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More Evidence of an Association between European Ancestry and *g* among African Americans: An Analysis of a Nationally Representative Sample of American Youth

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This report examines the National Longitudinal Study of Youth 1979 data. Self-reported European ancestry among Black Americans is found to have a positive yet moderate correlation with cognitive ability. Of the 2935 screener-identified African Americans, 53 had self-reported ancestry from a specific European ethnicity. This group had an advantage of .41*d* over African Americans who did not report any European ancestry. Consistent with previous results, the effect of European ancestry exhibited a positive correlation with subtest *g*-loadings. The findings were corroborated by results from the Adolescent Brain Cognitive Development (ABCD) Study, which used genetically assessed ancestry. In both cases, African Americans with more European ancestry were overrepresented, by a factor of two, in the right tail of the cognitive distribution.

Key Words: Ancestry, Cognitive ability, Race, African-American, USA

An earlier study using the National Longitudinal Study of Youth 1997 found that both parent-reported European ancestry and lighter skin color were associated with higher levels of general cognitive ability (*g*) among African Americans. Moreover, both the ancestry and color effects were strongest on more *g*-loaded subtests, thus exhibiting a so-called Jensen effect (Hu et al., 2019). More recently, European genetic ancestry was found to be positively (and African and Amerindian ancestry negatively) associated with *g* within self-identified African and Hispanic American groups in a large national sample (Fuerst, Hu & Connor, 2021).

Taken together, these results are consistent with the hypothesis which predicts that differences in genes inherited from continental ancestry populations are related to socially-identified race/ethnic group differences in tests of cognitive ability. However, the association between European ancestry and *g* has been disputed (Colman, 2016; Nisbett, 2009). As such, we examine the National Longitudinal Study of Youth 1979, which asked participants about ethnic descent and contains a reliable measure of *g*. Moreover, we report corroborating results based on the Adolescent Brain Cognitive Development Study (ABCD) in which continental ancestry was measured genetically.

African Americans reporting European ethnicity in the NLSY79

Methods

Race and descent in the NLSY 1979 sample.

We use the National Longitudinal Study of Youth 1979, a nationally representative sample of American adolescents and young adults. Individuals were aged 14 to 21 at the start of the interviews. We restricted our analysis to non-Hispanic African Americans, using the official R02147 (Race78) variable, or "R's racial/ethnic cohort from screener." Light and Nandi (2007, pp. 131-132) detail the method of classification for this variable: "respondents were coded as black if they chose 'Black, Negro, or Afro-American' as their origin or descent, or were identified by the interviewer as black."

In the NLSY79, self-reported ethnicity variables also assessed the respondents' first and second ethnic descent (variables R0009600 and R0009700): "What is your Origin or Descent?" This variable allowed for multiple choices. Those African Americans who selected a European ethnicity (English, French, German, Greek, Irish, Italian, Polish, Portuguese, Russian, Scottish, or Welsh) for one of their choices were coded as having some European background.

Thus, we identified two groups: African Americans without self-reported European descent, and African Americans with reported European descent. The

assumption is that self-reported European ethnic descent indexes recent genetic admixture (i.e., within the last few generations). That is, it is assumed that African Americans who mark having e.g., French or English descent have a European-origin parent, grandparent, or great-grandparent and so have more European ancestry than the African American average. For the rationale, see Witty and Jenkins (1934), Jenkins (1936), and Nisbett (2009).

We did not look at White Americans who reported African ancestry, because there were no such cases. This is because NLSY79 coded anyone who chose "Black, Negro, or Afro-American" for one of their origin or descent groups as being Black or African American (unless they also reported a Hispanic descent).

Cognitive ability

We use the ASVAB subtest scores as a measure of cognitive ability. The ASVAB is designed to measure aptitudes in four domains: Verbal, Math, Science and Technical, and Spatial. This cognitive battery is composed of ten subtests: Arithmetic reasoning, Mathematics knowledge, Paragraph comprehension, Word knowledge, General science, Electronics information, Auto and shop information, Mechanical comprehension, Coding speed, and Numerical operations. For the ASVAB subtests, we regressed out the effects of sex and age. To obtain a measure of this *g* factor, we factor analyzed, with principal factor analysis, the ten subtests of the ASVAB and produced two unrotated factors, the first explaining 58% of the variance, which we recognize as *g*, and the second explaining 11%, which we recognize as non-*g* variance.

Analysis

As a preliminary test, we checked for data normality. We produced skewness and kurtosis values of -0.506 and -0.380, respectively, for *g* scores, in the combined sample of African and White Americans ($N = 10{,}071$). As the normality condition is met, we then computed mean scores for the African Americans with and without reported European ancestry. We provide scores normed relative to the White mean. We additionally computed the point-biserial correlations between reported European ancestry and ASVAB subtest scores. We report these along with the corresponding subtest *g*-loadings and reliabilities. The subtest reliabilities are taken from ASVAB Technical Bulletin No. 1 CAT-ASVAB Forms 1 & 2, Table 7.3 (Defense Manpower Data Center, 2006). The *g*-loadings are derived from factor analysis applied to the African American sample. The relevant formulas for correcting unequal sample sizes in point-biserial correlations are provided by Hunter & Schmidt (2004, p. 280). To test for a Jensen effect (Rushton, 1998), the effect of ancestry on subtest scores is then correlated with the subtest *g*-loadings, after both vectors are corrected for square root of the subtest reliability (see:

Jensen, 1998). This is known as the correlated vector method. It is assumed that, since these are all African Americans, they share a similar culture; this common culture will make score differences on less *g*-loaded, and presumably less genetically influenced, subtests more similar across groups.

As an alternative test, we restrict the data to respondents with *g* scores above the African American mean by two standard deviations and calculate the proportion of African Americans with European ancestry. If European ancestry is associated with cognitive ability in the African American population, then there should be an increased proportion of European ancestry at high levels of cognitive ability (Jenkins, 1936; Nisbett, 2009; Witty & Jenkins, 1934).

Results

There were 2882 African Americans without reported European ancestry; they had a mean *g* score of $M = -1.004$ ($SD = 0.818$). There were 53 African Americans with self-reported European ancestry; the mean *g* score of this group was $M = -0.668$ ($SD = 1.020$). The Cohen's *d*[1] between the two groups was $d = 0.41$. We computed a point-biserial correlation between each subtest and a dichotomized biracial variable, coded as 1 = Black, 2 = Black_w/_European Ancestry. Because our sample sizes are unequal, a correction needs to be applied (Hunter & Schmidt 2004, p. 280). The correlations and corrected correlations are shown in Table 1 along with subtest *g*-loadings and reliabilities.

Table 1. g-*loadings, reliability coefficients, and point-biserial correlations (rpbs) between ASVAB subtest scores and the dichotomous ancestry variable (African American with and without European ancestry).*

Subtest	*g*-loading	Reliability	rpbs	rpbs corrected
General science	0.822	0.86	0.069	0.251
Arithmetic reasoning	0.756	0.89	0.055	0.202
Word knowledge	0.869	0.86	0.044	0.163
Paragraph comprehension	0.806	0.67	0.044	0.163
Numerical operations	0.712	0.79	0.011	0.041
Coding speed	0.634	0.81	0.050	0.184
Auto and shop information	0.656	0.89	0.024	0.089
Mathematics knowledge	0.768	0.92	0.027	0.101
Mechanical comprehension	0.661	0.80	0.036	0.134
Electronics information	0.742	0.74	0.069	0.251

[1] The formula is: $(Mean_1 - Mean_2) / SQRT(((N_1 * SD_1^2) + (N_2 * SD_2^2)) / (N_1 + N_2))$

The correlation between the *g*-loadings and point-biserial correlations, with both corrected for subtest reliability, was $r = .40$. This represents a relatively modest Jensen effect compared to various meta-analyses reporting a Jensen effect of $r \sim .60$ (Jensen, 1998, pp. 381-383; te Nijenhuis and van den Hoek, 2016; te Nijenhuis, van den Hoek & Willigers, 2017; te Nijenhuis, van den Hoek & Dragt, 2019). The general consensus indicates that the advantage of Black with European ancestry tends to be larger on more *g*-loaded tests.

As an alternative test, we restrict the data to respondents with *g* scores two standard deviations or more above the African American mean. Out of the 99 individuals, three had reported European ancestry. This is equivalent to 3.03% of the sample, which is almost twice as high as the 1.81% in the total sample.

Race and genetic ancestry in the ABCD sample

The NLSY79 analysis could be criticized on the grounds that self-reported European descent does not correspond with elevated genetic European ancestry, despite it usually being taken as such (e.g., Lee, 2010; Nisbett, 2009). Considering this, we also report data from a formally unpublished side analysis of the Adolescent Brain Cognitive Development Study (ABCD) data done in conjunction with Fuerst et al. (2021). The ABCD is a recent collaborative longitudinal project. It involves 21 sites from around the USA. Children were 9-10 years at baseline in approximately 2016. The methods and variables have previously been extensively detailed (Fuerst et al., 2021).

To exclude confounding due to factors related to recent immigration, only individuals with US-born families (including children, parents, and grandparents) were included. This allows for comparison with older studies, such as Witty and Jenkins (1934) and also the NLSY79 results. As with the NLSY79 analyses, children coded as being Hispanic were excluded.

Parents were asked 18 questions about the child's specific race and ethnicity. For the purpose of this analysis, an individual was defined as White American if they were marked as being White and no other race. Thus "White Americans" were non-Hispanic mono-racial Whites. An individual was defined as an African or Black American if they were marked as being Black or African whether or not they were also identified as being another race. Thus "Black Americans" were non-Hispanic mono- and multi-racial Blacks. This follows the convention of NLSY79. Additionally, Black Americans were subdivided into those who were identified as also being White (i.e., multiracial Black and White) and those who were not so identified.

Methods

Cognitive ability

General cognitive ability (*g*) scores were based on eleven subtests. Multi-group confirmatory factor analysis (MGCFA) was used to verify measurement invariance. The *g*-scores were outputted from the MGCFA model. Fuerst et al. (2021) note:

> ABCD baseline data contain the following cognitive subtests, the first seven of which are from the NIH Toolbox® cognitive battery: Picture vocabulary, Flanker, List sorting, Card sorting, Pattern comparison, Picture sequence memory, Oral reading recognition, Wechsler Intelligence Scale for Children's Matrix reasoning, The Little Man Test (efficiency score), The Rey Auditory Verbal Learning Test (RAVLT), Immediate recall, and RAVLT delayed recall. For details about these measures, see Thompson et al. (2019). We conducted multi-group confirmatory factor analysis (MGCFA) on these subtests, …. Briefly, we first checked whether outliers and missing data had any impact, and whether our results remained strong after correction. We then conducted exploratory factor analysis and multigroup confirmatory factor analysis on the aforementioned set of subtests as a check for bias. After adjustment for age, we did not find any non-linear effects of age. Adjustment for sex did not reveal any evidence of meaningful differences in fit between the competing models, the *g*-model and the correlated factors model. We find that a three broad factor model (memory, complex cognition, and executive function) with *g* at the apex fits the data well. Moreover, strict measurement invariance holds between SIRE groups. The best fitting model (M6A, Table S2 of Supplementary File 1; CFI = .954, RMSEA = .044) was one in which *g* alone explains SIRE group differences. We output the *g*-factor scores from this model for use in the analyses. These score magnitudes are approximately the same as those derived from exploratory factor analysis.

Genetic ancestry

Genetic ancestry was computed using 99,642 autosomal SNP variants and the Admixture program (Alexander, Novembre & Lange, 2009). A k = 5 solution for continental ancestry (European, Amerindian, African, East Asian, and South Asian) was used. Fuerst et al. (2021) note:

> Imputing and genotyping was done by the ABCD Research Consortium using Illumina XX. 516,598 variants survived the quality control. Before global admixture estimation, we applied quality control using PLINK 1.9.

We used only directly genotyped, bi-allelic, autosomal SNP variants (494,433 before, 493,196 after lifting). We pruned variants for linkage disequilibrium at the 0.1 R^2 level using PLINK 1.9 (--indep-pairwise 10000 100 0.1). This variant filtering was done in the reference population dataset to reduce bias from sample non-representativeness. 99,642 variants were left after pruning. We merged the target samples from ABCD with reference population data for the populations of interest. A k = 5 solution with European, Amerindian, African, East Asian and South Asian components provides the most comprehensive but parsimonious model of the US population, capturing all the predominant ancestral backgrounds in the US population. We merged our sample with relevant samples from 1000 Genomes and from the HGDP to perform the cluster analysis and identify these k = 5 components. The following populations from 1000 Genomes and from the HGDP reference populations were excluded: Adygei, Balochi, Bedouin, Bougainville, Brahui, Burusho, Druze, Hazara, Makrani, Mozabite, Palestinian, Papuan, San, Sindhi, Uygur, Yakut. We excluded these populations because they were overly admixed or because the individuals in the ABCD sample lacked significant portions of these ancestries (e.g., Melanesians and San). We split the ABCD target samples into 50 random subsets (222 persons each) and merged them sequentially with the reference data. Admixture at k = 5 was run on each of the 50 merged subsets. This repeated subsetting was done to avoid skewing the admixture algorithm to European ancestry which was predominant in the ABCD sample.

Analysis

The following variables are reported: sample sizes, general intelligence scores, European genetic ancestry percentages, percent of children with 50% or more European genetic ancestry, and percent of children identified by their parents as both Black and White. Results were decomposed by multi-racial Black & White and Black-only African American status and also by equal and/or greater than two standard deviations above the African American mean. These were supplementary analyses from Fuerst et al. (2021). No new analyses were performed for this sample.

For purposes of reporting, the data was transformed into IQ-metric scores, with a standard deviation of 15 and the white mean set to 100. To transform the data, we first pooled the African and White American standard deviations, and then computed Cohen's *d*-values based on the means and this pooled standard deviation, and finally converted these *d*-values into IQ-metric scores.

Results

The results are shown in Table 2. As can be seen, in this sample, parent-identified race tracks genetic ancestry. Additionally, groups with more European genetic ancestry perform better. Moreover, high-IQ African Americans are disproportionately Black & White and also have elevated levels of European ancestry relative to the African American average. Thus, these results agree with those from the NLSY79.

Table 2. *Supplementary results from the ABCD study. All included subjects are from US-born families.*

Parent-identified child race	*N*	IQ	% European ancestry	% with European ancestry ≥50%	% identified as Black & White
Mono-racial White American	4858	100	98 ± 03	100.0% (4856/4858)	0%
African American	1813	85.95	24 ± 18	15.9% (288/1813)	18%
≥ 2 SD above mean IQ	57	124.97	34 ± 23	35.1% (20/57)	37%
Black without White	1486	84.39	17 ± 1	2.0% (30/1486)	0%
Black & White	327	92.98	56 ± 13	78.9% (258/327)	100%

Discussion

In a large representative sample, African Americans with reported European ancestry had higher *g* scores than those with no reported European ancestry. This was assessed using various methods including Jensen's correlated vectors, which has been criticized for its inability to test appropriately for measurement invariance as well as alternative, non-*g* models (Wicherts, 2017). Using the same NLSY79 data, a recent study by Lasker, Kirkegaard and Nyborg (2021) employed multi-group confirmatory factor analysis, as suggested by Wicherts (2017), to test for both invariance and Spearman's model. Their finding that measurement invariance holds and the weak version of Spearman's hypothesis fits the data better than a non-*g* model, following a bifactor model, provides solid grounds for the findings about ancestry effects in the present study, notwithstanding the shortcomings of the correlated vectors method. Consistent with the results of Hu et al. (2019), this ancestry effect tended to be larger on the more *g*-loaded subtests. The findings from the NLSY79 study were corroborated by results from the ABCD study, which contained both genetic ancestry and parent-reported child race(s). These results are congruent with those of other recent studies based on genomic admixture analysis, a widely used method for investigating the causes of group differences in various complex traits (Fuerst et al., 2021).

These results also suggest that the general approach proposed by Witty and Jenkins (1934) and Jenkins (1936) is valid: If ancestry is associated with

intelligence among admixed populations, then the right tail should be overrepresented with more admixed individuals. This is what was found to be the case in both the NLSY79 and ABCD samples. Witty and Jenkins' analysis, in contrast, suffered from failing to compare the ancestry of the selected group to the ancestry of the group from which it was selected. Instead, their comparison sample was a completely different and, moreover, socioeconomically selected one (Mackenzie, 1984), a point which is highly relevant since socioeconomic status positively correlated with European ancestry in admixed American groups (Kirkegaard, Wang & Fuerst, 2017). Had the authors made the correct comparison, they likely would have found results similar to the current ones. As it is, their data implies a reported mean European ancestry for their selected sample quite similar to the genetic ancestry of our intelligence-selected ABCD sample (30% vs. 34%; see Loehlin, Lindsay & Spuhler 1975, p. 130).

There is now a large body of evidence that European ancestry — whether self-reported, parent-reported, indexed by race-associated phenotype, or assessed genetically — is related to *g* in admixed American populations. These findings contradict previous narrative reviews (e.g., Colman, 2016; Nisbett, 2009) and suggest systematic bias in past narrative reviews. A systematic review of the 20th-century literature on admixture and cognitive ability is in order.

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