The Aetiology of High Cognitive Ability in Early Childhood

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Both the environment and genetics are likely to influence the development of cognitive talent during the preschool years. It is not known to what degree or how these influences differ from those throughout the range of ability. 1943 twin pairs were assessed at 2, 3 and 4 years of age using diverse verbal and nonverbal cognitive measures. Consistently high scoring children were selected on a general cognitive factor. From behavioural genetic model fitting analyses, substantial shared environmental (70%) and modest genetic influences (20%) were found in the high group and this matched the aetiology of the entire sample. Strong genetic predisposition was not apparent. Individual differences in cognitive ability and high ability is largely due to shared environment during the preschool years.

Introduction

The role of nature and nurture in the aetiology of high ability has been widely discussed, particularly between the proponents and opponents of 'the talent account' (Howe et al., 1998, p. 399). Proponents refer to biological factors predisposing individuals to a potential for talent—a 'special biological potential' that can be identified in some children but not others (Howe et al., 1998, p. 399). Opponents of this view lay emphasis on skill acquisition through early exposure, practice, and other processes that appear to rely more on environmental factors.

Which of these views is most relevant to cognitive development in early childhood? The goal of the present study was to approach this issue from a behavioural genetic perspective, to investigate the genetic and environmental influences on high cognitive ability. Furthermore, it allows us to ask to what extent is the aetiology of high cognitive ability related to the aetiology of cognitive ability throughout the normal range. A 'special biological potential' for high ability would contribute to the portion of variation explained by genetic factors.

At the genetic level, a 'special biological potential' for extreme cognitive ability might be caused by specific patterns of genetic effect that are distinct from those causing the trait variation across the distribution. Superior talents have been ex-
plained by a process called emergenesis, which involves common genes acting configurally rather than additively (Lykken et al., 1992). The twin design provides a good empirical test because if genetic influences were emergenetic in nature, monozygotic (MZ) twins who share all their additive as well as non-additive genetic effects should be more than twice as similar on a measured trait as dizygotic (DZ) twins, who share on average 50% of their polymorphic genes but are much less similar with regard to specific gene configurations (Lykken, 1982). However, previous research has not investigated the possibility of these effects being evident in early childhood.

An alternative view hypothesises that high cognitive ability represents the high end of a continuous dimension of cognitive ability (Plomin & Price, 2003). From this perspective, high ability during the preschool years might be best explained as the high extreme of individual differences in precocity and maturation, with the same relative genetic and environmental influences as for the whole spectrum of variation. In molecular genetics the quantitative trait loci (QTL) perspective refers to the combined additive effect of a large number of genes contributing to complex traits, and thus creating a quantitative (continuous) trait (Plomin et al., 2001).

The twin method compares resemblance for MZ and DZ twin pairs. It has several underlying assumptions that have been widely discussed and tested (e.g. Scarr & Carter-Saltzman, 1979; Morris-Yates et al., 1990). It involves partitioning phenotypic variance into genetic, shared environmental, and nonshared environmental variance (Plomin et al., 2001). Shared environment represents the factors responsible for resemblance between family members, and nonshared environment represents the factors responsible for differences between family members. Heritability typically refers to the proportion of phenotypic differences among individuals that can be attributed to genetic differences in a particular population.

Throughout the whole range of cognitive ability, heritability is about 0.25 in early childhood (Spinath et al., 2003) and rises during adolescence to above 0.50 in adulthood (McGue et al., 1993). Shared environmental influence is substantial for the normal range in childhood (accounting for as much as 70% of the phenotypic variance when twins are studied) and by adolescence it decreases dramatically. The first family study addressing the etiology of high cognitive ability was published more than a century ago (Galton, 1869). However, there is still little known about the etiology of high cognitive ability in early childhood.

In the field of high ability research, cognitive skill has always been considered one of the major phenotypes of interest. The present study refers to general cognitive ability rather than intelligence, as the former refers specifically to what is in common among tests of diverse cognitive ability, whereas the latter can mean different things in different contexts (Plomin, 1999).

A standard method to estimate genetic influence for extreme groups is called DF extremes analysis (DeFries & Fulker, 1985, 1988). Using this method, two earlier twin studies investigated the link between the etiology of high cognitive ability and the etiology in the normal range in early childhood and concluded there was not any aetiological difference (Cherny et al., 1991; Petrill et al., 1998). However, both studies lacked power because their relatively small sample sizes (about 300 pairs)
meant that the number of high ability children within these samples was extremely small.

The present analyses capitalised on a large twin sample known as the Twins Early Development Study (TEDS; Trouton et al., 2003). Earlier reports from this study have investigated the aetiology of cognitive abilities in the normal range (Price et al., 2000; Spinath et al., 2003) and of cognitive disabilities (e.g. Dale et al., 1998).

It is noted that this study examined high cognitive ability and not other specific domains of talent such as music or mathematics, and it did not study exceptional children individually, for example those with rare savant skills. However a broad view of high ability in the population is equally useful in that it allows us to understand the general pattern of such development. Because the highest ability children were selected from the sample, this made the choice of cut-offs somewhat arbitrary and it was possible and instructive to compare several high group cut-offs.

Method

Participants

TEDS is a longitudinal population-based study of twins born in England and Wales between 1994 and 1996 (Trouton et al., 2003). A total of 16810 families were contacted, of whom 13428 (79.9%) agreed to participate. These families filled in an initial booklet, and then just before the twins’ second, third, and fourth birthdays questionnaire booklets were sent to them. Informed consent was obtained at each stage. Exclusions occurred for the following reasons: unascertained zygosity, severe medical, genetic or perinatal problems, incomplete booklets or booklets returned later than 6 months after the relevant birthday, and if English was not the first language spoken in the home. Physical similarity ratings by parents were used to determine zygosity, and this was validated with a sample of same-sex pairs by identification of polymorphic DNA markers — a method which assigns zygosity with more than 95% accuracy (Price et al., 2000).

The TEDS sample at 2 to 4 years is suitably representative in terms of education, parental ethnicity, and employment status, of the UK population of parents of young children (Trouton et al., 2003). This was ascertained by comparing the sample to age-weighted 1994 census data from the Office of National Statistics (ONS).

The sample after exclusions consisted of 1943 twin pairs with complete data at 2, 3 and 4 years: 657 MZ pairs, 648 DZ same-sex pairs, and 638 DZ opposite-sex pairs (DZOS). Equal numbers of the three types is an indication of representativeness, since selection effects in volunteer twin samples usually favour disproportionate numbers of MZ twins (Lykken, Tellegen, & DeRubeis, 1978).

Measures

Non-verbal performance. Age-appropriate versions of the Parent Report of Children’s Abilities (PARCA) were used for assessing non-verbal cognitive performance. The PARCA is an hour-long test developed from several standard measures (e.g. McCarthy Scales of Children’s Abilities; McCarthy, 1972; the Bayley Scales of
Infant Development; Bayley, 1993), and other novel items designed specifically for the PARCA.

In the first section, parents administered to their children a battery of standard cognitive tasks. At 2 years this consisted of block building, drawing designs, design copying, matching, and paper-folding tasks. In the second section, parents reported on the ability of their children to perform specific cognitive tasks (e.g. 'Does your child recognise himself/herself when looking in the mirror?'). Age-appropriate versions of the 2-year PARCA were used at ages 3 and 4.

Good internal consistency and validity of these measures have been shown. Both sections of the PARCA showed internal consistencies of 0.67 or higher at ages 2 and 3. The 2-year PARCA showed a multiple correlation of 0.55 when compared with the Mental Development Index (MDI) of the Bayley Scales of Infant Development-II (BSID-II; Bayley, 1993) (Saudino et al., 1998). The 3-year PARCA correlated 0.54 with a non-verbal composite from the McCarthy Scales of Children's Abilities (McCarthy, 1972) (Oliver et al., 2002). Analyses are in progress for the 4-year extension of the PARCA validation. The reported results are consistent with a meta-analysis supporting the validity of parent-based measures (Dinnebeil & Rule, 1994).

Verbal performance. The MacArthur Communicative Development Inventory: UK Short Form (MCDI:UKSF) was used to assess vocabulary production and grammar. This is an abbreviated and anglicised adaptation of the widely used MacArthur Communicative Development Inventory (MCDI) (Dale et al., 1998).

Vocabulary production was measured in the MCDI:UKSF by means of a 100-item checklist asking parents to report on their children's production of root words (e.g. dog, game, gentle). A composite score was calculated by summing the number of words checked. The 2-year measure predicted the 680-word original MCDI with very high accuracy ($r = 0.98$) (Fenson et al., 2000). The 3- and 4-year measures were similar and were taken from an upward extension of the MCDI, consisting of 100 and 48 items, respectively.

Grammar was assessed by asking parents about their children's sentence complexity. At 2 and 3 years an initial question asked whether the child was able to combine words, and then the parent indicated in the next 12 items which of two sentences carrying the same meaning most resembled what their child was able to say. The first represented a developmentally simpler form, e.g. 'I want truck', and the second a more advanced form, e.g. 'I want truck like Billy has'. At age 4, parents described the way their child talked using one of six categories, from 'not yet talking' through to 'talking in long and complicated sentences'.

The test–retest reliability, internal consistency, and concurrent validity with tester-administered measures have been described elsewhere for the MCDI:UKSF (Fenson et al., 2000). It has been found to offer a valid and cost-effective measure of early linguistic development that is suitable for use with UK samples.

Analysis

The two nonverbal total scores (parent-administered PARCA and parent-reported PARCA tests) and the two verbal total scores (expressive vocabulary and expressive
grammar measures) were submitted to principal component analyses separately at each age. These factor analyses indicated the appropriateness of a single component to describe over 50% of the variance in the measures (Spinath et al., 2003). Finally, the standardised factor scores from each age were combined into an average score across the three ages.

This standardised average factor score was the basis for the selection of high scoring children across all three years. Four high group cut-offs were used: above 2.5%, above 5%, above 10%, and above 15% of the distribution. A dichotomous distinction was made between individuals in the selected extreme groups, called the probands, and those not in this group. The ratio of the number of probands in concordant pairs to the total number of probands, called the probandwise concordance, was calculated for each cut-off. Probandwise concordances based on categorical data lose information about the quantitative trait scores but are a commonly used preliminary index. More sophisticated genetic analyses described next used the quantitative trait scores.

In accordance with standard behavioural genetics procedure, the cognitive ability scores were age- and sex-corrected and standardised residuals were used in the following analyses (Eaves et al., 1989).

For analyses on the whole sample, twin similarity coefficients [intraclass correlations (ICC 1.1); Shrout & Fleiss, 1979] were calculated for the total group of male and female MZ and DZ same-sex twin pairs as well as DZOS twin pairs. Parameter estimates were obtained from univariate ACE model-fitting (Neale & Cardon, 1992). This apportions the phenotypic variance into the three components, additive genetic (A), shared environmental (C), and nonshared environmental (E) factors, assuming no effects of non-additive genetics, nonrandom mating, or gene–environment interaction. These were similar analyses to those published by Spinath et al. (2003), which found the heritability of general cognitive ability to be 0.23 at age 2, 0.30 at age 3, and 0.24 at age 4. Our results across the whole range of abilities were to some extent a replication of these, but used an aggregate of the factor scores from the three ages. A second analysis included DZOS pairs, and used a sex-limitation model (Neale & Cardon, 1992), as well as nested submodels.

For the analyses on the high extreme, group heritability for same-sex twin pairs was estimated by means of DF extremes analysis (DeFries & Fulker, 1985, 1988). This is a regression-based approach that uses quantitative scores to assess family resemblance on a measured continuous trait for a selected group. It focuses on mean differences of the quantitative trait scores between the probands compared to their co-twins, and the unselected sample (see Figure 1). The critical question concerns the mean scores of the probands' cotwins, for MZ and DZ twin pairs separately. If there is genetic influence on the quantitative trait at the extreme, we expect the MZ co-twin mean score to regress less towards the population mean score than the DZ co-twin mean score. That is, the MZ co-twin mean score should be more similar to the proband mean than the DZ co-twin mean. The extent to which genetic factors account for the mean difference between probands and the population is called group heritability. Group common environment refers to the extent to which the
Table 1. Twin transformed cotwin means for each high ability group and twin similarity coefficients (ICC1.1) for the total unselected sample

<table>
<thead>
<tr>
<th>Sample</th>
<th>MZM</th>
<th>DZM</th>
<th>MZF</th>
<th>DZF</th>
<th>DZOS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Top 2.5% group</td>
<td>0.88</td>
<td>0.81</td>
<td>0.97</td>
<td>0.89</td>
<td>0.92</td>
</tr>
<tr>
<td>Top 5% group</td>
<td>0.92</td>
<td>0.80</td>
<td>0.94</td>
<td>0.92</td>
<td>0.90</td>
</tr>
<tr>
<td>Top 10% group</td>
<td>0.95</td>
<td>0.87</td>
<td>0.95</td>
<td>0.87</td>
<td>0.83</td>
</tr>
<tr>
<td>Top 15% group</td>
<td>0.96</td>
<td>0.87</td>
<td>0.97</td>
<td>0.91</td>
<td>0.87</td>
</tr>
<tr>
<td>Total sample</td>
<td>0.96</td>
<td>0.83</td>
<td>0.95</td>
<td>0.85</td>
<td>0.81</td>
</tr>
</tbody>
</table>

Note: All similarity coefficients are based on age- and sex corrected scores. MZM = MZ male pairs, MZF = MZ female pairs, DZM = DZ male pairs, DZF = DZ female pairs, DZOS = opposite-sex DZ pairs.

Figure 1. To illustrate DF analysis, hypothetical mean scores of monozygotic co-twins of probands (C_MZ, —), same-sex dizygotic co-twins (C_DZS, —), and opposite-sex dizygotic co-twins (C_DZO, —) in the quantitative trait distribution are shown, with the population mean (μ) standardised to 0 and the proband mean (P) standardised to 1. The proband group is represented as the shaded area.

mean difference between the extreme group and the unselected population is due to shared environmental factors.

A second extremes analysis employed a model-fitting implementation of DF that allows the inclusion of DZOS pairs (Purcell & Sham, 2003). Parameters and their 95% confidence intervals were estimated by fitting the models to variance/covariance matrices using Mx (Neale, 1997). From these analyses transformed cotwin means can be derived. These are calculated by dividing the quantitative trait scores of the cotwins by the proband mean specific to each sex and zygosity group which can be interpreted as group correlations (DeFries & Fulker, 1985).
Results

The high cognitive ability proband groups showed a representative proportion of MZ, DZ and DZOS twin pairs at all cut-offs used. An excess of girls in all the high groups was noted, with the average ratio of girls to boys in the proband groups being 62:38, whereas it was practically even (52:48) in the whole sample.

Probandwise concordances at each threshold are shown in Figure 2, along with the individual differences intraclass correlations. These are presented separately for MZ, DZ same-sex and DZOS twin groups, in order to facilitate inferring the genetic and environmental influences on the trait. Slightly higher MZ compared to DZ and DZOS concordances across all cut-offs suggested modest genetic influence on high cognitive ability, whereas shared environmental influences were also indicated because DZ twin concordance exceed half the MZ concordance. The rightmost column shows that a similar pattern as the one found for concordances was obtained for the intraclass correlations in the full sample. The larger difference between MZ and DZ same-sex concordances at the 2.5% cut-off was viewed with caution due to the small number of probands in each zygosity group here.

The transformed cotwin means (group correlations) for each sex-zygosity group in the four high cut-off groups were calculated, together with the twin correlations for the entire sample, as shown in Table 1. Similar to the results for twin concordances,
the higher MZ than DZ transformed cotwin means were interpretable as indications of modest genetic influence on the high groups.

Figure 3 presents the genetic and environmental estimates from DF extremes analyses and from the individual differences analyses. Figure 4 shows the results from the second analyses that included DZOS. Across all thresholds, group heritabilities were very close to or lower than the heritability estimates for the whole sample (0.21 and 0.24 in Figures 3 and 4, respectively). Group heritabilities for the various cut-offs in Figures 3 and 4 ranged from 0.09 to 0.20. Group shared environmental estimates ranged from 0.75 to 0.84. It was noted that the 5% group heritability was lower compared to the estimates at other cut-offs in Figure 3, and the 2.5% and 5% cut-off group heritabilities were lower compared to the estimates at other cut-offs in Figure 4.

Discussion

To summarise, over 70% of the mean difference between the high scoring group and the whole sample was explained by shared environmental influences. Only a fifth of the mean difference was due to genetic factors. These results lend support to the argument that early ‘talents’ as discussed by Howe et al. (1998, p. 399) are driven
by shared environmental factors in the cognitive domain. These are influences that make children growing up in the same family similar. Potential candidates for such influences may include exposure to stimulating environments, parental support and encouragement, and early education.

In terms of genetic influence, this study suggests that high cognitive ability is the quantitative extreme of the same genetic factors that operate throughout the distribution. It does not provide support for theories suggesting that high cognitive ability in early childhood is uniquely influenced by rare genes of major effect or strong emergenic effects. The ‘special biological potential’ was not evident in the investigated sample assessed during the preschool years.

Our results appeared robust in several ways. First, the general pattern was highly comparable when two different regression methods were used. Furthermore, across four high group cut-offs we found a fairly consistent aetiological pattern. Proband-wise concordances, based on a categorical approach to the data, demonstrated a similar pattern to the twin correlations and quantitative genetic results. Taking an aggregate of the assessments from across three timepoints improved reliability because it meant that being selected in the high group reflected a stable tendency to
score high for the duration of the preschool years compared to the other children in the sample. Finally, this study is strengthened by the diverse cognitive tests designed to capture both language-based and nonverbal cognitive development, that together make up a strong general cognitive ability measure (Spinath et al., 2003).

Possible limitations of our study include the following: first, this study only investigated the preschool age group, when shared environment is known to be important for individual differences in cognitive ability. Second, the cognitive measures used were designed to assess cognitive ability across the whole range, not to differentiate among highly gifted children. At the same time, this procedure allowed high ability to be investigated in the context of normal development. All the measures showed a normal distribution, without ceiling effects or significant skew (Spinath et al., 2003) and the TEDS sample is representative of the general population.

Turning to environmental influences, all the estimates of shared environment were high. It cannot be ruled out that part of this result reflected method or design variance because we involved parents in the assessment process, and because we used a twin sample. Although it is reasonable to suggest that parent-administered measures might have led to inflated estimates of shared environment, nearly identical results were reported in another twin study in the normal range that used traditional measures administered in the laboratory by testers (Wilson, 1983).

In order to test for effects specific to the twin design TEDS obtained data on younger siblings of the twins. An initial analysis comparing DZ twins and twin-sibling pairs indicated that about half of the estimate of shared environment was specific to twins. This is likely to be due to prenatal or postnatal effects brought about by being exactly the same age (Koeppen-Schomerus et al., 2002). Interestingly the remaining shared environmental influence was still substantial in early childhood.

The larger proportion of girls in the high cognitive group was an interesting and unexpected finding. It is usually reported that males show more variance than females, and that groups of high and low scoring individuals on cognitive trait scores tend to have a majority of males (Hedges & Nowell, 1995). One possible explanation is that females mature slightly faster than males in early childhood with regard to cognitive development.

To conclude, this study investigated the aetiology of high ability in the cognitive domain in preschool children. The influence of shared environment was shown to be considerable. There was only modest genetic influence on the difference between the high group and the whole sample. Future studies could investigate in more detail specific sources of environmental influence on high cognitive ability in early childhood. The aetiology of other high ability domains, such as musical ability, could also be studied. Would other domains of talent show comparable aetiologies to the whole spectrum of ability in the preschool years? Perhaps some would appear qualitatively different, suggesting the existence of an early 'special biological potential' in those domains.

Finally, future studies could investigate the aetiology of cognitive talent in later childhood, when complex cognitive processes are developing such as reading and
conceptual understanding, and children enter formal education. Will an aetiological
distinction between the high ability group and the normal distribution emerge later
in development when different genes come into play? The TEDS sample is currently
being assessed at 7 and 9 years to address these issues. In terms of the aetiology of
talent, we predict that during development genetic influence increases, and shared
environment becomes less important.

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