

An Examination of Genotype-environment Interactions for Academic Achievement in an U.S. National Longitudinal Survey

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We examined whether genetic and environmental effects on academic achievement changed as a function of the quality of the children's environment. The study included a variety of observed environmental measures such as parental cognitive stimulation and poverty level, longitudinal information about previous environmental conditions, and a larger than average number of children who grew up in deprived environments. The sample consisted of 1664 pairs of full siblings, 366 pairs of half siblings, and 752 pairs of cousins who were on average 9.58 years old. Both a simple descriptive approach as well as significance tests performed with multilevel regression analyses showed little evidence for genotype-environment interactions. There was only a slight trend consisting of a linear decrease of total variance or nonshared environmental effects from deprived to good environments.

It has long been recognized, that rather than examining how much variance is explained by genetic and environmental factors, the more important scientific questions pertain to the mechanisms that describe how genes and environments work together in producing developmental outcomes (Anastasi, 1958). These mechanisms can roughly be subdivided into genotype-environment correlations and genotype-environment interactions (Wachs & Plomin, 1991). Genotype-environment correlations imply that environments of individuals are

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correlated with their genetic propensities whereas genotype-environment interactions refer to differential effects of the same environments on individuals with different genotypes (or the differential effects of different environments on individuals with the same genotype).

GENOTYPE-ENVIRONMENT CORRELATIONS

In literature there is cumulating evidence that genotype-environment correlations are important for children's development. For example, a number of studies have shown that when environmental measures such as parenting behaviors are used as the dependent variable in a behavior genetic analysis, the correlations between the environments of relatives increase with the degree of genetic relatedness (Baker & Daniels, 1990; Bouchard & McGue, 1990; Braungart, Fulker, & Plomin, 1992; Goodman & Stevenson, 1991, Plomin, Reiss, Hetherington, & Howe, 1994; Rende, Slomkowski, Stocker, Fulker, & Plomin, 1992; Rowe, 1981, 1983). This suggests that environmental measures tend to reflect the differential genetic resemblance of relatives and that they are dependent on the genetic propensities of individuals. Furthermore, this same phenomenon seems to apply to correlations between environmental variables and developmental outcomes that may not represent pure causal effects and could be confounded by genetic effects as well (Braungart et al., 1992; Cherny, 1994; Coon, Fulker, DeFries, & Plomin, 1990; Scarr & Weinberg, 1978).

These empirical findings can be explained by a third variable, or child effect and suggest genotype-environment correlations. The third variable explanation implies that genes shared by parents and children influence both environmental measures and child outcomes, and account for the higher correlation for groups of relatives that are more similar on the third variable. To illustrate that this is a form of genotype-environment correlations, consider the association between poverty and IQ. Genetic influence on parental intellectual ability could affect both the household income and the IQs of the biological children in that household, so that 'genetically' brighter children grow up in less poverty (better environments). Genetic influence on environmental measures can also be caused by child effects, if children are not passive recipients of care but active partners in their interaction with their environments (Bell, 1968; Ge et al., 1996). To the extent that the relevant behaviors are heritable, children who are genetically more alike will therefore create or experience more similar environments. This is another form of genotype-environment correlations because it implies that, for instance, brighter children grow up in "better" environments due to their choosing to read more books or their capacity to filter more effectively information from instruction.

GENOTYPE-ENVIRONMENT INTERACTIONS

Genotype-environment interactions are a second way genes and environments could coact to produce developmental outcomes. Whereas, in the case of genotype-environment correlations, specific genotypes are just more common in certain environments, interactions imply real effects of a specific combination of genes and environments. A first example can be found in literature that pertains to vulnerability and protective factors, and indicates that children who are biologically at risk may be especially vulnerable to the effects of unfavorable environments. In some situations the disorder could even remain unexpressed unless it is released by a specific environmental stressor. A second example of genotype-

environment interaction is present in so-called "goodness of fit" models (e.g. Thomas & Chess, 1977; Lerner, 1984). In these models the quality of the relation between dispositions of the child, whether learned or biological in origin, and characteristics of the environment are assumed to affect developmental outcomes.

Whereas most authors wouldn't deny the existence of genotype-environment interactions, there is considerable more disagreement about how influential they are for normal development. According to Scarr (1992) genotype-environment interactions are only important in severely deprived environments that are so extreme as to be outside of the normal range of rearing environments. Consequently they would have few implications for the vast majority of children who experience normal environments. Other social scientists endorse the opposite view (Bronfenbrenner & Ceci, 1994; Baumrind 1993; Jackson, 1993). For example, Bronfenbrenner and Ceci (1994) presented a developmental model in which relations between genes and environments are mediated by a mechanism called proximal process. Proximal processes should be viewed as progressively more complex reciprocal effects between the child and persons or objects in his or her immediate environment. A concrete example of such a process is the quality of interactions between child and caretakers. A proximal process must occur on a fairly regular basis over extended periods of time to be effective, and its power depends on the availability of resources (e.g. financial, intellectual). Because proximal processes actualize genetic potentials for effective psychological functioning, they imply that genetic effects will be greater in "good" environments. This differential genetic effect shows that Bronfenbrenner and Ceci's model can be considered as an example of the view that genotype-environment interactions are a common mechanism underlying normal development.

To avoid confusion it is important to note that in the above discussion the term interaction is used in the *statistical* "analysis of variance" sense of the word and that it reflects systematic effects on *differences* between children in a population. Another use pertains to interaction with the *physical* environment as may be relevant for an *individual* child. Obviously a child cannot develop without environment and interactions in this latter sense are always a necessity. However, although the relation between these two different perspectives is not fully understood (Burgess & Molenaar, 1995; Turkheimer & Gottesman, 1996), it seems likely that these latter types of interactions do not necessarily show as statistical interactions in a population. For instance, dynamic system models, that view individual development as emergent properties of nonlinear developmental systems, show that specific individual interactions may contribute to differences between children in a population but in an unpredictable and "chaotic" way (Gottlieb, 1991; Molenaar, Boomsma, & Dolan, 1993; Turkheimer & Gottesman, 1991).

STUDYING GENOTYPE-ENVIRONMENT INTERACTIONS USING NATIONAL LONGITUDINAL SURVEY DATA

In contrast to studies of genotype-environment correlations, there have been relatively few studies examining the importance of genotype-environment interactions for children's developmental outcomes (Wachs & Plomin, 1991). For this reason we will focus on genotype-environment interactions. Our data consisted of assessments of academic achievement in children of the female participants in the National Longitudinal Survey of Youth (NLSY, Center for Human Resource Research, 1993).

The NLSY, which started in 1979 with a national sample of men and women (ages 14-21), has a number of qualities that facilitate the examination of genotype-environment interactions. First, due to the sample design, children in the NLSY were born of relatively young mothers who were on average more likely to be less educated or belong to minority groups than those of a full cross-section of mothers (Chase-Lansdale, Mott, Brooks-Gunn, & Phillips, 1991). Compared to other studies that are more often comprised of white middle-class children, this survey is, therefore, more suitable to study ethnic and socioeconomic diversity and the differential effects of environments. Second, the survey comprises a variety of instruments to assess the quality of the environment that have demonstrated to be related to levels of academic achievement (e.g. Korenman, Miller, & Sjaastad, 1995; Luster & Dubow, 1992; Moore & Snyder, 1991; Mott, 1994; Parcel & Menaghan, 1994; Plotnick, 1992). To assess the child's immediate environment, information is gathered about parental cognitive stimulation and emotional support. At a more distant level, data are available about poverty, parental occupation and education, and father absence. These variables can be viewed as measures of financial and intellectual resources and the (emotional) stability of the children's environments. Third, because the NLSY is a longitudinal survey, data about previous points in time are available. This is important because not only the type but also the persistence of an environmental stressor over extended periods of time may be a relevant aspect of genotype-environment interactions (Bronfenbrenner & Ceci, 1994). For the distant variables information was gathered yearly since 1979, and for these variables it was therefore even possible to reconstruct complete "environmental histories" for each child. Fourth, the NLSY comprises a sizable number of siblings and cousins. Although there is no explicit information about genetic relatedness, classification algorithms can be applied to distinguish groups of full siblings, half siblings, and cousins in order to obtain a genetically informative design (see Rodgers, Rowe, & Li, 1994).

To examine genotype-environment interactions we used (multilevel) regression analyses. As the dependent variable, we used for each child the academic achievement assessment from the last survey year in which he or she participated. To account for the possible relevance of previous environmental conditions, *all* observed environmental information from the child's birth to his or her last academic achievement assessment was used to construct the independent variable. Next, significance tests were performed to examine linear and quadratic nonlinear changes in genetic and environmental effects as a function of the quality of the environments in which children grow up. Finally we would like to note that by calling the independent variables "environmental," we do not want to imply that they represent pure environment and are independent of genetic effects (Plomin, 1995; Reiss, 1995). This terminology was chosen to avoid confusion and to be consistent with the common usage of the term "environment" for the type of observed measures that were used in this article.

METHOD

Participants

Many NLSY mothers have more than one child and the survey therefore comprises a sizable number of siblings. Although there is no explicit information about paternity, a

classification algorithm can be used to distinguish full and half siblings and obtain a genetically informative design (see e.g. Rodgers et al. 1994). The algorithm assumes that mothers don't live simultaneously with different fathers, and classifies children who live with both biological parents as full siblings. In families where the father of one member of a sibling pair lives at home and the other's father not, children are classified as half siblings. If neither father lives in the home, a second variable is used that indicated how far away each child's father lives (with four or five categories: within one mile, 1-10 miles..., more than 200 miles). If the distance does not match the children are classified as half siblings, otherwise their status is considered as indeterminate.

For this article, six separate survey years were available that gave information to distinguish full and half siblings. To deal with these multiple survey years, we first identified full and half siblings for each year separately. Children who were classified as full siblings on at least *two* occasions and *never* classified as half siblings were considered to be full siblings. Children who were classified as half siblings on at least *two* occasions and *never* classified as full siblings were considered to be half siblings.

Classification errors attenuate the differences between groups of full and half siblings and result in overestimates of shared environmental effects and underestimates of genetic influences. Rodgers et al. (1994) and Rodgers, Rowe, and May (1994) validated their algorithm, which was also used in the present article, by showing that it yields heritability estimates that are quite close to those reported in the behavior genetic literature for frequently studied characteristics such as weight, height, and IQ. To check for possible errors, we also compared the sibling status obtained with our program with the sibling status obtained with the program of Rodgers (personal communication). The number of misclassifications was almost zero per cent (e.g. siblings classified as full siblings by our program and as half siblings by Rodger's program). The only difference was that a number of sibling pairs who *were* classified as full or half siblings by Rodger's program, were classified as *indeterminate* by our program and excluded from the present analyses. The explanation is that for the present article more waves of NLSY data were available. To avoid classification errors as much as possible, we choose to use this additional information conservatively by excluding all sibling pairs who showed any inconsistencies across the additional survey years.

In 1979 all youths who were in the appropriate age range were sampled from the households. Some mothers are therefore sisters and their children cousins. In terms of this hierarchical structure, the total sample from the present article comprised 3266 children from 2000 fathers, 1692 mothers, and 1591 families. In terms of pairs there were 1664 pairs of full siblings, 366 pairs of half siblings, and 752 pairs of cousins.

Measures

Academic achievement was assessed by means of three subtests of the Peabody Individual Achievement Test (PIAT) which is among the most widely used brief assessment instruments for children aged five and over (Center for Human Resource Research, 1993, p. 133). The three subtests were PIAT Mathematics, PIAT Reading Recognition, and PIAT Reading Comprehension, that measure quantitative reasoning, reading achievement, and ability to derive meaning from written sentences respectively. In addition, we constructed a general measure of academic achievement by computing the mean of three PIAT sub-

scales. The PIAT manual indicates medium reliability for the three subscales (Center for Human Resource Research, 1993, pp. 125-149). The one month test-retest reliability of the PIAT measures depends somewhat on the child's age, with median values of .74 for PIAT Mathematics, .89 for PIAT Reading Recognition, and .64 for PIAT Reading Comprehension. For the composite measure that we used in this article, Cronbach's alpha was .85. This suggested that the overall scale was a reliable measure for general academic achievement in the NLSY sample. To use the data of all children in a single analysis, regression analyses were used to adjust the PIAT scales for sex and age effects.

As a measure of the quality of the immediate environment, the Home Observation for Measurement of the Environment-Short Form (HOME-SF) was used. The HOME-SF is a modification of Caldwell and Bradley's HOME inventory and consists of two subscales that are labeled: Intellectual Stimulation and Emotional Support. The HOME-SF is completed for each child separately and comprises interviewer observations plus maternal ratings. The specific content of the HOME-SF items depends on the age of the child, but normed scores based on a single year of age are available. With respect to the reliability, a distinction needs to be made between the HOME-SF version that is appropriate for children younger than three years of age and the versions for children older than three years of age (Center for Human Resource Research, 1993, p. 170). Cronbach's alphas for the Total HOME-SF score, Intellectual Stimulation, and Emotional Support are in the younger/older group .55/.71, .50/.67, and .35/.58 respectively. This indicates a low reliability for young children and a somewhat below average reliability for older children.

As measures for the quality of the environment at a more distant level, seven variables were used that indicated whether a father figure was absent in the household, whether the marital status of the mother had changed compared to the previous year, family poverty status, the highest grade completed by the mother and highest grade completed by the father figure, and the employment level of the father figure. Father figure absent was scored one if there was no father figure in the household and scored zero if a father figure was present. Change in marital status was scored one when there was a divorce, re(marriage), new partner in the household, or death of a spouse and scored zero if the marital status of the mother had not changed compared to the previous year. Family poverty status was scored one if the total family income was below the poverty level as reported by the U.S. Department of Health and Human Services and scored zero if it was above the poverty level. Highest grade completed was measured in 21 categories that ranged from "no grade" to "eighth grade college or more." Employment level father figure was scored one to three representing respectively: unemployed, employment at intermediate level (e.g. laborer, office worker, craftsman, salesman), employment at higher level (e.g. manager, technical professional). The reliability of these measures is unknown but there were several indications that it was quite high. For instance, at the beginning of each NLSY interview a control question was asked whether the marital status reported in the previous interview was correct. In most survey years, over 99% of the respondents replied that this was the case. In addition, although there could have been actual changes, correlations between the reported Highest grade completed by mother in two adjacent survey years were about .99.

Finally, two variables were constructed that distinguished groups of NLSY children that were likely to have experienced different environments. The 1979 NLSY sample comprised a nationally representative cross-sectional sample plus supplementary samples of blacks, Hispanics, low income white youth, and respondents who were in the military at

Table 1. Descriptive Statistics for "Environmental Histories" and Group Membership

	<i>Mean</i>	<i>Standard Deviation</i>	<i>N</i>
Father figure absent	.26	.35	3266
Changes in marital status mother	.32	.14	3266
Family poverty status	.31	.35	3258
Highest grade completed mother	11.61	2.19	3261
Highest grade completed father	11.94	2.38	3258
Employment level father	2.09	.34	3253
Supplementary sample	.48	.50	3266
Minority group	.47	.50	3266

that time. It seems reasonable to suppose that children from mothers in the supplementary samples grow up in more disadvantaged environments, and we therefore created a variable labeled Supplementary sample that was one for children with a mother who belonged to the supplementary sample and zero for the other children. In addition, there is ample literature showing that economic and cultural factors may be different in whites compared to minority groups (e.g. see Child Development, Special Issue on Minority Children, 1990). For this reason we constructed a variable Minority group which was one for Hispanic and black children and zero for white children.

Multiple assessment years

The PIAT and HOME-SF were completed for all children in 1986, 1988, 1992, and 1994. Information about the distant environmental variables was obtained yearly since 1979. As the dependent variable in our analyses, we used for each child the PIAT scores from the last survey year in which he or she participated. To account for the possible relevance of previous environmental conditions, the mean of *all* observed environmental scores from the child's birth to his or her last PIAT assessment was used as the independent variable. At the time of their last PIAT assessment, the children were on average 9.58 years of age ($SD = 3.08$) and there were about 3.3 HOME-SF ($SD = .86$) assessments for each child. Because 83% of the children were born after 1979 and the percentage missing values was quite small (e.g. for almost every variable this was less than 10%), fairly complete information was available about the children's whole lives with respect to the distant environmental variables. Table 1 shows some interpretable descriptive statistics of these "environmental histories."

For Father figure absent, the mean was .26. To interpret this number it is important to recall that in each of the separate survey years the variable Father figure absent was originally scored one for a child if a father figure was absent and zero if a father figure was present. Next, for each child we had computed the mean of the variable Father figure absent across all survey years from the child's birth to his or her last PIAT assessment. This longitudinal mean, therefore, represented the proportion of the total number years in the children's lives that a father figure was absent. For instance, a value one would indicate that during the whole live of a child a father figure was absent and value zero that a Father figure was never absent. Thus, the sample mean of .26 reported in Table 1 for these longi-

tudinal means indicated that on average father figures were absent during 26% of the lives of the children. Results for Change in marital status and Family poverty status can be interpreted in an analogous way and showed that in about one-third of the children's lives there had been a change in the marital status of the mother and they lived in poverty. These descriptive statistics indicated that a substantial number of children in this sample grew up in disadvantaged environments. On the other hand standard deviations were quite large. This indicated that there were considerable individual differences in the conditions that children had experienced during their lives, and that the sample was suitable to study possible differential effects of environments.

On average parents completed 11th grade and the employment level of the fathers was at the intermediate level (laborer, office worker, craftsman, salesman). For Highest grade father and Employment level father, Table 1 reports the mean of the years father figures were present. However, because only fathers that are present in the household contribute to the quality (e.g. intellectual resources) of the child's environment, a weighted mean was used in the remainder of the analyses with weight one if a father figure was present in that survey year and weight zero if he was absent.

Finally, the variables Supplementary sample and Minority groups are by definition constant across time, and for these variables Table 1 simply reports percentages. These percentages showed that almost half of the sample consisted of children born to mothers that belonged to the 1979 supplementary sample and children from minority groups.

Modeling Genotype-environment Interactions

Genotype-environment interactions imply that genetic and environmental effects are different for children who grow in different environments. This situation can be illustrated with regression analysis. A general form of a regression equation is:

$$P = a + bX + R \quad (1)$$

in which P is the dependent variable, a the constant, b the regression coefficient, and R the error or residual component. Equation 1 can be visualized through a fictitious plot. In Figure 1 we have drawn such a plot for a *fictitious* example which has academic achievement as the dependent variable and Poverty as the independent variable.

The line in the middle of Figure 1 is the regression line, $a + bX$, that shows the predicted academic achievement given a certain amount of poverty. Because we assumed a negative relation between academic achievement and Poverty, predicted scores decrease from children in rich families to children in poor families. Poverty explains only part of the differences among children in academic achievement, and there remains a considerable amount of individual variation around the predicted score. This residual variance, R, is represented by the lines on the outside, that bound the region within which the academic achievement scores of 95% of children who experienced the same amount of Poverty lie. The upper bound of this region equals the predicted score plus two times the square root of the residual variance (standard deviation), and the lower bound equals the predicted score minus two times the square root of the residual variance. Figure 1 shows that the size of the 95% region increases with the amount of poverty. Thus, individual differences among children are larger for children who grow up in more Poverty. This indicates that genetic and

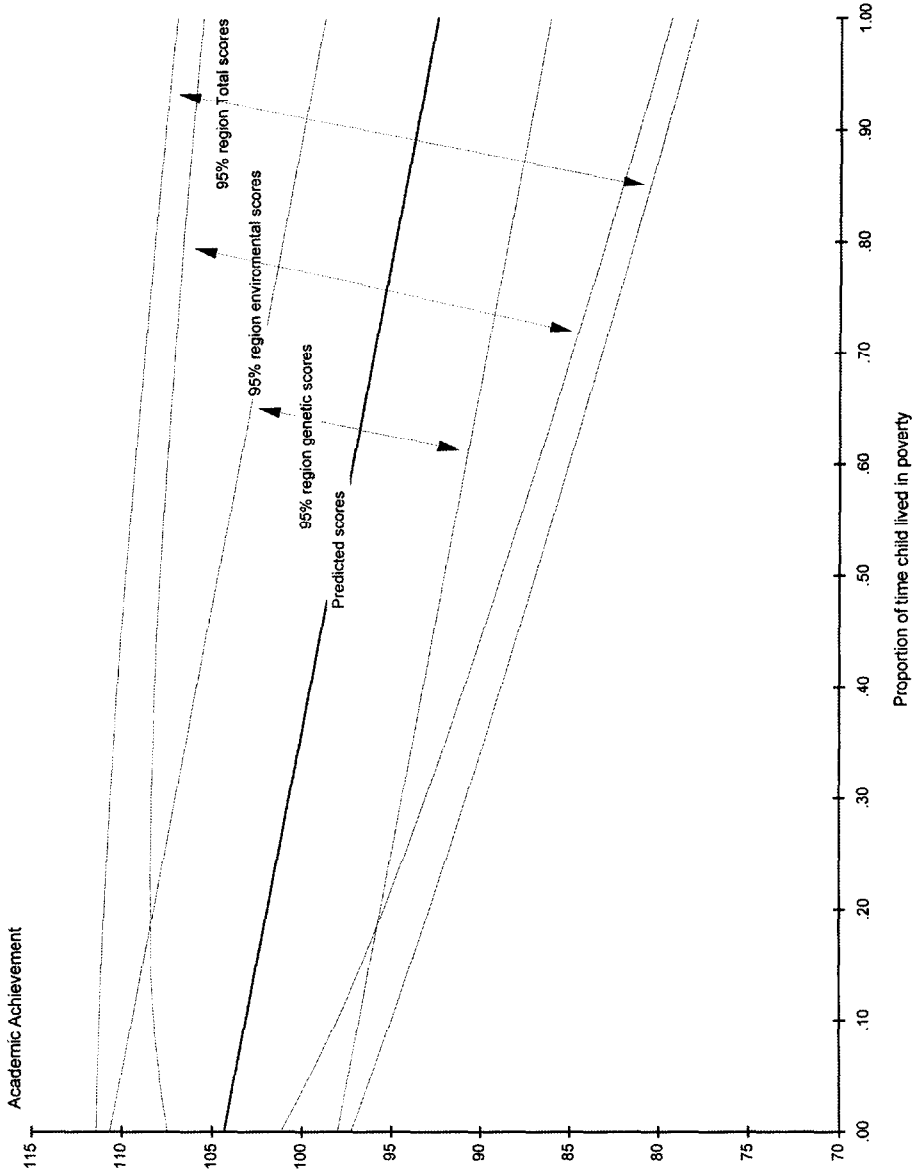


Figure 1. Proportion of Time Child Lived in Poverty

environmental effects, that cause these individual differences, depend on Poverty and implies interaction effects.

The residual variance or individual variation around the predicted score can be viewed as an additive sum of genetic and environmental effects. Analogous to the procedure for the total residual variance, it is therefore possible to construct a region within which the residual environmental scores of 95% of the children lie and a region within which the residual genetic scores of 95% of the children lie. Figure 1 shows that the genetic region is equally large for all values of Poverty. This indicates that genetic effects or genetic differences among children are independent of the amount of poverty, and that there are no interactions between Poverty and genetic effects. However, for environmental influences the size of the 95% region increases with the amount of poverty, implying an interaction between Poverty and the magnitude of environmental effects. Figure 1 also demonstrates that for children from rich families the 95% region is larger for genetic scores than for environmental scores whereas for children from poor families this region is larger for environmental scores than for genetic scores. This indicates that the heritability or proportion of genetic variance is larger for rich children, and illustrates that genotype-environment interactions affect the relative importance of genetic and environmental effects. Finally, we would like to note that although the total residual variance is the sum of residual environmental and genetic variance, the size of the overall region is not the sum of the genetic plus environmental regions. This is because the regions are computed using the *square root* of the residual variance, and the sum of two variances does not equal the sum of the square root of two variances.

Data analysis

The above section shows that an evaluation of genotype-environment interactions requires the decomposition of the residual variance into genetic and environmental components plus a test to study changes in the size of the genetic and environmental components as a function of the quality of the environment. In behavior genetic studies, phenotypic scores are usually decomposed into the additive sum of genetic influences *A* and two types of environmental influences. The environmental influences are denoted by symbols *E* and *C*, that represent environmental influences that are not shared by children in the same family and environmental influences that are shared by children in the same family respectively (Plomin, DeFries, & McClearn, 1990; Neale & Cardon, 1992). However, in contrast to most behavior genetic studies that involve relatives who grow up in the same household, our sample comprised cousins who grow in different households. Due to familial resemblance in parenting behavior or neighborhoods, some environmental influences may also be shared by cousins. For this reason we specified two separate shared environmental components instead of the usual shared environmental component *C*. The first component represented the environmental influences that are only shared by children in the nuclear family *N*, whereas the second component represented the shared family environment *F* that is similar for both siblings and cousins. Substituting these four components for the overall residual term *R* in Equation 1, yields the following regression equation:

$$P = a + bX + (E + A + N + F) \quad (2)$$

Thus, academic achievement is predicted by an independent variable X plus a residual part consisting of genetic and various environmental effects. In our study, the independent variable X is one of the observed environmental variables discussed in the Measures section, and the estimation of regression coefficients b could be realized by ordinary regression analysis. The decomposition of the residual term in genetic and environmental effects is more unusual. To illustrate how this can be done, it is convenient to drop the term bX from Equation 2. Note that this does not make any fundamental difference, and that instead of deviations from the regression line, $a + bX$, we are studying deviations from the general mean or regression line, a . To put this more simply, the removal of the term bX results into a decomposition of the total variance of P so that :

$$\text{var}(P) = \text{var}(E) + \text{var}(A) + \text{var}(N) + \text{var}(F) \quad (3)$$

A next step is to express the correlations among full siblings, half siblings, and cousins as a function of these components. Component E comprises nonshared environmental influences that are unique for each child as well as errors of measurement, and does not contribute to the resemblance between relatives. Under the assumption that genetic effects are the sum of the effects of many genes, it can be shown that genetic correlations are .5 for full siblings, .25 for half siblings, and .125 for cousins (Falconer, 1989, pp. 149-162). Component N correlates 1 in both sibling groups and .0 for cousins, because it pertains to environmental influences that are only shared by children in the nuclear family. The shared family influences F are identical for sibling as well as cousins and correlates 1. in all three groups. This yields the following equations:

$$\begin{aligned} r'_{\text{full siblings}} &= .5\text{var}(A) + \text{var}(N) + \text{var}(F) \\ r'_{\text{half siblings}} &= .25\text{var}(A) + \text{var}(N) + \text{var}(F) \\ r'_{\text{cousins}} &= .125\text{var}(A) + \text{var}(F) \end{aligned} \quad (4)$$

The symbol r is given an accent ($'$) to show that it is not standardized and should still be divided by the total variance $\text{var}(P)$ in order to get the (intraclass) correlation.

Formula 4 already suggests a first descriptive and indirect way to explore whether genetic and environmental effects change as a function of the quality of the environment. The approach consists of computing the absolute or unsigned differences between the academic achievement scores of pairs as an index of similarity and the average score of the pairs on the environmental variable as indicator for the quality of the environment. Next, this absolute academic achievement difference is correlated with the average environmental score, to examine whether the resemblance between relatives changes as a function of within-pair environmental mean. Analogous to the usual procedure in regression analyses, possible quadratic nonlinear changes can be studied by regressing the absolute within pair differences on the within-pair environmental mean plus the square of the within-pair environmental mean.

To illustrate the interpretation of possible results obtained with this approach, assume that there is a positive correlation between the absolute within pair differences and within-pair environmental means. This would indicate that relatives become increasingly dissimilar at the high end of the environmental continuum, and that the variance of component(s) that influence the similarity between relatives is larger in good environments and smaller in deprived environments. The relative sizes of correlations between the absolute within

pair differences and within-pair environmental means in the groups of full-siblings, half-siblings, and cousins give further information about which specific component interacts with the observed environmental quality. Genetic effects A would yield correlations that rank order in the opposite way as the biological relatedness of the pairs, that is, from full-siblings to half-siblings and then to cousins. This is because for children who are genetically more alike, genotype-environment interactions will be more alike. For instance, in the most extreme case of monozygotic twins who are genetically identical, the genotype-environment interaction effect would be the same for both twins and the correlation between the absolute within pair differences and within-pair environmental means would be zero. Interactions between nuclear family effects N and quality of the environment would be indicated by similar correlations in both sibling groups and zero correlations for cousins. Equal correlations in all three groups would imply effects of shared family factor F. Finally, we would like to mention that nonshared environment E does not affect the resemblance between relatives, and that therefore this indirect descriptive approach cannot detect possible interactions with this component.

The above approach gives merely a crude indication about possible changes in genetic and environmental effects as a function of the quality of the environment. For a thorough examination of genotype-environment interactions a procedure would be required that makes optimal use of all data, replaces visual inspection by statistical estimation, performs clear-cut significance tests for each of the model components separately, can handle linear as well as nonlinear changes, and can address changes in nonshared environmental effects and total variance as well as changes in shared environmental and genetic influences. A problem is that most behavior genetic methods assume pairs of relatives, whereas many families in our study comprised more than two children. The use of existing behavior genetic methods would therefore force us to select just one pair per family, and result in a substantial loss of information. One reason is that with multiple pairs from the same family, we would not have independent observations which makes it impossible to perform accurate significance test (e.g. the same child could simultaneously form a full sibling, half sibling, and cousin pair). Instead of analyzing pairs of relatives, we therefore studied whole families simultaneously using multilevel analysis (Goldstein, 1995). Multilevel analysis has specifically been developed to deal with dependent observations that are the result of a hierarchical data structure. Because the survey includes the children of NLSY *mothers* and a number of NLSY mothers are *sisters*, some children have the same father, children with different fathers can have the same mother, and groups of children with different mothers may belong to the same family. In our sample the children can therefore be grouped at four hierarchical levels, with as units at the different levels the individual child, the father, the mother, and the whole family.

Hereditary and environmental influences create differences in academic achievements between children that belong to different groups. Therefore, at each of the four levels there can be variance and the overall phenotypic variance can be viewed as the sum of the variances at each level. Another way to look at these differences is that they are caused by factors that make children who belong to the same group more alike compared to children from other groups. Thus, the resemblance between these groupings of related individuals can be looked at either as similarity of individuals in the same group, or as difference between individuals in different groups (Falconer, 1989, p. 148). The advantage of focusing on within group resemblance is that it facilitates the expression of the variance at each

Table 2. Expectations for the Genetic Multilevel Model

<i>Level</i>	<i>Unit</i>	<i>Observed Statistics</i>	<i>Contribution to Variance</i>
4	Family (cousins)	r'_{cousins}	$= .125\text{var}(A) + \text{Var}(F)$
3	Mother (half siblings)	$r'_{\text{half siblings}} - r'_{\text{cousins}}$	$= .125\text{var}(A) + \text{Var}(N)$
2	Father (full siblings)	$r'_{\text{full siblings}} - r'_{\text{half siblings}}$	$= .25\text{var}(A)$
1	Child	$\text{Var}(P) - r'_{\text{full siblings}}$	$= .5\text{var}(A) + \text{Var}(E)$

level in terms of the components E, A, C, and F. So at the highest level, the unit is family and all children within the same group are cousins. Differences between the units at this level therefore equal the (intraclass) correlation for cousins reported in Equation 4. The groupings one level lower represent half siblings because children within a group live in the same household and have the same mother. However, some of the differences are already explained by the highest level. This “explained” variance, that equals the correlation for cousins, needs to be subtracted from the resemblance between half siblings to get the expectation for the net differences at the third level. At the second level, groups of children have the same mother and father and are related as full siblings. The resemblance between full siblings minus the differences that are already accounted for by the third and fourth level, that equals the half sibling correlation, yields the expectation for the second level. Finally, the expectation for the differences at the child level is the residual variance and can be computed by subtracting the sum of the variance components of all higher, that equals the full sibling correlation, from the total variance.

The expectations for the genetic multilevel model in our study are summarized in Table 2.

The table shows that the level two variance represents pure genetic effects and that the other levels contain genetic effects plus effects of one environmental component. To study each of the E, A, C, and F components separately, it is therefore necessary to subtract during the analyses half of the level two variance from the third and fourth level and two times the level two variance from the first level. This results in pure nonshared environmental variance at level one, pure genetic variance at level two, pure shared nuclear family variance at level three, and pure shared family environment at level four. To perform this analysis we used the multilevel software MLn (Woodhouse, Rashbash, Goldstein, Yang, & Plewis, 1996). The specification of this genetic multilevel model in MLn is somewhat beyond the standard multilevel analysis, and we therefore included the MLn script in the Appendix.

The extension that is necessary to study genotype-environment interactions consists of including an observed environmental measure as explanatory variable in the regression equation for academic achievement (see Equation 2), and testing whether the amount of pure variance at each level depends on the environmental score. The examination of changes in variances at a given level is quite common in multilevel analyses and easy to implement in MLn (Woodhouse et al., 1996, pp. 30-31). Technically it can be achieved by estimating at each level one additional parameter (the correlation between the regression coefficient of the environmental variable and the unit means) to study linear effects and two additional parameters to study quadratic nonlinear effects (the correlation between the regression coefficient of the environmental variable and the unit means plus a variance for the environmental regression coefficient). To test whether the linear and quadratic effects were

Table 3. Correlations between Environmental Variables and PIAT Measures

	<i>Total score</i>	<i>Mathematics</i>	<i>Reading Recognition</i>	<i>Reading Comprehension</i>
HOME-Total score	.40	.35	.36	.36
HOME-Cognitive stimulation	.38	.32	.33	.33
HOME-Emotional support	.30	.26	.26	.26
Father figure absent	-.21	-.18	-.19	-.20
Changes in marital status mother	-.06	-.04	-.08	-.07
Family poverty status	-.36	-.30	-.33	-.33
Highest grade completed mother	.29	.27	.23	.23
Highest grade completed father	.29	.25	.26	.27
Employment level father	.27	.23	.25	.25
Supplementary sample	-.16	-.17	-.12	-.13
Minority group	-.21	-.24	-.15	-.19

Note: Except for Change in marital status mother versus Total score and Mathematics, all correlation were significant at $p < .05$. Total sample size was 3266, but due to nonresponse analyses for Total score, Mathematics, Reading Recognition, and Reading Comprehension were respectively based on 98.9%, 100%, 98.9%, and 83.0% of the total sample.

Table 4. Pairwise Correlations between Relatives and Multilevel Estimates of Proportion Genetic and Environmental Variance

	<i>Full siblings</i>	<i>Half siblings</i>	<i>Cousins</i>	<i>E</i>	<i>A</i>	<i>N</i>	<i>F</i>
PIAT Total score	.48	.30	.35	.24*	.60*	.00	.16*
Mathematics	.43	.23	.35	.25*	.70*	.00	.06
Reading Recognition	.41	.28	.24	.42*	.38	.00	.20*
Reading Comprehension	.40	.22	.31	.35*	.56*	.00	.09

Note: E is nonshared environment, A genetic influences, N shared nuclear family environment, and F shared family environment. * indicated $p < .05$. Correlations were based 1664 pairs of full siblings, 366 pairs of half siblings, and 752 pairs of cousins. Multilevel analyses involved 3266 children from 2000 fathers, 1692 mothers, and 1591 families. Due to nonresponse, analyses for Total score, Mathematics, Reading Recognition, and Reading Comprehension were respectively based on 98.9%, 100%, 98.9%, and 83.0% of the total sample

significant we used a chi-square difference test. This test compares the fit of the model that allows changes in variances at a specific level versus the fit of a model that does not allow changes in variances at that level. This difference in fit has a chi-square distribution with one degree of freedom for the model that specifies one additional parameter and examines linear effects, and two degrees of freedom for the model that specifies two additional parameters and examines quadratic effects. Both tests were performed at each of the four levels separately. In addition, we performed a general test that examined linear and quadratic effect for all components simultaneously. This was achieved by constraining the parameters to be equal across all four levels. For each test we used a significance level of .05.

RESULTS

Table 3 displays the correlations between the environmental variables and the PIAT measures.

Except for Change in marital status, tests performed with multilevel analysis indicated that the correlations were significant. The average correlation was .25, and suggested that our study comprised a set of relevant predictors for academic achievement. Among the highest correlations were the ones found for the HOME-SF and Family poverty status.

To give an impression about the relative importance of genetic and environmental factors, Table 4 shows the correlations between the academic achievement scores of relatives and multilevel estimates of the proportions genetic and environmental variance. The correlations were Pearson correlations based on all possible full sibling, half sibling, and cousin pairs in our sample, and in the multilevel analysis no measured environmental variables were included.

The full sibling correlation was larger than the half sibling correlation. This indicated genetic effects because, as shown in Table 2, the difference between the two correlations is an estimate of .25 times the genetic variance. The average cousin correlation was .31 and even slightly larger compared to the average half sibling correlation of .26. Table 2 shows that the difference between the correlations for cousin and half siblings, equals .125 times the genetic variance plus all shared nuclear family environmental variance. Therefore, the most important conclusion is that there is little evidence for nuclear family influences *N*. These above described trends were also reflected in the multilevel estimates of genetic and environmental components that indicated on average 31% nonshared environmental effects, 56% genetic variance, .0% shared nuclear family environmental effects, and 13% shared family environmental effects.

The estimates in Table 4 assumed that cousins were full cousins and therefore that the NLSY mothers were full sisters. A violation of this assumption would have resulted in underestimates of the correlations between cousins. This is because the genetic correlation between half cousins is .0625, whereas the genetic correlation between full cousins equals .125. However, because the contribution to a correlation equals the genetic correlation times the heritability, violation of this assumption can only have a very small effect on the correlation between cousins. For instance, even if we compare the two most extreme situations in which all cousins are full cousins versus all cousins are half cousins, a heritability of 56% would result in a difference between the correlations in these groups of only .035 ($= (.125 - .0625) * .56$). Furthermore, as an empirical check of this assumption, we also computed the cousin correlation in Table 4 by making a selection of mothers. For this purpose we used additional information that allowed us to select NLSY mothers who were very likely to be full sisters. Sisters who indicated that they lived with both biological parents in the same period during the first 13 years of their lives were considered to be full sisters. Similar to the assumption that was made to classify full siblings, this assumed that the mothers of the sisters did not live simultaneously with different fathers. The children of these (full) sisters were classified as full cousins. The correlation for this group, that very likely consisted completely of full cousins, was on average .31. This correlation was exactly equal to the average cousin correlation reported for the full group in Table 4, and suggested that our assumption that all cousins were full cousins may not have had an important impact on our results.

The correlations between within-pair absolute differences in total PIAT scores and the within pairs environmental means are shown in Table 5. Supplementary sample and Minority group are dichotomous variables. In this situation, correlations indicate whether the within-pair absolute differences for academic achievement are different in one group

Table 5. Pearson and Multiple Correlations between Average Environmental Score and Resemblance in PIAT Total score

PIAT Total score	<i>Full siblings</i>		<i>Half siblings</i>		<i>Cousins</i>	
	Pears.	Mult.	Pears.	Mult.	Pears.	Mult.
HOME-Total score	-.04	.04	.00	.01	-.04	.09
HOME-Cognitive stimulation	-.06	.06	-.03	.03	.00	.03
HOME-Emotional support	.00	.03	.02	.03	-.08	.11
Father figure absent	.01	.04	-.01	.02	-.08	.11
Changes in marital status mother	.02	.02	.07	.10	-.01	.05
Family poverty status	.02	.05	.02	.03	.02	.08
Highest grade completed mother	-.01	.03	.04	.08	-.04	.04
Highest grade completed father	-.02	.05	.02	.08	-.02	.07
Employment level father	-.01	.05	.06	.06	-.02	.04
Supplementary sample	-.02	-	.07	-	.01	-
Minority group	.00	-	-.06	-	.09	-

Note: The Pearson correlations indicate linear effects and the multiple correlations quadratic nonlinear effects. Correlations were based on 1664 pairs of full siblings, 366 pairs of half siblings, and 752 pairs of cousins. Due to nonresponse, analyses for Total score, Mathematics, Reading Recognition, and Reading Comprehension were respectively based on 98.9%, 100%, 98.9%, and 83.0% of the total sample

compared to the other. For dichotomous variables it does not make sense to examine quadratic nonlinear effects that require continuous ordinal information, and the corresponding cells are therefore empty in Table 5.

All correlations were (very) small. Unless the interaction involved nonshared environment or different components would mask each other's interactions, this suggested that genotype-environment interaction may not be very important. The increase from the Pearson correlations that examined linear effects to the multiple correlations that examined quadratic nonlinear effects was in most cases small (e.g. the average increase was .03). This small increase suggested that there was no clear evidence for quadratic nonlinear interaction effects. To check if the results were different for the PIAT subscales, we computed the same correlations for each subscale. However, results were very much the same as those presented for the PIAT Total score.

The chi-square difference tests, that were performed with genetic multilevel regression analyses, showed that 24% of the chi-square significance tests were significant at $p < .05$ and that 9% of the tests were significant at $p < .01$. This confirmed the conclusion derived from Table 5, and indicated that the vast majority of the tests showed no evidence of genotype-environment interactions. To examine the significant results more closely, we selected for each environmental variable on the basis of the smallest p -values the best fitting model. Results are shown in Table 6

To interpret Table 6 correctly, we would like to stress that we tested for both linear and nonlinear changes in the effects of the four components (E, A, N, and F) separately and all components simultaneously (E + A + N + F). With 10 tests for each scale the chance of obtaining at least one significant result for a scale is substantial, and we therefore used Table 6 only to detect general trends instead of interpreting all individual results. There

Table 6. Most Significant Results for Each Combination of Environmental Variable and PIAT Scales

	PIAT Total score		Mathematics		Reading Recognition		Reading Comprehension	
	Most sign. Compon.	type effect	Most sign. Compon.	type effect	Most sign. Compon.	type effect	Most sign. Compon.	type effect
HOME-Total score	E *	linear decr.	E *	nonlinear	E *	linear decr.	F	linear decr.
HOME-Cognitive stimulation	E *	linear decr.	E	linear decr.	E	linear decr.	-	-
HOME-Emotional support	All	linear decr.	-	-	E	linear decr.	F	linear decr.
Father figure absent	-	-	-	-	-	-	-	-
Changes in marital status	All	nonlinear	All	nonlinear	-	-	-	-
Family poverty status	E	linear incr.	-	-	-	-	E *	linear incr.
Highest grade completed mother	All *	linear decr.	-	-	All *	linear decr.	All *	linear decr.
Highest grade completed father	All *	linear decr.	-	-	A *	linear decr.	E	linear decr.
Employment level father	-	-	-	-	F	linear decr.	-	-
Supplementary sample	F	linear decr.	F *	linear decr.	-	-	-	-
Minority group	All	linear incr.	-	-	E *	linear incr.	A	linear incr.

Note: E is nonshared environment, A genetic influences, F shared family environment, All is all components, * is $p < .01$. Multilevel analyses involved 3266 children from 2000 fathers, 1692 mothers, and 1591 families. Due to nonresponse, analyses for Total score, Mathematics, Reading Recognition, and Reading Comprehension were respectively based on 98.9%, 100%, 98.9%, and 83.0% of the total sample

were three trends. First, the most significant results were either found for nonshared environmental effects (e.g. the HOME-SF scales) or the overall test that examined changes in all components simultaneously (e.g. Highest grade completed mother). These components did not only show more often significant results but were, with one exception, also the only components with p 's $<.01$. Second, the significant results seemed to indicate simple linear instead of nonlinear changes in variances. Third, except for Supplementary sample, variances decreased for variables of which high scores represented good environments and increased for variables of which high scores represented deprived environments. Thus, differences between children tended to be smaller in more favorable environments.

To give an impression of the magnitude of the effects, we discuss two examples. First, Table 6 shows that the overall variance of PIAT Total scores decreased linearly when Highest grade completed mother increased. To compute an index for the magnitude of this decrease we first computed the size of the 95% region for the lowest value (first grade) of Highest grade completed mother by subtracting the lower bound from the upper bound as depicted in Figure 1. Next, the size of the 95% region was computed for the highest value (eight grade college or more) of Highest grade completed mother. The ratio of the sizes of the most extreme 95% regions was .96. This indicated that even if the most extreme situations were contrasted, effect sizes were not large. The second example concerns Family poverty status that showed a linear increase in nonshared environmental variance for PIAT Total scores in children who grew up in more poverty. For the most extreme values of Family poverty status the ratio of the size of the 95% regions for the nonshared environment was 1.16. This indicated that the size of the 95% region for nonshared environment was 16% larger in children who lived in poverty their whole life compared to children who never lived in poverty. However, nonshared environment explains only part of the total variance, and the ratio of the sizes of the 95% regions for the total variance of 1.03 was therefore much smaller. A final way to interpret the increase in nonshared environmental effects is in terms of proportion explained variance. For children who never lived in poverty this proportion was 20% and for children who lived in poverty their whole life 25%. In sum, these calculations, that contrasted the most extreme situations, showed that the significant results that were found in our analyses were not very large.

DISCUSSION

In this article we examined whether genetic and environmental effects on academic achievement changed as a function of the quality of environment in which children grow up. Both simple descriptive indirect statistics as well as significance tests performed with multilevel regression analyses showed little evidence for genotype-environment interactions. There was only a slight trend consisting of a linear decrease of total variance or non-shared environmental effects from deprived to good environments.

Our study included a variety of observed measures, longitudinal data, and a relatively large number of children who grow up in deprived environments. Given that this design seemed to provide a suitable opportunity to study genotype-environment interaction, it was surprising to find so little evidence for it. To our knowledge there are no other papers that examined whether genetic and environmental effects depended on the quality of the environment. There are, however, a few papers that examined the more general hypothesis that genetic and shared environmental influences on IQ differ for children with different levels

of IQ. These studies show a slight tendency to result in nonsignificant findings (Cherny, Cardon, Fulker, & DeFries, 1992; Thompson, Detterman, & Plomin, 1993). Moreover, if significant interactions are found they seem to contradict each other. For example, Bailey and Revelle (1991) found evidence for higher heritability at the upper end, whereas Detterman, Thompson, and Plomin (1990) found evidence for higher heritability at the lower end of the IQ continuum. Thus, our results do not seem to be inconsistent with other genetic research that fails to identify consistent differences in genetic and environmental effects along the IQ continuum.²

At first sight our results do seem to contradict findings in nongenetic research showing an abundance of person-environment interactions in a variety of research areas (Rutter & Pickles, 1991). To understand this discrepancy it may be helpful to elucidate some typical features of situations in which these interactions are more commonly observed (McCall, 1991). With the possible exception of interactions associated with sex and age, many examples in literature involve *rare* genetic or environmental circumstances. A frequently mentioned example is Phenylketonuria (PKU). PKU is a metabolic disorder that gives rise to a mental handicap only when phenylalanine is present in the diet. The required genetic circumstance for PKU, however, is very rare (approximately 1 in 10,000 live births). Other examples of interactions sometimes also involve the timing of an event or sequence of events across time (Rutter & Pickles, 1991). This suggests another characteristic of situations in which interactions are more likely to occur. Because interactions often comprise unique combinations of person, environment, and timing, they usually apply only to a small proportion of individuals and may not have a noticeable impact on general population samples. A final point is that interactions sometimes involve "human intervention" such as experimental manipulation or treatment. In the PKU example, because phenylalanine is present in many foods under normal circumstances all children with the genetic defect will get PKU retardation unless they are given a special diet. If these typical characteristics are taken into account, the discrepancy between the abundance of person-environment interactions in nongenetic research and the lack of evidence in this study becomes understandable. Academic achievement is in general not determined by rare genetic or environmental conditions, we did not study very specific subgroups or individuals, and there were no interventions or special environmental manipulations.

A possible methodological explanation for the many nonsignificant findings could be a low power of our test so that very large genotype-environment interaction effects would have been necessary to obtain significant results. However, our calculations for the variable Family poverty status showed that we were able to detect that for children who never lived in poverty the proportion nonshared environmental variance was 20%, and that for children who lived in poverty during their whole life this percentage was 25%. In terms of phenotypic difference, this increase corresponded only with a 3% change in the size of the interval around the predicted score within which 95% of the children lie. We should also note that these changes pertained to the most extreme categories and that for all children with values in between, the numbers are smaller. These calculations suggest that the many nonsignificant genotype-environment interactions in our study cannot simply be explained by a lack of power. A second methodological explanation could be that our study did not include the relevant environmental variables. For instance, all our observed measures were "objective" measures whereas individual differences in the perception of the same environmental circumstances might be more relevant. Although we cannot exclude the possibility

that inclusion of other variables would have shown more evidence for genotype-environment interactions, the substantial correlations with children's academic achievements suggested that at least in terms of main effects our study comprised a set of relevant environmental measures.

Some caution is required to interpret the significant genotype-environment interactions we *did* find in this paper, that suggested a decrease of total variance or nonshared environmental effects from deprived to good environments. First, we found that 24% of our tests were significant at $p < .05$. Although this finding indicated that more than 5% of the tests were significant, it could still be a chance finding. The reason is that all tests were performed on the same data set with four correlated measures. The test results were therefore not independent of each other. For instance, if due to sample fluctuations the total variance was somewhat larger in good environments, this chance finding would increase the probability of finding a significant result on every test. Second, analytical strategies to detect genotype-environment interactions are usually very sensitive to floor and ceiling effects of the dependent variable. This is because these measurement artifacts can lead to a differential reduction of the (residual) variances across the continuum of the scale (Muthén, 1991; Van den Oord & Van der Ark, 1997). Because in good environments academic achievement scores were on average higher, our result indicating a decrease of total variance in good environments could be confounded with ceiling effects. An inspection of the distribution of the four PIAT scales showed that each scale was slightly skewed to the left (average skewness was $-.098$) which is the direction that would be expected if there were ceiling effects. Although the skewness was very small, the sensitivity of genetic studies for these measurement artifacts (Van den Oord & Rowe, 1997) suggests that ceiling effects could not be excluded as an explanation for the small decrease in total variance in good environment. Although ceiling effects may explain changes in total variances, it seems likely that its effects on the relative importance of genetic and environmental influences are generally less severe. Our trend that for some environmental variables nonshared environmental effects were larger in deprived environments could therefore imply that for instance children in low quality environments are more sensitive to accidental environmental hazards.

The tests that were performed in this article showed little evidence for genotype-environment interactions and if significant results were found the effects were, even if the most extreme environmental situations were contrasted, not large and could have been confounded by methodological factors. We would like to add that the trends that were found in this study were also different than predicted by existing theoretical ideas about the role of interaction processes in normal development. For instance, the model of Bronfenbrenner and Ceci (1994) predicts larger heritabilities in good environments whereas significant results in this article consisted of larger nonshared or overall variance in deprived environments.

In contrast to the negative results that we found with respect to genotype-environment interactions, many of the environmental variables that were studied in this article do seem to show evidence for genotype-environment correlations (Braungart et al., 1992; Cherny, 1994; Coon et al. 1990; Scarr & Weinberg, 1978). At a more theoretical level our results were therefore more consistent with the view that for normal development genotype-environment interactions may be less pervasive and important than genotype-environment correlations (Scarr, 1992). We should stress that our results do not exclude the possibility

that genetic or environmental variance may increase drastically at the extremes of the environmental continuum. The reason is that although disadvantaged environments were oversampled in our study, they could still not be extreme enough to detect genotype-environment interactions. The conclusion that for major characteristics such as IQ, genotype-environment correlations may be more important than genotype-environment interactions may also make evolutionary sense (see McCall, 1991). Genotype-environment correlations mean that individuals seek out or experience compatible and suitable environments, and it is therefore an adaptive mechanism. Genotype-environment interactions on the other hand more often consist of relatively rare combinations of person, environment, and time, and it seems more reasonable to suppose that nature would leave the regulation of important characteristics up to an adaptive mechanism instead of "chance" combinations.

APPENDIX

MLn script to decompose the total variance of PIAT scores into nonshared variance (level 1, idchild), 1/4th of the genetic variance (level 2, idfath), nuclear family variance (level 3, idmoth), and shared family variance (level 4, idfam):

```

logon = 1 piat.log
echo = 0
dinput c1-c5
c:\nlsy\piat.dat
echo = 1
name c1 'idchild' c2 'idfath' c3 'idmoth' c4 'idfam' c5 'piat'
calc c6 = 1+(c1-c1)
name c6 'cons'
iden 1 'idchild'
iden 2 'idfath'
iden 3 'idmoth'
iden 4 'idmoth'
expl 'cons'
RESP 'piat'
sete 1 'cons' 'cons'
sete 2 'cons' 'cons'
sete 3 'cons' 'cons'
sete 4 'cons' 'cons'
batch 1
maxi 40
start
pick 3 c96 b15
calc b16 = sqrt(2)*sqrt(b15)
calc b15 = sqrt(.5)*sqrt(b15)
aver 'idchild' count to b40
put b40 b15 c15
put b40 b16 c16
offs 1 c16
offs 3 c15

```

offs 4 c15
 next
 rand

NOTES

1. We would like to thank Min Yang of the Institute of Education, University of London for suggesting this MLn script to us.

2. To make a more direct comparison with our data, we computed correlations using the absolute differences between the PIAT Total scores of pairs and the average PIAT score of the pairs. These correlations were -.06 for full siblings, -.01 for half siblings, and -.12 for cousins. These negative correlations in all three groups suggested a trend of smaller genetic and environmental effects at the higher end of the IQ continuum. To test whether this trend was significant, the multilevel regression analyses in this article cannot be used (this is because the dependent and independent variable are both functions of PIAT scores and very highly correlated, so that regressing one on the other would explain all variance for at least one level making it useless to test for interaction effects at that level). We therefore used the extension discussed by Cherny et al. (1992) of the DF-method (DeFries & Fulker, 1985, 1988). Because this approach cannot deal with dependency in data caused by multiple children from the same family, we selected at random one pair of relatives per family. Results from these tests were nonsignificant.

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