

Genotype by Environment Interactions in Cognitive Ability: A Survey of 14 Studies from Four Countries Covering Four Age Groups

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Abstract A large part of the variation in cognitive ability is known to be due to genetic factors. Researchers have tried to identify modifiers that influence the heritability of cognitive ability, indicating a genotype by environment interaction (G×E). To date, such modifiers include measured variables like income and socioeconomic status. The present paper focuses on G×E in cognitive ability where the environmental variable is an unmeasured environmental factor that is uncorrelated in family members. We

examined this type of G×E in the GHCA-database (Haworth et al., Behav Genet 39:359–370, 2009), which comprises data of 14 different cognition studies from four different countries including participants of different ages. Results indicate that for younger participants (4–13 years), the strength of E decreases across the additive genetic factor A, but that this effect reverts for older participants (17–34 years). However, a clear and general conclusion about the presence of a genuine G×E is hampered by differences between the individual studies with respect to environmental and genetic influences on cognitive ability.

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Genetic and environmental influences on individual differences in cognitive ability have enjoyed extensive investigation (see Plomin and Spinath 2004, for an overview). Using family-based designs, in which phenotypic variance is decomposed into additive genetic, unique environmental, and common environmental effects shared by family members (denoted A, E, and C, respectively), heritability estimates have been reported between roughly 0.5 and 0.7 for adolescents and adults (see McGue 1997). For young children the heritability is somewhat lower than 0.5 (see Haworth et al. 2010), and for infants as young as 10 months, the heritability is appreciably lower (Tucker-Drob et al. 2011).

Having established that, at least beyond childhood, genetic factors explain a substantial part of the phenotypic variance in cognitive abilities, the question arises whether the heritability of cognitive ability is constant across the range of environmental effects. We consider variation in heritability as a function of an environmental variable to be

a potential manifestation of Genotype by Environment interaction ($G \times E$; Eaves et al. 1977). Measures that have shown to influence or moderate the heritability of cognitive ability include parental income (Harden et al. 2007), socioeconomic status (Tucker-Drob et al. 2011; Turkheimer et al. 2003), parental education (Grant et al. 2010; Rowe et al. 1999; Van der Sluis et al. 2008), and educational attainment (Johnson et al. 2009). It is clear that the moderators in these studies are not strict environmental measures, although they may have a strong influence on the effective environment (Plomin and Daniels 1987).

The present paper focuses on the detection of genotype by environment interaction in cognitive ability where the environment variable is unmeasured (Jinks and Fulker 1970; Van der Sluis et al. 2006; Molenaar et al. 2012). Testing for genotype by unmeasured environment is important for a number of reasons, discussed below.

Screening. $G \times E$ can be studied in phenotypic variables while relevant environmental variables—i.e., variables that interact with genotype—are unknown or data on these variables are lacking. This opens the possibility to screen phenotypic variables for $G \times E$, in the absence of any explicit theory identifying potential environmental moderators (see Molenaar et al. 2012). Once $G \times E$ is detected, one could investigate which environmental variables contribute to this interaction.

GWAS. Testing for gene by unmeasured environment is of interest in the context of Genome-wide association studies (GWAS). In GWAS, $G \times E$ interaction is usually not modeled, although the presence of unmodeled $G \times E$ is hypothesized to affect the power to detect genetic variants. Several authors have suggested that the failure of GWAS to detect associations between phenotypes and common genetic variants (i.e., the ‘missing’ or ‘hidden’ heritability problem) might at least partly be due to unmodeled $G \times E$ (e.g., Eichler et al. 2010; Maher 2008; Manolio et al. 2009). For those phenotypes that display $G \times E$, the identification of the environmental factors causing the $G \times E$ would be of biological interest, and could facilitate the detection of associated genetic variants in GWAS.

Ability differentiation. Genotype by unmeasured environment interactions are relevant to substantive hypotheses. Most notably, Molenaar et al. (2012) discussed how the ability differentiation hypothesis (Spearman 1927) can be investigated by testing for a $G \times E$ interaction on IQ test scores in the ACE-model. Ability differentiation concerns the hypothesis that correlations among IQ subtests scores decrease for increasing levels of the underlying general intelligence factor, g (Jensen 1998; Spearman 1927). Ability differentiation has been operationalized as a non-linear relation between g and the subtest scores (Tucker-Drob 2009), a non-normal g -distribution (Molenaar et al. 2011), heteroscedastic residual variances (Hessen and

Dolan 2009), or smaller g variance at higher g levels (Reynolds et al. 2010). $G \times E$ represents another important avenue to the conceptualization and analysis of ability differentiation. The observation that g is substantially heritable (e.g., McGue 1997) may imply that the additive genetic factor, A , underlying g is a relatively weaker source of individual differences as the level of g increases. This implication may result if the unique environmental variance is greater at higher levels of A , i.e., an interaction between A and E .

Tucker-Drob (2009) related ability differentiation to gene by observed environment interaction. Specifically, they showed that when the environmental measure is correlated with g (as is the case with SES for instance), ability differentiation can result in spurious interactions between genotype and the observed environment measures. Other research related to ability differentiation and $G \times E$ concerns studies into the differential heritability of IQ (Detterman 1990; Sundett et al. 1994; Thompson et al. 1993; Brant et al. 2012), which addressed the question whether A is an equally strong source of individual differences across all levels of IQ (i.e., $A \times IQ$ interaction). Here, we follow Jinks and Fulker (1970) and address the question whether the environmental influences on IQ are an equally strong source of individual differences across all levels of A .

In the present article, we test for a genotype by unmeasured environment interaction on cognitive ability in a large dataset on cognitive ability from the GHCA consortium (Genetics of High Cognitive Abilities; Haworth et al. 2009). These data comprise IQ scores from 14 studies conducted in four different countries: US, UK, Australia, and the Netherlands. We analyzed the GHCA database, taking into account the variability of the IQ measures within the individual studies. Note that the same data has also been analyzed by Haworth et al. (2010). In this prior study, a linear increase of heritability was found across age. In the present study, we test for $G \times E$ in these data using the method proposed by Molenaar et al. (2012). This method is related to the test of Jinks and Fulker (1970, see above; see also Van der Sluis et al. 2006), but has the advantage of including data of both MZ and DZ twins which increases power due to the separation of common and unique environmental factors. In the present paper we first present the $G \times E$ -model and describe the data in the GHCA database, and then present and discuss the results of fitting the $G \times E$ model to these data.

The heteroscedastic ACE-model

Let Y_{ij} denote the phenotypic score of the j th twin ($j = 1, 2$) of the i th twin pair ($i = 1, \dots, N$). In the standard ACE-model, Y_{ij} is described by the following linear equation:

$$Y_{ij} = v + A_{ij} + C_{ij} + E_{ij}, \quad (1)$$

where v is an intercept. The additive genetic factor (A_{ij}), the common environmental factor (C_{ij}), and the unique environmental factor (E_{ij}) are assumed to follow a normal distribution with zero-means and variances σ_A^2 , σ_C^2 , and σ_E^2 respectively. In addition, it holds that $\text{cor}(C_{i1}, C_{i2}) = 1$, $\text{cor}(E_{i1}, E_{i2}) = 0$, $\text{cor}(A_{i1}, A_{i2}) = 1$, in MZ twins, and $\text{cor}(A_{i1}, A_{i2}) = 0.5$, in DZ twins. Under the assumption that A_{ij} , C_{ij} , and E_{ij} are uncorrelated, the phenotypic variance σ_Y^2 can be decomposed as follows:

$$\sigma_Y^2 = \sigma_A^2 + \sigma_C^2 + \sigma_E^2. \quad (2)$$

Within the ACE-model, Molenaar et al. (2012) distinguished two possible G×E interactions, i.e., the interaction between A and C, and the interaction between A and E. To model these two interactions, we condition on A, i.e.,

$$\sigma_{Y|A}^2 = \sigma_{C|A}^2 + \sigma_{E|A}^2. \quad (3)$$

In Eq. (3), G×E can be modeled by allowing the variance of C and E to depend on the level of A. For instance, the variance of E can be decreasing across levels of A, which would mean that the heritability effectively increases. To this end, we specify a function to relate σ_E^2 and σ_C^2 to A. Van der Sluis et al. (2006) and Hessen and Dolan (2009) proposed to use the exponential function, as the range of this function is non-negative, which is desirable for a variance parameter. Thus, the ACE-model can be extended to include G×E in the following way:

$$\sigma_{Y|A}^2 = \sigma_{C|A}^2 + \sigma_{E|A}^2 = \exp(\gamma_0 + \gamma_1 A) + \exp(\beta_0 + \beta_1 A), \quad (4)$$

where γ_0 and β_0 are baseline parameters which account for the part of the variance of C and E that does not depend on A, while γ_1 and β_1 are linear interaction parameters, which model the possible dependency of respectively the variance of C and E on A. We refer to this model as the heteroscedastic ACE model, as the C and E factor are heteroscedastic across A. From now, we use the term ‘G×E’ to refer to the general concept of ‘genotype-by-environment interaction’ and we use the term A×C or A×E to refer to a specific operationalization within the heteroscedastic ACE model. Thus, G×E can be established by testing β_1 to be significantly different from 0 (indicating an A×E interaction) and/or by testing γ_1 to be significantly different from 0 (indicating an A×C interaction).

In the heteroscedastic ACE-model, we cannot simply use σ_A^2 as an estimate for the heritability as this parameter is not appropriately standardized. In the presence of G×E effects in the ACE model, σ_A^2 needs to be standardized by using

$$h^2 = \frac{\sigma_A^2}{\sigma_A^2 + \exp(\gamma_0 + \frac{1}{2}\gamma_1^2) + \exp(\beta_0 + \frac{1}{2}\beta_1^2)}$$

The two terms involving $\exp(\cdot)$ in the denominator concern the marginal variance of C and E respectively (see Hessen and Dolan 2009). If γ_1 and β_1 are 0 (i.e., no A×C and A×E interactions), the formula for h^2 reduces to the traditional formula for heritability, $\sigma_A^2/(\sigma_A^2 + \sigma_C^2 + \sigma_E^2)$. It can therefore be seen that h^2 and the traditional heritability estimate diverge when the absolute value of γ_1 and/or β_1 increases.

The tests of β_1 and γ_1 discussed above (Eq. 4) concern generalized linear G×E interactions.¹ It is possible to test for generalized curvilinear interactions by extending Eq. (4) into

$$\sigma_{Y|A}^2 = \sigma_{C|A}^2 + \sigma_{E|A}^2 = \exp(\gamma_0 + \gamma_1 A + \gamma_2 A^2) + \exp(\beta_0 + \beta_1 A + \beta_2 A^2) \quad (5)$$

Here, β_2 and γ_2 are curvilinear interaction parameters that can be tested on significance similarly as discussed above.

The statistical properties of the model in Eq. (4) are well documented (Jinks and Fulker 1970; Van der Sluis et al. 2006; Molenaar et al. 2012). It has been shown that parameter recovery is satisfactory, that both A×E and A×C interactions can be estimated together, and that power to detect A×E is generally good. The detection of A×C interactions, however, requires large samples (Molenaar et al. 2012).² It should be noted that the approach in Eq. (4) does not take into account the possibility that C and E interact (i.e., C×E). Molenaar et al. showed that the presence of C×E does not appreciably affect tests of A×C. However, if C is the main source of variation, the detection of A×E is affected by the presence of C×E (i.e., unmodeled C×E may be incorrectly detected as A×E). Nevertheless, we found that, when A is the main source of variation, the presence of C×E hardly affects the detection of A×E. As A can be considered the predominant source of variation in IQ data (at least from childhood onwards), the presence of C×E in the data is not expected to affect tests on G×E using the present method (see Molenaar et al. 2012). We note, however, that there is

¹ The interactions are not purely linear as we use exponential functions in Eq. (4). However the interactions are linear in the logarithm of the variance of E and C, we therefore refer to the interactions as generalized linear interactions.

² The exact sample size needed for sufficient power to detect A×C interactions depends on a number of aspects (e.g., strength of A, effect size of the A×C interaction, and the effect sizes of other interactions in the data). In a ‘basic setting’ (A is the predominant source of variation, A×C effect size is moderate, and there are no other interactions in the data) a total sample size of 4,000 is needed (2000 MZ and 2000 DZ twins) for a power of 0.8.

empirical support for C×E in cognitive ability (Kremen et al. 2005; Hanscombe et al. 2012). Thus, although presence of C×E does not appreciably affect tests on G×E, heritability estimates might be affected. In a small simulation study based largely on the setting of the simulation in the Molenaar et al. paper (results are available upon request), we found that the presence of C×E did not affect heritability estimates (percentage bias were close to 0). In addition, we found a minor effect on the estimate of σ_C^2 , i.e., percentages bias of 3 to 8 % for increasing effect size of the C×E effect. We believe that such biases are within the acceptable range given the purposes of the present undertaking. We therefore conclude that the presence of unmodeled C×E will not importantly affect the results as reported below.

The G×E model can be fitted to data of both MZ and DZ twins using marginal maximum likelihood (MML; Bock and Aitkin 1981). In this procedure, the observed data, conditional on A, are assumed to follow a normal distribution. Note that unconditionally, the phenotypic data may be non-normal, as the presence of G×E will generally result in non-normality (Eaves et al. 1977). In principle, a marginal test on normality could be conducted on singleton data to test for G×E (e.g., the Shapiro-Wilks test on normality, Shapiro and Wilks 1965). However, as the present tests on non-normality are more specific, power to detect non-normality is larger as compared to the marginal tests (see Molenaar et al. 2010). In addition, to be able to distinguish A×C from A×E, singleton data is not sufficient and twin data is required. The model from Eq. (5) is fitted using the freely available software package Mx (Neale et al. 2006). As both A×C and A×E can be combined in a single model, the free parameters to be estimated are: σ_A^2 , β_0 , β_1 , β_2 , γ_0 , γ_1 and γ_2 . Example script are available on the website of the first author.

Application to GHCA data

Description of the data

The database comprises univariate IQ scores of 14 studies conducted in four countries: US (Colorado, three studies; Minnesota, two studies; Ohio, one study), UK (one study), Australia (one study), and the Netherlands (six studies). Aggregating all of these data yields a total of 10,897 twin pairs (4911 MZ pairs and 5986 DZ pairs). The age of the participants varies from 4 to 71. For each twin in the database, an IQ measure is available. Across the different studies, different test batteries have been used to obtain IQ score. For instance, in one of the US studies, the short form of the Stanford-Binet Intelligence Scale was used; in the UK study, Three subtests of the WISC-III were

administered together with Raven's progressive matrices; and in another study from the US, the full WISC-III was used. We refer to Haworth et al. (2009) and the references therein, for a detailed overview of the IQ test batteries used in the different studies.

Analysis

As the aggregated data are heterogeneous with respect to age, we follow Haworth et al. (2010), and perform the analysis within more age-homogenous subgroups. Haworth et al. considered Three age categories: 4–10, 11–13, and 14–34. All participants above age 34 are omitted as there were too few participants in this age range to construct a reasonably homogenous subgroup with respect to age. In our analysis, we modified the age categories of Haworth et al. because we considered it possible that the nature of G×E differs between adolescents (who presumably are still in school and live at home) and young adults. Specifically, we created the categories: 4–10, 11–13, 14–16, and 17–34. We note that the general pattern of results, as presented below, does not depend on the exact age categories that are used: results are generally the same for the Haworth et al. age categories. However, our categorization does provide a clearer picture of how G×E changes across age. See Table 1 for the sample sizes within the age groups of both Haworth et al. and our age categorization.

As can be seen in Table 1, in our alternative categorization, the third category of Haworth et al. (2010) is split into one relatively homogenous age group (14–16), and an additional group (age 17–34). We also considered a second alternative in which this additional group was made more homogenous (i.e., participants of ages 17–20), but this categorization did not alter the results.

The aggregated data are potentially heterogeneous as they originated from 14 different studies. To establish whether the results within the age groups hold across the different studies, we conduct the analyses on both the aggregated data and on the data of each of the 14 individual studies. Table 2 provides the distribution of participants

Table 1 Number of MZ and DZ twin pairs (N_{MZ} ; N_{DZ}) within the age categories as used by Haworth et al. and as used in the present study

Group no	Haworth et al.		Present			
	Age	N_{MZ}	N_{DZ}	Age	N_{MZ}	N_{DZ}
1	4–10	1,140	1,613	4–10	1,140	1,613
2	11–13	2,195	2,722	11–13	2,195	2,722
3	14–34	1,507	1,582	14–16	807	966
4	–	–	–	17–34	700	616
Total N	–	4,842	5,917	–	4,842	5,917

Table 2 Number of MZ and DZ twin pairs (N_{MZ} ; N_{DZ}) within each age category for each study in the GHCA database

Study	Total N	Age 4–10	Age 11–13	Age 14–16	Age 17–34
Netherlands #1	125; 112	125; 112	0; 0	0; 0	0; 0
Netherlands #2	49; 63	49; 63	0; 0	0; 0	0; 0
Netherlands #3	79; 111	0; 0	79; 111	0; 0	0; 0
Netherlands #4	79; 108	0; 0	0; 0	13; 14	66; 94
Netherlands #5	36; 58	0; 0	0; 0	0; 0	36; 58
Netherlands #6	69; 69	0; 0	0; 0	0; 0	0; 0
Colorado #1	752; 1,025	391; 534	204; 280	126; 173	31; 38
Colorado #2	215; 175	17; 6	13; 14	153; 125	32; 30
Colorado #3	332; 364	0; 0	30; 44	99; 140	203; 180
Minnesota #1	777; 469	43; 16	734; 453	0; 0	0; 0
Minnesota #2	410; 214	0; 0	0; 0	92; 31	318; 183
Australia	338; 515	0; 0	0; 0	324; 483	14; 32
Ohio	121; 171	121; 171	0; 0	0; 0	0; 0
UK	1,529; 2,532	394; 714	1,135; 1,818	0; 0	0; 0

Samples used for the analysis of the individual studies are in boldface

over age categories and studies. Some studies include only participants in one age category (e.g., Netherlands #1), while other studies include participants in multiple age categories (e.g., Colorado #1). In some cases, a study contained too few participants in a given age category to enable model fitting on this subsample (e.g., Netherlands #4 only contains 13 MZ twins and 14 DZ twins between 14 and 16 years old). Therefore, for our analyses, we only select 17 subsamples that we considered large enough to provide stable parameter estimates. These samples are shown in boldface print in Table 2. Note that we omitted Netherlands #5 because we considered the total sample size to be too small, and we omitted Netherlands #6, as this study only contains participants of age 40–70. In the analysis on the aggregated data however, we do include Netherlands #5. The data are standardized within each study by the original authors (Haworth et al. 2009). We additionally standardized the data within each age group. The resulting data thus are standardized in each age \times study cell of the design.

Results

MZ and DZ twin correlations of the IQ measures in the 17 subsamples are presented in Table 3. In the Table the skewness, kurtosis, and the Shapiro-Wilks test of normality are also given as non-normality could be an indication of $G \times E$. As can be seen, normality is rejected in the first two aggregated age categories. As indicated by the skewness, the IQ distributions have a heavier lower tail (negatively skewed), suggesting that the variance of E and or C might be decreasing across A. However, these are just indications; more elaborate tests are possible with the heteroscedastic ACE model. We present these results next.

Table 4 gives the parameter estimates of the heteroscedastic ACE model with linear and curvilinear effects for the $A \times E$ and $A \times C$ interactions on the aggregated data. In the aggregated data, we investigated within each age group, whether the linear and quadratic effects improved model fit. These results are in Table 5. As can be seen, the model with a linear $A \times E$ effect only is favored by the likelihood ratio test (LRT), AIC and BIC in all age groups except age group 14–16. In this age group, results are mixed as the AIC favors the full model and the BIC indicates that none of the $G \times E$ effects (i.e., $A \times E$ and $A \times C$) are significant. As the latter model is more parsimonious, we accept that in age group 14–16, no interactions are present. As none of the $A \times C$ interactions were significant and at most linear $A \times E$ interactions were found, we focused on the results of the ACE model with a linear $A \times E$ interaction in all age groups for the remaining analyses. See Table 6 for the heritability and standardized parameter estimates within each age group for each individual study and the aggregated data. As can be seen, in most cases h^2 is close to σ_A^2 indicating that heritability as operationalized in the ACE model (i.e., as the standardized estimate of σ_A^2) is only mildly affected by the $A \times E$.³

In Fig. 1, we plotted the heritability estimates within each of the 17 subsamples against the average age of the subsamples. The plot is consistent with the findings of Haworth et al. (2010) in this dataset, i.e., that heritability increases monotonically with age. As can be seen in the figure, there are substantial differences in the heritability estimates across studies. Some of these differences may be attributed to sample size (i.e., the small studies of approximately the same average age show differences due

³ In the absence of both $A \times E$ and $A \times C$ (i.e., $\beta_1 = 0$ and $\gamma_1 = 0$), h^2 and standardized σ_A^2 are equivalent, see the formula for h^2 above.

Table 3 MZ and DZ correlations, skewness, kurtosis and a test on normality of the IQ measures in the 17 subsamples within each age category

Cat	Study	Cor		Skewness		Kurtosis		<i>p</i> value S–W test	
		MZ	DZ	Twin 1	Twin 2	Twin 1	Twin 2	Twin 1	Twin 2
4–10	Netherlands #1	0.70	0.49	–0.41	–0.56	2.99	3.56	0.01	0.00
	Netherlands #2	0.78	0.51	–0.16	0.21	3.73	2.99	0.23	0.27
	Colorado #1	0.81	0.52	0.09	–0.12	3.12	3.19	0.05	0.03
	Ohio	0.76	0.55	0.10	–0.06	2.85	3.03	0.69	0.69
	UK	0.66	0.50	–0.33	–0.35	2.94	2.88	0.00	0.00
	Aggregated	0.74	0.54	–0.12	–0.21	3.14	3.12	0.00	0.00
11–13	Netherlands #3	0.86	0.53	–0.02	–0.06	3.26	2.84	0.37	0.39
	Colorado #1	0.87	0.55	0.10	0.17	2.74	2.75	0.29	0.09
	Minnesota #1	0.76	0.51	0.17	0.05	3.10	3.35	0.01	0.06
	UK	0.68	0.44	–0.58	–0.67	3.39	3.52	0.00	0.00
	Aggregated	0.73	0.47	–0.31	–0.38	3.20	3.29	0.00	0.00
14–16	Colorado #1	0.84	0.52	0.29	0.20	3.27	3.25	0.05	0.38
	Colorado #2	0.88	0.46	–0.12	–0.11	3.33	2.91	0.05	0.19
	Colorado #3	0.77	0.49	0.21	–0.05	3.48	3.73	0.03	0.03
	Minnesota #2	0.81	0.42	0.27	0.16	2.39	2.50	0.05	0.48
	Australia	0.82	0.45	–0.13	–0.09	2.46	2.46	0.00	0.00
	Aggregated	0.83	0.46	–0.02	–0.04	2.94	2.93	0.22	0.17
17–34	Netherlands #4	0.86	0.34	–0.21	–0.21	2.48	2.27	0.08	0.05
	Colorado #3	0.86	0.57	–0.03	–0.03	2.74	2.89	0.44	0.82
	Minnesota #2	0.80	0.52	0.53	0.52	3.23	3.07	0.00	0.00
	Aggregated	0.82	0.49	0.13	0.13	3.00	3.08	0.16	0.05

‘Cor’ denotes twin correlation. *p* values of the S–W (Shapiro-Wilks) test smaller than one’s alpha level indicate non-normality. Normality is characterized by skewness and kurtosis of 0 and 3, respectively. Note that the aggregated analysis does include the Netherlands #5 and Netherlands #6 studies

Table 4 Parameter estimates of the heteroscedastic ACE model with linear and curvilinear effects for the A×E and A×C interactions

Age group	β_0	β_1	β_2	γ_0	γ_1	γ_2
4–10	–1.46	–0.37	0.04	–1.15	0.02	0.03
11–13	–1.53	–0.47	–0.13	–1.53	–0.13	0.08
14–16	–1.81	–0.09	–1.08	–2.44	0.54	–0.04
17–34	–1.90	0.39	–0.27	–1.70	–0.03	0.06

to sampling fluctuations). However, results of some of the larger studies also show substantial differences, even though the average age is approximately the same over the studies. We return to this point below.

The A×E interactions as obtained in each study and in the aggregated data are depicted in Fig. 2 for each age group. From the results of the aggregated data in Fig. 2a, b, it appears that in age categories 4–10 and 11–13, the variance of E is decreasing across levels of A. The decrease is significant at $\alpha = 0.05$, according to both the likelihood ratio test and the 95 % confidence interval of β_1 (see Table 6).⁴ Within the individual studies some differences in the form of the G×E are apparent, but individual study results tend to follow the trend from the aggregated data.

Main departures are Colorado #1 in age group 4–10, and Minnesota #1 in age group 11–13. Both studies show a significant effect in the opposite direction as compared to the effect in the aggregated data, i.e., the variance of E increases with A. Other studies show no effect or an effect consistent with the aggregated result.

In age category 14–16, no effect is observed in the aggregated data according to the likelihood ratio test and the confidence interval of β_1 (see Table 6). Within the individual studies some differences in the form of the A×E are apparent, but results tend to follow the results from the aggregated data. Some studies show an effect in the opposite direction (i.e., Colorado #1, Ohio, Colorado #2, and Minnesota #1). However, none of these effects are significant at $\alpha = 0.05$ (see Fig. 2c; Table 6).

In age category 17–34, Fig. 2d, the aggregated data show an increase of σ_E^2 across A. This effect is significant according to the likelihood ratio test and the confidence

⁴ We considered 95 % one-at-a-time confidence intervals as an exploratory tool to see which parameters are significantly different from 0 for $\alpha = 0.05$. We also conducted likelihood ratio tests on β_1 which can be used to provide a stricter test on the significance of this parameter for any α (see Table 4).

Table 5 Model fit indices for the heteroscedastic ACE-model

Model	Description	Age group Statistic	4–10	11–13	14–16	17–34
$\beta_1, \beta_2, \gamma_1, \gamma_2$	Full model	LRT	–	–	–	–
		AIC	3,121	5,657	1,795	1,239
		BIC	–14,706	–29,099	–8,789	–6,172
$\beta_1, \beta_2, \gamma_1, -$	Drop curvilinear A×C	LRT	0.28	1.83	6.76	2.97
		AIC	3,120	5,656	1,799	1,240
		BIC	–14,710	–29,102	–8,790	–6,174
$\beta_1, -, \gamma_1, -$	Drop curvilinear A×E	LRT	0.06	0.03	0.12	0.01
		AIC	3,118	5,654	1,797	1,238
		BIC	–14,714	–29,106	–8,793	–6,177
$\beta_1, -, -, -$	Drop linear A×C	LRT	1.87	0.07	2.55	0.17
		AIC	3,118	5,652	1,798	1,237
		BIC	–14,717	–29,110	–8,796	–6,181
$-, -, -, -$	Drop linear A×E	LRT	42.06	258.91	0.01	18.93
		AIC	3,158	5,909	1,796	1,253
		BIC	–14,699	–28,985	–8,800	–6,175

For the AIC and BIC, best values are in boldface. The unrounded AIC value for the third and fourth model equal respectively 3,117.691 and 3,117.565. The likelihood ratio test (LRT) concerns one degree of freedom

interval of β_1 (see Table 6). The effect in the aggregated data is reproduced in the Minnesota #3 study. However, the Colorado #3 study shows an effect in the opposite direction.

If we compare the results from Table 6 to those from Table 3, we can conclude that generally, G×E is present in the data (Table 6) if normality is rejected (Table 3). However, for some cases this does not hold. For instance, the Colorado #3 study in age group 14–16 is not associated with a G×E interaction, but normality is rejected. The opposite is also observed, e.g., in the Colorado #3 study G×E is present but normality is not rejected.

Conclusion on aggregated data

In the aggregated data, we observed that for participants between the age of 4–10 and 11–13, the influence of the unique environmental factor, E, decreases with increasing levels of the additive genetic factor, A. In participants between the age of 14 and 16, no effect was detected. In the participants between 17 and 34, the influence of factor E increased with increasing levels of A. Taken at face value, this pattern of results suggests that the direction of the A×E on IQ reverts during adolescence and young adulthood. However, as we discuss next, given the differences in the results between the samples, this conclusion should be drawn with care.

Different results across studies

The pattern of results as presented in Table 6 reveals substantial differences between the individual

studies.⁵ First, estimates of the additive genetic effects, σ_A^2 , within each age group vary considerably over the studies. For age 4–10, 11–13, 14–16, and 17–34, estimates range from 0.32 to 0.65, from 0.49 to 0.64; from 0.54 to 0.79; and from 0.53 to 0.85, respectively. Part of these differences can be explained by the small sample size of some of the studies, which renders the estimate of σ_A^2 subject to large sampling error. Still, some of the larger studies within the same age group show substantial differences in the estimates of σ_A^2 . For instance, in the age category of 4–10, the estimate is 0.32 in UK study ($N = 1,108$), but 0.65 in the Colorado #1 study ($N = 925$). In addition to the differences with respect to σ_A^2 , we see some differences with respect to the effect of the common environment, σ_C^2 . For age 4–10, 11–13, 14–16, and 17–34, estimates of σ_C^2 range from 0.19 to 0.34; from 0.16 to 0.27; from 0.00 to 0.24; and from 0.06 to 0.31, respectively. Again, some of these differences may be due to sampling error, yet, large studies do show variable results, for instance, the estimate of σ_C^2 is

⁵ Our implementation of A×C involves fitting the model subject to $\text{var}(C_j) = \exp(\gamma_0 + \gamma_1 A_j)$ where $j = 1, 2$, with $\text{cov}(C_1, C_2) = \sqrt{\exp(\gamma_0 + \gamma_1 A_1)} \times \sqrt{\exp(\gamma_0 + \gamma_1 A_2)}$, (see Molenaar et al. 2012). This can be interpreted as a scalar effect of A_j on the variance of C. In the light of comments by an anonymous reviewer, we also fitted the AT-model with A×T interaction, where ‘T’ denotes the total environment, i.e., $T = C + E$, as proposed by Carey (2009). Our results in terms of the interactions and their heterogeneity over samples do not depend on our specific modeling choice. That is, in the AT analyses, the direction of the effects in Table 6 were replicated for all studies. These additional results are available from www.dylanmolenaar.nl

Table 6 Age descriptives, heritability, standardized parameter estimates, and number of MZ and DZ twins within each age category for both the aggregated data and the data within each study

Cat	Study	N_{MZ}	N_{DZ}	Age		Heritability h^2	Variance of A σ_A^2	Variance of E baseline and A×E parameter		Variance of C σ_C^2	$\chi^2(1)$
				Mean	sd			β_0 (baseline)	β_1 (A×E)		
4–10	Netherlands #1	125	112	5.80	0.06	0.43	0.42 (0.18; 0.68)	-1.43 (-1.77; -1.13)	-0.70 (-1.09; -0.34)	0.26 (0.03; 0.50)	14.62
	Netherlands #2	49	63	9.10	0.10	0.53	0.52 (0.18; 0.98)	-1.54 (-1.92; -1.11)	-0.16 (-0.64; 0.29)	0.24 (0.00; 0.60)	0.53
	Colorado #1	391	534	8.92	0.80	0.64	0.65 (0.51; 0.84)	-1.82 (-2.04; -1.59)	0.42 (-0.17; 0.68)	0.19 (0.05; 0.32)	2.65
	Ohio	121	171	6.07	0.68	0.42	0.42 (0.21; 0.65)	-1.46 (-1.71; -1.20)	0.13 (-0.19; 0.46)	0.34 (0.12; 0.55)	0.62
	UK	394	714	10.59	0.24	0.32	0.32 (0.18; 0.46)	-1.21 (-1.37; -1.06)	-0.53 (-0.72; -0.37)	0.34 (0.22; 0.45)	42.52
	Aggregated	1,140	1,616	9.06	1.79	0.42	0.41 (0.34; 0.49)	-1.42 (-1.52; -1.33)	-0.33 (-0.45; -0.22)	0.34 (0.26; 0.41)	33.98
11–13	Netherlands #3	79	111	12.02	0.08	0.64	0.64 (0.41; 0.87)	-1.95 (-2.25; -1.62)	-0.02 (-0.49; 0.51)	0.21 (0.00; 0.47)	0.01
	Colorado #1	204	280	11.85	0.81	0.65	0.64 (0.50; 0.80)	-2.06 (-2.26; -1.85)	0.14 (-0.13; 0.43)	0.22 (0.08; 0.38)	1.01
	Minnesota #1	734	453	11.82	0.40	0.49	0.49 (0.36; 0.62)	-1.44 (-1.55; -1.33)	0.23 (-0.001; 0.42)	0.27 (0.14; 0.40)	3.82
	UK	1,135	1,818	11.78	0.40	0.50	0.49 (0.41; 0.57)	-1.37 (-1.47; -1.28)	-0.73 (-0.83; -0.64)	0.16 (0.09; 0.23)	306.29
	Aggregated	2,195	2,720	11.83	0.47	0.56	0.52 (0.46; 0.59)	-1.45 (-1.52; -1.38)	-0.52 (-0.60; -0.45)	0.21 (0.15; 0.27)	203.10
14–16	Colorado #1	126	173	14.74	0.77	0.80	0.79 (0.63; 0.93)	-2.12 (-2.36; -1.86)	0.09 (-0.26; 0.46)	0.08 (0.02; 0.26)	0.27
	Colorado #2	153	125	16.00	0.00	0.75	0.76 (0.49; 0.96)	-2.03 (-2.31; -1.76)	0.57 (0.25; 0.93)	0.10 (0.02; 0.36)	11.58
	Colorado #3	99	140	14.75	0.84	0.54	0.54 (0.28; 0.81)	-1.54 (-1.97; -1.21)	-0.33 (-0.95; 0.12)	0.24 (0.00; 0.50)	1.89
	Minnesota #2	92	31	16.84	0.10	0.81	0.77 (0.62; 0.93)	-1.70 (-1.95; -1.42)	0.19 (-0.16; 0.52)	0.00 (0.00; 0.34)	1.13
	Australia	324	483	15.93	0.26	0.73	0.72 (0.59; 0.82)	-1.75 (-1.91; -1.59)	-0.24 (-0.45; -0.03)	0.09 (0.02; 0.22)	5.12
	Aggregated	807	966	15.66	0.81	0.71	0.71 (0.63; 0.78)	-1.77 (-1.86; -1.67)	-0.05 (-0.20; 0.10)	0.12 (0.06; 0.20)	0.41
17–34	Netherlands #4	66	94	17.62	0.38	0.80	0.85 (0.62; 1.00)	-1.93 (-2.28; -1.55)	-0.11 (-0.53; 0.35)	0.06 (0.00; 0.23)	0.24
	Colorado #3	203	180	19.46	2.00	0.53	0.53 (0.36; 0.73)	-1.85 (-2.11; -1.61)	-0.38 (-0.74; -0.05)	0.31 (0.11; 0.50)	4.94
	Minnesota #2	318	183	17.63	0.36	0.57	0.56 (0.38; 0.76)	-1.76 (-1.97; -1.57)	0.53 (0.27; 0.82)	0.23 (0.07; 0.43)	17.21
	Aggregated	700	615	18.78	2.71	0.69	0.69 (0.57; 0.80)	-1.77 (-1.88; -1.65)	0.19 (0.01; 0.37)	0.14 (0.05; 0.26)	4.39

$\chi^2(1)$ denotes a likelihood ratio test on parameter β_1 . 95 % confidence intervals are in brackets. In a few cases we experienced numerical difficulties in estimating the lower bound of γ_0 because the number of DZ twins was too small. 'Aggregated' is based on the aggregated data within the corresponding age category including the Netherlands #5 and Netherlands #6 studies. As some samples are omitted in the analysis of the individual studies (see Table 2), N_{MZ} and N_{DZ} will not necessarily add up to the aggregated N_{MZ} and N_{DZ} .

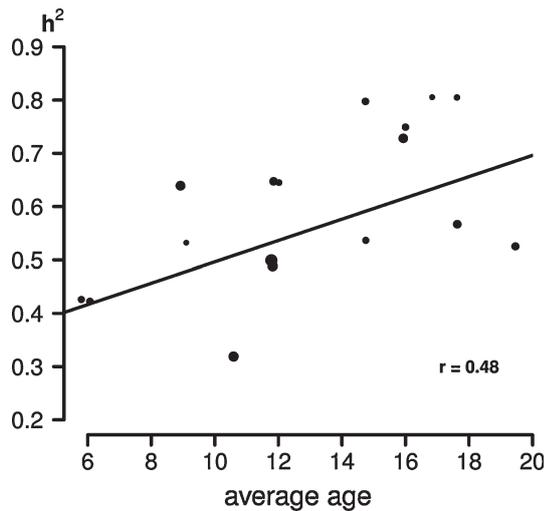


Fig. 1 Heritability (h^2), as estimated in the 17 samples from the 14 individual studies, plotted against the average age of the sample. Sizes of the *dots* are proportional to the sample size of the corresponding sample. Both the regression line and correlation coefficient take the differences in sample size into account

0.34 in the UK study, and 0.19 in the Colorado #1 study in the age range 4–10.

Finally, we see similar variability with respect to the estimates of the $A \times E$ effect, β_1 . Within age groups,

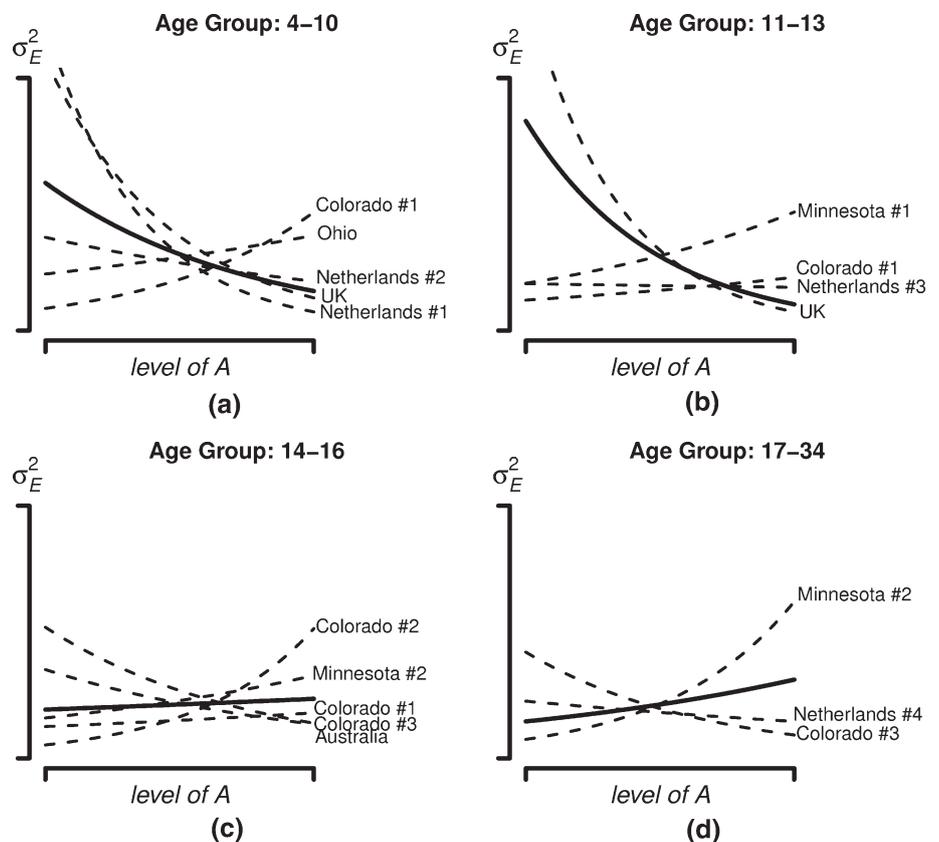
estimates vary widely and can even be of opposite sign. Large studies also show substantial differences, e.g., within age group 17–34, the β_1 of the Colorado #3 study equals -0.38 , while the Minnesota #2 study is associated with an opposite effect ($\beta_1 = 0.53$).

Differences in additive genetic and shared environmental influences

Given the variability we observed with respect to estimates of σ_A^2 and σ_C^2 , even in the larger studies, the question arises how these differences come about. Here, we discuss possible causes.

First, studies differ substantial in the IQ measures that were used. Some studies used full test batteries (Colorado #1, Colorado #2, Netherlands #3, and Netherlands #4); others used only two subtests (Colorado #3), four subtests (Ohio, UK, Minnesota #1, Minnesota #2), five subtests (Australia), or six subtests (Netherlands #1 and Netherlands #2). These psychometric differences result in variation in the exact composition of the IQ measure. For instance, some studies rely only on the subtest from the Verbal Comprehension and Perceptual Organization domain (e.g., the Minnesota studies), while in other studies (e.g., Colorado #1 and #2 studies) measures are included from all major cognitive domains (working memory, perceptual speed, etc.). This variation is

Fig. 2 Variance of E (σ_E^2) as a function of A within each age group. *Dashed lines* represent the results of the individual studies; the *solid bold line* represents the results of the aggregated data



important as genetic, unique and common environmental influences and $G \times E$ may differ across specific cognitive abilities (e.g., Finkel et al. 1995).

Another source of differences in results between the individual studies are the possible differences on background variables which are known to be related to heritability, e.g., parental income, educational attainment, or SES (Turkheimer et al. 2003). First, representativity of the samples may differ across countries. For instance, in the Australia study, twins are mainly from the entire Brisbane area while in the Minnesota studies, all twins lived close to the laboratory where testing took place. Thus the Minnesota sample is from a specific region (i.e., where the laboratory was located), while in the Brisbane sample, participants are from much more varied regions. In addition, there are differences between the individual studies in the way in which participants were recruited. Some studies relied on birth records (e.g., Colorado #2), others relied on primary and secondary schools (e.g., Australia) or media advertisements (e.g., Ohio). Such variability in recruitment might have resulted in differences on background variables across countries.

Differences in genotype by environment interaction across studies

The differences in the estimates of the $A \times E$ effect, β_1 , are such that they defy substantive explanation. From Table 6, it appears that the β_1 estimates vary, with opposite effects across studies within the same age group. For instance, in age group 14–16, the Colorado #2 study shows a significant effect with $\beta_1 = 0.57$, while the Australia study is associated with a significant effect in the opposite direction, $\beta_1 = -0.24$. Similarly, in age category 17–34, two opposite yet significant effects are observed: Colorado #3 with $\beta_1 = -0.38$ and Minnesota #2 with $\beta_1 = 0.53$. Such differences across studies render substantive conclusion in terms of genuine genotype-by-environment interaction difficult. Whether the $A \times E$ effects on the aggregated data can be interpreted substantively remains an open question. We discuss this further below.

Discussion

In this study we used a heteroscedastic ACE model to investigate the presence of $G \times E$ in cognitive ability in 14 different studies conducted in Four countries covering four different age groups.

Similar to the standard ACE model, the heteroscedastic ACE model assumes that A, C, and E are uncorrelated and the question arises whether violations of this assumption affect results on $G \times E$ (i.e., tests on $A \times C$ and/or $A \times E$). In the Molenaar et al. (2012) study, we showed that a linear

correlation between A and E due to shared genetic effects between the phenotype and a measure of E did result in spurious $G \times E$. However, it remains to be investigated whether a direct correlation between A and E influences tests on $G \times E$. For instance, it is possible that $A \times E$ as operationalized in the heteroscedastic ACE model, could arise due to difference in the A-E or A-C correlation across environments or genotypes. This would imply a nonlinear relation between A and E or A and C which can possibly influence the results concerning $A \times E$ and $A \times C$ respectively. This is an interesting topic for further research.

In the present study, it appeared that results on the aggregated data are difficult to interpret in terms of a genuine $G \times E$ effect because results differed considerably with respect to presence, as well as direction of the $G \times E$ effect, across countries and ages. The possibility that differences in measurement instruments across countries caused artificial $G \times E$ in different directions cannot be ruled out (see Eaves et al. 1977). We would have been more confident about the genuineness and interpretation of the $G \times E$ results on the aggregated data if we had observed consistent effects across countries, studies, and age groups.⁶

Representativeness of the samples analyzed in a $G \times E$ analysis is another important issue. As mentioned by Turkheimer et al. (2003) and Hanscombe et al. (2012) unrepresentativeness can affect $G \times E$ results if the sample under consideration differs from the population on important background variables. For instance, it has been argued that the direction of $G \times E$ may be different at the extremes of SES (Scarr 1992), suggesting that $G \times E$ results can diverge across samples that differ with respect to SES. Another problem with unrepresentative samples is that the unrepresentativeness itself may be a spurious source of non-normality (e.g., by oversampling either extreme of the IQ distribution), which in turn may result in the detection of spurious $G \times E$.

Given its relative statistical and substantive importance, it is remarkable to see that the detection of $G \times E$ in general, and genotype by unmeasured environment interactions in particular, is a challenging task (see Eaves et al. 1977; Eaves 2006). A main problem is that measurement issues such as floor or ceiling effects, and poor scaling may give rise to spurious $G \times E$. The question rises how we may overcome these problems. First, univariate applications, as in this paper, are particularly vulnerable to scale problems as the unique environment factor E in an ACE decomposition includes measurement error (Turkheimer and Waldron 2000; Loehlin and Nichols 1976). As a result,

⁶ Note that in such a situation, in principle, one still should be careful as the same artificial scale effects could have been replicated across countries (see Eaves 2006). However, as –in this study– different instruments were used across countries, we think that this would not have been the case.

heteroscedastic measurement error due to floor, ceiling, and poor scaling effects can give rise to $G \times E$ (see also Tucker-Drob 2009). A possible solution to this problem is to use multiple measures of the same phenotypic construct (e.g., multiple subtests scores of a given IQ domain). Given multiple measures, measurement error can be separated from the E component in the common-pathway model (McArdle and Goldsmith, 1984; see also Eaves et al. 1977). To this end, a measurement model needs to be specified, linking the observed phenotypic measures to the latent phenotypic construct. In the measurement model, residuals may be heteroscedastic to accommodate poor scaling effects. $G \times E$ can then be tested at the level of the latent phenotype, in a similar way as above. Results pertaining to $G \times E$ at this level can then be more confidently interpreted in terms of a true $G \times E$ effect, as all measurement problems are captured in the residuals (Molenaar et al. 2012).

Another possible solution is to test for $G \times E$ on the phenotypic item level instead of on test or subtest level. Using the appropriate measurement models, e.g., a Rasch model (Rasch 1960) or a two-parameter model (Birnbaum 1968), each answer category of the item is modeled explicitly. As a result, floor, ceiling, and poor scaling effects cannot give rise to spurious $G \times E$. Tests for $G \times E$ on item level are readily available in the case of a measured environmental variable, see Medland et al. (2009), and in case of an unobserved environment (the methodology proposed by Molenaar et al. 2012, could be used).

Taking all together, using the heteroscedastic ACE model we did not find a consistent pattern of results between age groups, datasets, and countries. We think that these results are a clear illustration of the profound scale issues that make investigations on $G \times E$ a challenging undertaking. However, we hope to have touched on some promising possibilities above, to address these scale issues in future research.

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Study (Australia): Australian Research Council (A7960034, A79906588, A79801419, DP0212016 and DP0343921) and The Human Frontier Science Program (RG0154.1998-B). Netherlands Twin Register: Dutch Organization for Scientific Research (NWO) 051.02.060, NWO 480-04-004, NWO 575-25-012 and NWO/SPI 56-464-14192) and Human Frontiers of Science Program (RG0154/1998-B). The Mx syntax file of the models described in this paper are available from the site of the first author, www.dylanmolenaar.nl.

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