Polygenic Score of Intelligence is More Predictive of Crystallized than Fluid Performance Among Children

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Abstract

Scores on intelligence tests have been reported to correlate significantly with educational, occupational and health outcomes. Twin and genome wide association studies in adults have revealed that intelligence scores are moderately heritable. We aimed to better understand the relationship between genetic variation and intelligence in the context of the developing brain. Specifically, we questioned if a genetic predictor of intelligence derived from a large GWAS dataset a) loaded on specific factors of cognition (i.e. fluid vs. crystallized) and b) were related to differences in cortical brain morphology measured using MRI scans. To do this we calculated an intelligence polygenic score (IPS) for the Adolescent Brain Cognitive Development (ABCD) baseline data, which consists of 11,875 nine- and ten- year old children across the US. We found that the IPS was a highly significant predictor of estimates of both fluid ($t=8.7$, $p=3.0\times10^{-18}$, 0.8% variance explained) and crystallized ($t=17.1$, $p=2.0\times10^{-64}$, 3.1% variance explained) cognition. Critically we found greater predictive power for crystallized than fluid ($z=5.1$, $p=3.1\times10^{-7}$), this result replicated in ancestry stratified analysis: for Europeans ($z=4.7$, 3.2×10^{-8}) and non-Europeans ($z=2.6$, $p=9.4\times10^{-3}$). This indicates a stronger loading of IPS on crystallized cognition. IPS was significantly related to total cortical surface area ($t=5.5$, $p=2.5\times10^{-8}$, 0.4% variance explained), but not mean thickness ($t=2.0$, $p=0.045$) – after Bonferroni correction. These results replicated in the European subsample (area: $t=5.4$, $p=6.3\times10^{-8}$, mean thickness: $t=2.3$, $p=0.021$), but not in the non-European subsample (area: $t=2.4$, $p=0.016$, mean thickness: $t=-0.41$, $p=0.68$). Vertex-wise analyses within the European group showed that the surface area association is largely global across the cortex. The stronger association of IPS with crystallized compared to fluid measures is consistent with recent results that more culturally dependent measures of cognition are more heritable. These findings in children provide new evidence relevant to the developmental origins of previously observed cognitive loadings and brain morphology patterns associated with polygenic predictors of intelligence.

Introduction

Intelligence is an important indicator of health and societally defined measures of success[1–3] that has been shown to be moderately heritable at around 50%[4]. In intelligence research two latent factors are often distinguished: crystallized and fluid[5]. Crystallized intelligence is related to aspects of cognition that are developed through experience, such as vocabulary, academic skills, and general knowledge. Conversely, fluid intelligence is related to an individual's ability to perform well cognitively in novel situations. Traditional views of these factors predicted that crystallized intelligence would be less influenced by genetics as it was thought to be more impacted by experience and environment[6]. However, recent evidence in adults has shown that this is not the case. A meta analysis across adult twin samples demonstrated that more culturally dependent measures of cognition are more heritable[7]. Kan et al.[7] speculated that these results may reflect the presence of gene-environment correlation (rGE). In this case rGE might reflect the fact that individuals with genotypes that initially bias them toward higher cognitive performance are more likely to end up in environments, or have experiences, that further develop these functions. This could occur, for example as a result of streaming students into classes by aptitude. rGE can thus increase heritability estimates. It has been argued that rGE more strongly impacts culturally-dependent measures of intelligence, as society more readily creates environments that facilitate rGE for crystalized intelligence[7]. Higher heritability for more culturally dependent measures of intelligence has been shown for adults, but not for children[7]. As rGE is presumed to accumulate over time[8] we hypothesize that this differentiation in heritability between fluid and crystallized intelligence might develop across childhood. We thus aimed to investigate the relationship between genetic variation and factors of intelligence in the early adolescent brain.

A recent genome wide association study (GWAS) in 269,867 adults of European ancestry associated 205 genomic loci and 1,016 genes to variability in intelligence[9]. By generating an intelligence polygenic score (IPS) they explained up to 5.2% of the variability in intelligence in independent samples. They found that associated genes were strongly expressed in the brain, and specifically associated with hippocampal pyramidal neurons and striatal medium spiny neurons. Additionally, studies have found that total brain volume and intelligence are correlated at 0.24-0.33[10,11], with both gray and white matter volume contributing to this association[12]. This correlation between intelligence and both gray and white matter volume has been shown to be largely determined by genetics[13,14]. For adults, thicker cortex has sometimes been associated with greater intelligence[13–15]. A recent study, however, in children reported that at age 9 there was no significant relationship between intelligence and cortical thickness, but at age 12 a negative correlation between intelligence and thickness across the cortex was observed[16]. Conversely, cortical area has been shown to be positively associated with intelligence scores in adolescents[17]. Both thickness and area have been shown to be genetically correlated with intelligence in children and adolescents[16,17]. These findings suggest that brain morphology is related to intelligence and that the two share a common genetic basis.

We aimed to further disentangle the associations between genetics, brain morphometry and intelligence in a large cohort (N= 9,511 individuals) of 9- and 10-year-old children obtained from the Adolescent Brain Cognitive Development (ABCD) study. To investigate these associations, we generated an IPS for each individual in the ABCD dataset using summary statistics from a GWAS of intelligence on 269,867 individuals[9]. After controlling for socioeconomic and demographic differences, we predicted that the IPS would: 1) significantly predict cognitive performance in the ABCD sample; 2) be more associated with crystallized than

with fluid intelligence; and, 3) be associated with cortical morphology. The ABCD sample is ancestrally diverse and the portability of polygenic scores to different ancestry groups has been shown to detrimentally impact prediction[18–20], as such for any discovered associations in the full sample we will investigate if they replicate in European and non-European subsets of the dataset.

Methods and Data

2.1 ABCD data

The ABCD study (http://abcdstudy.org) consists of N=11,875 individuals aged 9/10 years old at baseline[21]. This longitudinal study was designed to follow the development of children at 21 sites across the US for ten years. The cohort exhibits a large degree of socio-economic and demographic diversity. Exclusion criteria were limited to: 1) lack of English proficiency; 2) the presence of severe sensory, neurological, medical or intellectual issues that would inhibit the child's ability to comply with the protocol; and, 3) an inability to complete an MRI scan at baseline.

Here, we utilized baseline data from ABCD release 2.0 (DOI: 10.15154/1503209). A wide range of measurements were collected for each individual. In addition to demographic and socio-economic variables, for the current study we utilized three data sources: 1) cognitive assessments from the NIH Toolbox[22]; 2) whole-genome genotyping data[23]; and, 3) magnetic resonance imaging[24,25]. Each of these data types will briefly be described below.

2.1.1 NIH Toolbox Cognitive Assessment:

The NIH Toolbox® Cognition Battery (http://www.nihtoolbox.org)[26], herein referred to as 'the Toolbox', consists of seven different tasks that test executive function, working memory, episodic memory, attention, processing speed and language ability. The Toolbox® was normed on individuals between 3 and 85 years old. The total time to complete the battery is approximately 35 minutes. The ABCD study administers the Toolbox in English[27], as eligibility criteria requires that youth participants are fluent in English.

The Toolbox Reading Recognition Task® is a test in which individuals pronounce single words. The Toolbox Picture Vocabulary Task®[28] tests participants vocabulary by asking them to match spoken words to pictures. The Toolbox Pattern Comparison Processing Speed Test®[29] measures processing speed by asking them to identify if two side by side pictures are the same or different as rapidly as possible. The Toolbox List Sorting Working Memory Test ® tests participants working memory by requiring them to order presented objects in size order. The Toolbox Picture Sequence Memory Test® assesses episodic memory by asking participants to reproduce a sequence of items in the correct order[30]. The Toolbox Flanker Task®, a variant of the Eriksen Flanker task[31], is designed to measure cognitive control by requiring individuals to identify the direction of a central arrow that is flanked by either congruent or incongruent arrows. The Toolbox Dimensional Change Card Sort Task® is designed to measure cognitive flexibility[32]. All tasks provide raw scores, uncorrected standard scores, and age-corrected standard scores[27]. Uncorrected task scores were used for all our analyses.

Two summary scores also provided are the Crystallized Composite and Fluid Composite. The Crystallized Composite score is derived from performance on the Reading Recognition and the Picture Vocabulary tasks, the Fluid Composite score from performance on the five remaining measures. These composite scales have been shown to have high convergent validity with 'gold standard' measures of fluid and crystallized intelligence in both adults[33] and children[34].

2.1.2 Genetic Data

Saliva samples were collected at the baseline visit and sent to Rutgers University Cell and DNA Repository for storage and DNA isolation. Genotyping was performed using the Smokescreen array[35], consisting of 646,247 genetic variants. Before variant imputation, quality controls (QC) on the genotyping were performed to ensure each genetic variant has been successfully called in more than 95 percent of the sample and that missingness for each individual was not higher than 20%. After this QC 517,724 SNPs and 10,659 individuals remained. Based on genotyped data, we derived genetic ancestry using fastStructure[36] with four ancestry groups. Genetic relatedness and principal components were calculated using PLINK.

We then performed imputation using the Michigan Imputation Server[37] using hrc.r1.1.2016 reference panel, Eagle v2.3 phasing and multiethnic imputation process. PLINK[38] was used to convert dosage files to plink files using a best guess threshold of 0.9 for each loci. After best guess conversion, we used post imputation variant QCs of minor allele frequency above 5%, Hardy-Weinberg threshold of 10^{-6} and missingness of 10%. Additionally, we enforced no greater than 10% missing SNPs for each individual. These QCs were performed using PLINK[38] and resulted in 1,427,972 SNPs and 10,659 individuals remaining.

2.1.3 Neuroimaging Data

The imaging component of the ABCD study was developed by the ABCD Data Analysis and Informatics Center (DAIC) and the ABCD Image Acquisition Workgroup. Imaging methods were developed and optimized to be harmonized across all 21 sites and 3 scanner platforms: Siemens Prisma, General Electric 750 and Phillips. Details of these data collection methods and scanning protocols can be found at [25]. Image postprocessing was conducted by the ABCD DAIC[24]. For each subject, a 3D model of their cortical surface was reconstructed using Freesurfer (http://surfer.nmr.mgh.harvard.edu/). Vertex-wise cortical thickness was estimated after defining the cortical surface and underlying white/gray matter boundary. Vertex estimates of cortical area were computed by calculating the area of elements of the standardized tessellation mapped to each subject's native space. Details of this procedure can be found at [39–43].

2.2 Methods

2.2.1 Computing the Polygenic Score

Polygenic scores aggregate the effects of individual SNPs estimated from a previous GWAS discovery analysis, to produce a single score for each individual. The discovery dataset was computed on 269,867 individuals by Savage et al, using a meta-analysis in which neurocognitive tests primarily gauged fluid cognitive performance[9]. The summary statistics from this analysis were downloaded from (https://ctg.cncr.nl/software/summary_statistics). As nearby SNPs are correlated with one another these are removed before polygenic scoring; this process is known as clumping and pruning. After imputation was performed for the ABCD sample we performed clumping and pruning of SNPs using PRSice[44] with a clumping window of 250 kb, clumping r^2 of 0.1 and no thresholding of significance on the summary statistics. SNPs from the major histone compatibility complex were also removed from the analysis. This resulted in 692,685 SNPs remaining. The polygenic score for each individual was then computed as a sum of their SNPs, with each SNP being weighted by the effect in the discovery sample.

2.2.2 Ancestry Stratified Analysis

The ABCD study contains individuals from multiple ancestry groups. However, the discovery sample for the IPS was European individuals. Training and testing polygenic scores in different ancestry groups have been shown to reduce predictive power[18–20]. The ABCD study has made specific efforts to collect individuals from ethnically diverse backgrounds and in service of this effort we wanted to prevent the total exclusion of non-Europeans from the current analysis. As such we perform analyses for three strata of ancestry: 1) full sample, 2) Europeans only (proportion above 90%) and 3) non-European (the remainder of the sample).

2.2.3 Statistical Model for Behavioral Tasks

To assess the association between the IPS and cognitive performance in ABCD, we fit Generalized Linear Mixed-Effect Models (GLMMs). Each model had a different task or composite score from the NIH Toolbox as the dependent variable. In addition to the IPS, all models included the fixed effects of sex at birth, parental marital status, age, education level of parent/caregiver, household income and top ten components of genetic ancestry. Data collection site and family were input as random effects. Continuous variables were z-scored before model fitting to allow coefficients to be interpreted as standardized effect sizes. GLMMs were implemented using the R gamm4 package[45]. In order to assess the increased predictive power of the IPS beyond the covariates alone, we calculated the change in variance explained between the null model (just covariates) and the full model (covariates + IPS). To test if standardized regression coefficients differed between analogous regressions we performed a z-test on the difference between coefficients, based on the propagated standard error for the two regression coefficients. This test assumes the standard errors are not correlated and so provides a conservative estimate of significance.

2.2.4 Neuroimaging Analysis

In order to test the association between IPS and global measures of brain morphology, we used the same GLMMs described for predicting Toolbox measures, with the addition of scanner id as a fixed effect, to predict total cortical surface area and mean thickness. To explore regional brain morphology features associated with individuals' IPS, we fit univariate general linear models to predict vertex-wise area and thickness from IPS. The fixed effects were the same as those used for behavioral data. We used scanner ID instead of study site as a covariate, as this is more relevant for imaging measures. All covariates were treated as fixed effects due to the large computational burden of fitting vertex-wise mixed models. Family was excluded as a covariate as treating it as a fixed effect would have drastically increased the number of estimated parameters. Once again predictors and responses were z-scored to allow coefficients to be mapped and interpreted as standardized effect sizes. False discovery rate (FDR) corrected p-values were calculated for each vertex to allow thresholding at a corrected level of 0.05.

Results

Sample

Due to missing demographic information and/or Toolbox scores 1,319 individuals were removed, with 1,018 of those being due to missing declared household income. Failure of individuals' genetic data to pass QC metrics resulted in a further 1,414 individuals being removed. Table 1 shows behavioral and demographic statistics for the remaining individuals

used in this analysis. Note: self-declared race is in this table for the readers' information, however for statistical models principal components of genetics ancestry were used (see methods). This left 9,142 individuals in the full sample, 5,212 in the European sample and 3,930 in the non-European sample.

	Full Sample	*Europeans*	*Non-Europeans*
Total N	9142	5212	3930
	Mean (SD)		
Toolbox Fluid Composite Score	92.11 (10.47)	93.95 (9.61)	89.67 (11.05)
Toolbox Crystallized Composite Score	86.84 (6.92)	88.60 (6.28)	84.50 (7.07)
Age - months	119.04 (7.47)	119.19 (7.47)	118.84 (7.46)
Gender	**N (%)**		
M	4775 (52.2)	2751 (52.8)	2024 (51.5)
Parent Married = Yes	6436 (70.4)	4325 (83.0)	2111 (53.7)
Parental Education			
< HS Diploma	339 (3.7)	21 (0.4)	318 (8.1)
HS Diploma/GED	703 (7.7)	150 (2.9)	553 (14.1)
Some College	2302 (25.2)	966 (18.5)	1336 (34.0)
Bachelor	2473 (27.0)	1649 (31.6)	824 (21.0)
Post Graduate Degree	3325 (36.4)	2426 (46.5)	899 (22.9)
Household Income			
[<50K]	25543(27.9)	643 (12.3)	1910 (48.6)
[>=50K & <100K]	2627 (28.7)	1587 (30.4)	1040 (26.5)
[>=100K]	3962 (43.3)	2982 (57.2)	980 (24.9)
Race Ethnicity			
White	5102 (55.9)	4944 (95.0)	158 (4.0)
Hispanic	1745 (19.1)	136 (2.6)	1609 (41.0)
Black	1144 (12.5)	1 (0.0)	1143 (29.1)
Asian	195 (2.1)	0 (0.0)	195 (5.0)
Other	946 (10.4)	125 (2.4)	821 (20.9)

Table 1: Summary of demographics and composite toolbox scores for individuals with full data used in behavioral analysis. (Self declared race is reported here, however top 10 principal components of genetic ancestry were used instead in statistical models)

Behavioral Results

Table 2 displays the regression results for associating the IPS with fluid and crystallized composite scales, using GLMMs, across each ancestry strata. The IPS was significantly predictive of both subscales across all groups. Critically, the standardized regression coefficient was significantly higher for crystallized than fluid composite scores regardless of ancestry group (full sample: $z=5.1$, $p=3.1\times10^{-7}$, Europeans: $z=4.7$, $p=3.2\times10^{-6}$ and non-Europeans: $z=2.6$, $p=9.4\times10^{-3}$). A table of all outputs from these two regression models for each ancestry group can be found in supplementary materials.

Sample	*Fluid Composite*				*Crystallized Composite*			
	Standard. β	T-stat	P value	% Var. Explained	Standard. β	T-stat	P value	% Var Explained
Full Sample	0.29	8.7	3.0×10^{-18}	0.8	0.52	17.1	2.0×10^{-64}	3.1
Europeans	0.32	8.1	4.9×10^{-16}	1.3	0.59	15.4	3.1×10^{-52}	4.4
Non-Europeans	0.22	3.8	1.6×10^{-4}	0.37	0.42	8.2	3.9×10^{-16}	1.7

Table 2: Regression results for GLMMs associating IPS and a) fluid composite and b) crystallized composite scores within i) full sample (N=9142), ii) Europeans (N=5212) and iii) non-Europeans (N=3930).

Fitting separate regression models for each individual test of the Toolbox, we found that the IPS was a significant predictor for each cognitive measure individually for the full sample and European individuals (all p values<10^{-3}), surviving the Bonferroni-corrected significance threshold of 0.05/9=0.006. Within the non-Europeans only three measures were individually significantly predicted by the IPS (surviving Bonferroni correction): List Sorting Working Memory (t=4.2, p=3.1×10^{-5}), Picture Vocabulary (t=6.2, p=4.9×10^{-10}) and Reading Recognition tasks (t=7.5, p=3.1×10^{-14}). Standardized regression coefficients of IPS predicting each of the

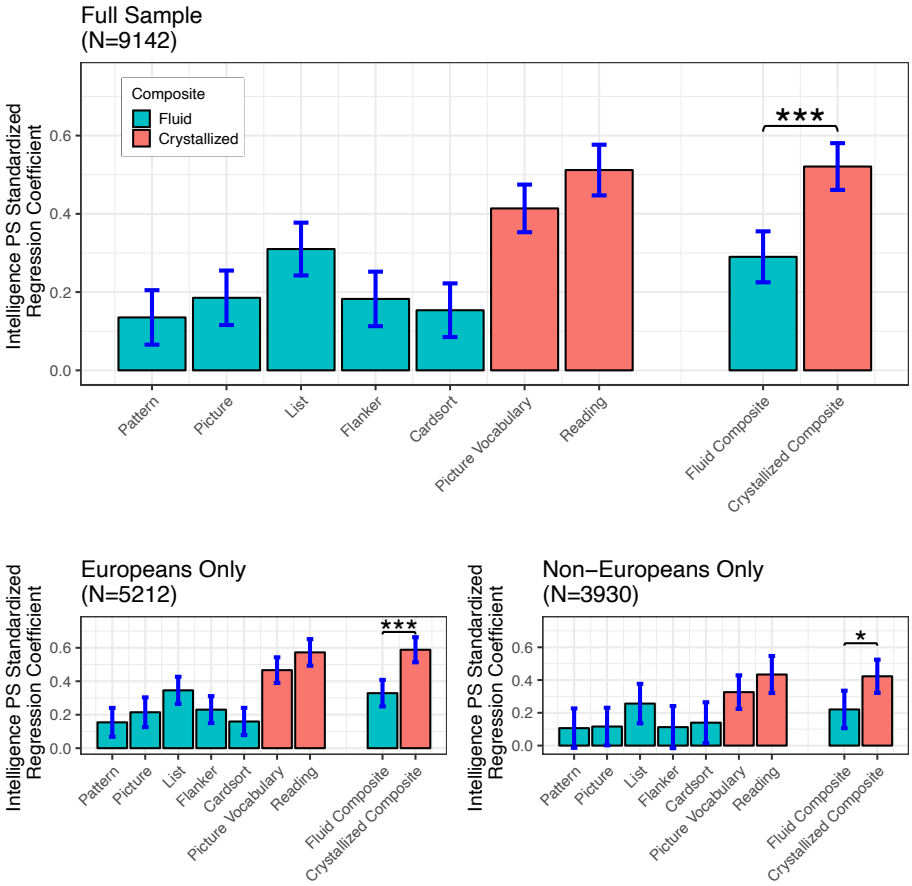

Figure 1 Standardized regression coefficeints of IPS for *fitting linear mixed models to each Toolbox measure and the two composite scales (fluid and crystallized) – Full sample (top), European sample (bottom left), non-European sample (bottom right). Error bars indicate 95% confidence intervals from 1.96 × standard errror. Tasks making up the fluid subscale have consistantly lower regression coefficients than those making up the crystallized subscale.*

toolbox measures and composite scales are displayed in Figure 1 for the full sample (top panel), Europeans (lower left) and non-Europeans (lower right). In blue are those measures making up the fluid composite and in red are those making up the crystallized composite. In this figure there is a clear separation where the cognitive measures used to produce the fluid composite score have consistently lower IPS standardized regression weights than the measures used to produce the crystallized composite score. Both Figure 1 and Table 2 demonstrates attenuation of predictive performance of IPS from Europeans to non-European samples in line with previous findings.

Neuroimaging Results

For the neuroimaging analyses an additional 775 individuals were excluded due to missing or failed QC of MRI scans (European: 281, non-European: 395 individuals). Within the full sample at the level of the whole brain, IPS was significantly associated with larger total cortical surface area (t=5.5, p=2.5×10^{-8}) explaining 0.4% of variance in cortical surface area above and beyond the socioeconomic and demographic covariates. IPS was nominally significant when associated with mean thickness but did not survive Bonferroni corrected significance (t=2.0, p=0.045). Within ancestry stratified analyses we found similar associations within Europeans for IPS and total cortical surface area (t=5.4, p=6.3×10^{-8}) and mean thickness (t=2.3, p=0.021), respectively explaining 0.6% and 0.1% of variance. Conversely, for non-Europeans we saw a greatly reduced association between IPS and cortical surface area (t=2.4, p=0.016) explaining 0.2% of variance, and no association with mean thickness (t=-0.41, p=0.68). This suggests the majority of the signal between IPS and total cortical area in the full sample was being driven by the European group, as such for vertex-wise analysis of cortical area we focused

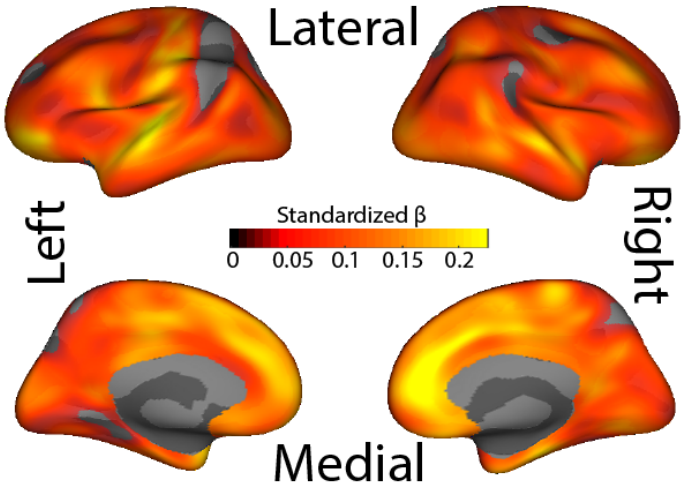

Figure 2 Vertex-wise associations between IPS and area for European subsample. Units are Standardized Effect Sizes (predictors and response variables z scored – i.e. units of standard deviation). Map is thresholded at 0.05 FDR corrected p value.

on the European sample. Figure 2 shows the regional pattern of cortical area associations with higher IPS. The map shows standardized regression coefficients (as in Figure 1) thresholded at an FDR-corrected p-value of 0.05. It suggests a distributed and global cortical area phenotype associated with high IPS, characterized by slightly larger associations in medial frontal regions.

Discussion

Results reveal that an IPS is more predictive of crystallized than fluid cognitive performance in a large sample of 9- and 10-year-old children, despite the fact that the discovery GWAS to produce the IPS was trained predominantly on fluid dimensions of cognition[9]. Conventional theories of general intelligence would predict that more culturally-dependent cognition should be more impacted by one's environment and therefore less heritable[6]. We show here, however, that this is not the case, which is similar to heritability estimates from a prior twin study[7]. It is in fact the more culturally-mediated measures of crystallized intelligence that are more strongly predicted by genetics in the ABCD sample at baseline. A plausible explanation that has been suggested for this unexpected result attributes the effect to gene-environment correlation[7]. For example, individuals with an initial slight bias toward higher cognitive performance may be more likely to end up in environments or having experiences (e.g., reading more or taking more advanced classes in school) that are likely to exaggerate the effect of this initial genetic predisposition. It is argued that the reason for this effect being stronger for culturally-loaded factors of intelligence is that these factors represent societal demands[46]. As such, society creates environments that facilitate gene-environment correlations (rGE) for culture-mediated factors, in a way that it does not for culture-reduced factors. If this argument holds, we expect that as participants in ABCD get older the effects of gene-environment correlation will become greater and the association presented here should become larger (i.e. a larger difference in predictive power of IPS between fluid and crystallized factors). In a recent study, Beam and Turkheimer modeled the effects of increasing rGE and showed that it could explain often observed increases in the heritability of measures of cognitive function between childhood and adolescence[8]. We anticipate testing this hypothesis in later time points of this longitudinal study.

Ancestry stratified analyses revealed the results in the full dataset replicated within European and non-European subsets of the dataset. This indicates that these effects are unlikely driven by either: a) solely European individuals; or, b) the admixture of ABCD. Problems with training and testing polygenic scores in different ancestry groups is well documented[18–20], and although the IPS does significantly predict cognition in the non-European group we find a reduction in effect sizes when compared to Europeans. As has been discussed in human genetics[47,48], this once again underscores the importance of collecting genetic data from ancestrally diverse populations and developing methods that can be used across ancestry groups.

In the full sample we also found that total cortical area was associated with higher IPS. This is consistent with the findings in adults that total brain volume (area x thickness) is positively correlated with intelligence[10,11] and that they share a common genetic basis[13,14]. This result replicated in the European sample, but not in the non-European sample suggesting the full sample result was driven by the European individuals, once again highlighting issues of portability of polygenic scores across ancestry groups. Additionally, previous work has demonstrated that cortical surface geometry is highly predictive of genetic ancestry[49,50] and it is possible that that shared genetic basis between brain morphology and intelligence differs between ancestry groups. Within the European sample, the vertex-wise analysis showed that the pattern of cortical area associated with higher IPS was global across the cortex with medial frontal regions showing slightly higher associations. Neither mean nor vertex-wise cortical thickness were found to be significantly associated with IPS. This is consistent with a recent study's finding that in 9-year-old children that there was no relationship between cortical thickness and intelligence[16]. The same study showed the emergence of a negative correlation

between thickness and measures of intelligence at 12 years of age. We may therefore find that the IPS is negatively correlated with cortical thickness at future time points as brain development proceeds in the ABCD sample.

A note of caution should be added when interpreting the IPS: it should not simply be thought of as a proxy for genetics or 'nature'. Each individual in this study inherited half of their genome from each parent and so these genetic associations can also have indirect influences on their cognitive performance through the cognitively enriching environments that parents provide. Indeed a recent study demonstrated that up to 30% of a polygenic score based on individuals can be explained through a score based on non-transmitted alleles of parents[51]. Furthermore, it should be emphasized that in addition to one's DNA sequence, epigenetic effects of chromatin and histone modifications as well as DNA methylation are also biological factors that have been shown to impact cognition[52]. These are biological mechanisms that can be impacted by one's environment and influence one's cognitive function and brain structure dynamically over the lifespan.

Although the association between IPS and cognitive performance is highly significant, the effect is a moderate one (full sample - fluid:0.29σ and crystallized: 0.52σ). It is possible that these effects will become larger for later time points collected in the ABCD study. This expectation is based on the finding that heritability of intelligence increases over age[55–57] and studies finding that a IPS based on educational attainment (the number of years completed in education) has stronger correlations with school performance of older children[58,59]. The predictor with the largest effect size in our analysis was parental education, with children of highly educated parents (post graduate) on average having crystallized scores 0.91 standard deviations higher than those of low educated parents (<high school diploma; see supplementary tables). Parental education is an important socioeconomic measure that is partially a proxy for material resources. However, it is also confounded by genetics: highly educated individuals are likely to possess genotypes that are advantageous for performing better in school and this in turn will be passed on to their children. It will be important to leverage the wealth of data available in ABCD and other studies to develop new methods that can partial socioeconomic and environmental effects from genetic ones. More precisely characterizing these components will enable us to investigate modifiable factors that can benefit the cognitive development of adolescents.

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The ABCD data repository grows and changes over time. The ABCD data used in this report came from [NIMH Data Archive Digital Object Identifier (10.15154/1503209)].

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Bibliography

1. Deary, I. J. & Gottfredson, L. S. Intelligence Predicts Health and Longevity, but Why? *Curr. Dir. Psychol. Sci.* **13**, 1–4 (2004).
2. Kuh, D., Richards, M., Hardy, R., Butterworth, S. & Wadsworth, M. E. J. Childhood cognitive ability and deaths up until middle age: A post-war birth cohort study. *Int. J. Epidemiol.* **33**, 408–413 (2004).
3. Kell, H. J., Lubinski, D. & Benbow, C. P. Who Rises to the Top? Early Indicators. *Psychol. Sci.* **24**, 648–659 (2013).
4. Polderman, T. J. C. *et al.* Meta-analysis of the heritability of human traits based on fifty years of twin studies. *Nat. Genet.* **47**, 702–709 (2015).
5. Cattell, R. B. Theory of Fluid and Crystalized Intelligence: A Critical Experiment. *J. Educ. Psychol.* **54**, 1–22 (1963).
6. Cattell, R. B. *Intelligence: Its structure, growth and action*. *Advances in Psychology, No. 35.* (1987).
7. Kan, K. J., Wicherts, J. M., Dolan, C. V. & van der Maas, H. L. J. On the Nature and Nurture of Intelligence and Specific Cognitive Abilities: The More Heritable, the More Culture Dependent. *Psychol. Sci.* **24**, 2420–2428 (2013).
8. Burgess, A., Shah, K., Hough, O. & Hynynen, K. Phenotype–environment correlations in longitudinal twin models. *Dev Psychopathol.* **25**, 7–16 (2013).
9. Savage, J. E. *et al.* Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. *Nat. Genet.* **50**, 912–919 (2018).
10. McDaniel, M. A. Big-brained people are smarter: A meta-analysis of the relationship between in vivo brain volume and intelligence. *Intelligence* **33**, 337–346 (2005).
11. Pietschnig, J., Penke, L., Wicherts, J. M., Zeiler, M. & Voracek, M. Meta-analysis of associations between human brain volume and intelligence differences: How strong are they and what do they mean? *Neurosci. Biobehav. Rev.* **57**, 411–432 (2015).
12. Thompson, P. M. *et al.* Genetic influences on brain structure. *Nat. Neurosci.* **4**, 1253–1258 (2001).
13. Posthuma, D. *et al.* The association between brain volume and intelligence is of genetic origin. *Nat. Neurosci.* **5**, 83–84 (2002).
14. Hulshoff Pol, H. E. *et al.* Genetic Contributions to Human Brain Morphology and Intelligence. *J. Neurosci.* **26**, 10235–10242 (2006).
15. Haier, R. J., Jung, R. E., Yeo, R. A., Head, K. & Alkire, M. T. Structural brain variation and general intelligence. *Neuroimage* **23**, 425–433 (2004).
16. Brouwer, R. M. *et al.* Genetic associations between intelligence and cortical thickness emerge at the start of puberty. *Hum. Brain Mapp.* **35**, 3760–3773 (2014).
17. Schmitt, J. E. *et al.* A Comprehensive Quantitative Genetic Analysis of Cerebral Surface Area in Youth. *J. Neurosci.* **39**, 2248–18 (2019).
18. Martin, A. R. *et al.* Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. *Am. J. Hum. Genet.* **100**, 635–649 (2017).
19. Duncan, L. *et al.* Analysis of polygenic risk score usage and performance in diverse human populations. *Nat. Commun.* **10**, (2019).

20. Carlson, C. S. *et al.* Generalization and Dilution of Association Results from European GWAS in Populations of Non-European Ancestry: The PAGE Study. *PLoS Biol.* **11**, (2013).
21. Morgan, G. D. *et al.* The conception of the ABCD study: From substance use to a broad NIH collaboration. *Dev. Cogn. Neurosci.* **32**, 4–7 (2017).
22. Bleck, T. P., Nowinski, C. J., Gershon, R. & Koroshetz, W. J. What is the NIH Toolbox, and what will it mean to neurology? *Neurology* **80**, 874–875 (2013).
23. Uban, K. A. *et al.* Biospecimens and the ABCD study: Rationale, methods of collection, measurement and early data. *Dev. Cogn. Neurosci.* **32**, 97–106 (2018).
24. Hagler, D. J. *et al.* Image processing and analysis methods for the Adolescent Brain Cognitive Development Study. *bioRxiv* (2018). doi:10.1101/457739
25. Watts, R. *et al.* The Adolescent Brain Cognitive Development (ABCD) study: Imaging acquisition across 21 sites. *Dev. Cogn. Neurosci.* **32**, 43–54 (2018).
26. Weintraub, S. *et al.* Cognition assessment using the NIH Toolbox Cognition assessment using the NIH Toolbox. (2013). doi:10.1212/WNL.0b013e3182872ded
27. Casaletto, K. B. *et al.* Demographically Corrected Normative Standards for the English Version of the NIH Toolbox Cognition Battery. *J Int Neuropsychol Soc.* **21**, 378–391 (2015).
28. Gershon, R. C. *et al.* NIH toolbox cognition battery (CB): Measuring language (vocabulary comprehension and reading decoding). *Monogr. Soc. Res. Child Dev.* **78**, 49–69 (2013).
29. Carlozzi, N. E., Beaumont, J. L., Tulsky, D. S. & Gershon, R. C. The NIH Toolbox Pattern Comparison Processing Speed Test: Normative data. *Arch. Clin. Neuropsychol.* **30**, 359–368 (2015).
30. Dikmen, S. S. *et al.* Measuring Episodic Memory Across the Lifespan: NIH Toolbox Picture Sequence Memory Test Sureyya. *J Int Neuropsychol Soc* **20**, 1–22 (2014).
31. Eriksen, B. & Eriksen, C. Effects of noise letters upon the identification of a target letter in a nonsearch task. *J. Child Psychol. Psychiatry Allied Discip.* **16**, 143–149
32. Zelazo, P. D. *et al.* NIH Toolbox Cognition Battery (CB): validation of executive function measures in adults. *J. Int. Neuropsychol. Soc.* **20**, 620–629 (2014).
33. Heaton, R. K. *et al.* Reliability and validity of composite scores from the NIH toolbox cognition battery in adults. *J. Int. Neuropsychol. Soc.* **20**, 588–598 (2014).
34. Akshoomoff, N., Beaumont, J. L., Bauer, P. J. & Dikmen, S. NIH Toolbox Cognitive Function Battery (CFB): Composite Scores of Crystallized, Fluid, and Overall Cognition. *Monogr Soc Res Child Dev.* **78**, 119–132 (2013).
35. Baurley, J. W., Edlund, C. K., Pardamean, C. I., Conti, D. V. & Bergen, A. W. Smokescreen: A targeted genotyping array for addiction research. *BMC Genomics* **17**, 1–12 (2016).
36. Raj, A., Stephens, M. & Pritchard, J. K. FastSTRUCTURE: Variational inference of population structure in large SNP data sets. *Genetics* **197**, 573–589 (2014).
37. Das, S. *et al.* Next-generation genotype imputation service and methods. *Nat. Genet.* **48**, 1284 (2016).
38. Chang, C. C. *et al.* Second-generation PLINK: rising to the challenge of larger and richer datasets. *Gigascience* **4**, (2015).
39. Dale, A. M., Fischl, B. & Sereno, M. I. Cortical Surface-Based Analysis: I. Segmentation and Surface Reconstruction. *Neuroimage* **9**, 179–194 (1999).
40. Fischl, B., Sereno, M. I. & Dale, A. M. Cortical Surface-Based Analysis: II: Inflation,

Flattening, and a Surface-Based Coordinate System. *Neuroimage* **9**, 195–207 (1999).
41. Fischl, B. *et al.* Sequence-independent segmentation of magnetic resonance images. *Neuroimage* **23**, S69–S84 (2004).
42. Dale, A. M. *et al.* Automatically Parcellating the Human Cerebral Cortex. *Cereb. Cortex* **14**, 11–22 (2004).
43. Fischl, B. & Dale, A. M. Measuring the thickness of the human cerebral cortex from magnetic resonance images. *Proc. Natl. Acad. Sci.* **97**, 11050–11055 (2000).
44. Euesden, J., Lewis, C. M. & O'Reilly, P. F. PRSice: Polygenic Risk Score software. *Bioinformatics* **31**, 1466–1468 (2015).
45. Wood, S. & Scheipl, F. gamm4: Generalized additive mixed models using mgcv and lme4. R package version 0.2-3. (2014).
46. Dickens, W. T. What is g? Paper presented at the annual meeting of the Behavior Genetics Association. in (2008).
47. Martin, A. R. *et al.* Clinical use of current polygenic risk scores may exacerbate health disparities. *Nat. Genet.* **51**, 584–591 (2019).
48. Petrovski, S. & Goldstein, D. B. Unequal representation of genetic variation across ancestry groups creates healthcare inequality in the application of precision medicine. *Genome Biol.* **17**, 16–18 (2016).
49. Bakken, T. E., Dale, A. M. & Schork, N. J. A geographic cline of skull and brain morphology among individuals of european ancestry. *Hum. Hered.* **72**, 35–44 (2011).
50. Fan, C. C. *et al.* Modeling the 3D Geometry of the Cortical Surface with Genetic Ancestry. *Curr. Biol.* **25**, 1988–1992 (2015).
51. Kong, A. *et al.* The nature of nurture: Effects of parental genotypes. *Science (80-.).* **359**, 424–428 (2018).
52. Day, J. J. & Sweatt, J. D. Epigenetic mechanisms in cognition Jeremy. *Neuron* **70**, 813–829 (2011).
53. Vilhjálmsson, B. J. *et al.* Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. *Am. J. Hum. Genet.* **97**, 576–592 (2015).
54. Márquez-Luna, C., Loh, P. R. & Price, A. L. Multi-ethnic polygenic risk scores improve risk prediction in diverse populations. *Genet. Epidemiol.* **41**, 811–823 (2017).
55. McClearn, G. E. *et al.* Substantial Genetic Influence on Cognitive Abilities in Twins 80 or More Years Old. *Science (80-.).* **276**, 1560–1563 (1997).
56. Trzaskowski, M., Yang, J., Visscher, P. M. & Plomin, R. DNA evidence for strong genetic stability and increasing heritability of intelligence from age 7 to 12. *Mol. Psychiatry* **19**, 380–384 (2014).
57. Haworth, C. M. A. *et al.* The heritability of general cognitive ability increases linearly from childhood to young adulthood. *Mol Psychiatry* **15**, 1112–1120 (2011).
58. Krapohl, E. *et al.* The stability of educational achievement across school years is largely explained by genetic factors. *npj Sci. Learn.* **3**, 1–10 (2018).
59. Selzam, S. *et al.* Predicting educational achievement from DNA. *Mol. Psychiatry* **22**, 267–272 (2017).