramson, PhD (PI), Florin Vaida, PhD, Reena Deutsch, PhD; Johns Hopkins University Site: Justin McArthur (PI), Vincent Rogalski; Icahn School of Medicine at Mount Sinai Site: Susan Morgello, MD (Co-PI) and David Simpson, MD (Co-PI), Letty Mintz, NP; University of California, San Diego Site: J. Allen McCutchan, MD (PI), Kaoi Phillips, BSN; University of Washington, Seattle Site: Ann Collier, MD (Co-PI) and Christina Marra, MD (Co-PI), Trudy Jones, MN, ARNP; University of Texas, Galveston Site: Benjamin Gelman, MD, PhD (PI), Eleanor Head, RN, BSN; and Washington University, St. Louis Site: David Clifford, MD (PI), Muhammad Al-Lozi, MD, Mengsha Teshome, MD.


Financial support. This work was supported by grant number R01 MH095621 from the National Institute of Mental Health/National Institutes of Health (NIH). The CHARTER study is also supported by awards N01 MH22005, HHSN271201000036C, and HHSN271201000036C from the NIH.

Disclaimer. The study sponsors/funding sources had no role in the study design, data collection, analyses, interpretation of data, writing of the report, or the decision to submit for publication. The views expressed in this article are those of the authors and do not reflect the official policy or position of the NIH or the United States Government.

Potential conflicts of interest. T. H. has served as PI of research grants to Vanderbilt University from Merck & Co. R. J. E. gave sponsored talks and received honoraria for serving on the scientific advisory board of GlaxoSmithKline. D. B. C. has received support for consulting/advisory boards from Sanofi, Genentech, Quintiles, Inhibikase, Bristol-Myers-Squibb (BMS), GlaxoSmithKline, Millennium, Biogen Idec, Amgen, Pfizer, AstraZeneca, Cytheris and Merck, has received speaker honorarium from Sun Pharmaceuticals and Biogen Japan, and receives research support from Lilly, Roche, Bayer, Sanoﬁ, Gilead, and the Alzheimer Association. A. C. C. has current or past research support from Merck & Co, National Institutes of Health, Roche Molecular Systems, and Schering-Plough. She is a member of Data, Safety, and Monitoring Boards for 2 Merck-sponsored studies. She previously owned stock in Abbott Laboratories, BMS, Johnson & Johnson, and Pfizer. C. M. M. receives royalties from Lippincott Williams and Wilkins and from UpToDate. J. A. M. authors chapters on HIV for the Merck Manual. D. M. S. provided served as a consultant for Astellas, Acorda, Allergan, Merz, and Ipsen. He has received speaking honoraria from Allergan and Acorda, and research grants from Merz, Allergan, Ipsen, Acorda, and Astellas. S. L. L. has received support for research projects from Abbott, Merck & Co, Tibotec, Schering-Plough, and GlaxoSmithKline. He has received honoraria for speaking from Abbott, GlaxoSmithKline, and Tibotec. The other authors have no potential conflicts of interest to declare. All other authors report no potential conflicts.

All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

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