



# Increased environmental sensitivity in high mathematics performance



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## ABSTRACT

Results of international comparisons of students in studies such as PISA (*Program for International Student Assessment*) and TIMSS (*Trends in International Mathematics and Science Study*) are often taken to indicate that mathematical education in Dutch schools is not appropriate for mathematically talented students. However, there has been no empirical study yet that investigated this hypothesis. If indeed, Dutch students with a genetic predisposition for high mathematical ability are not nurtured to their full potential, their mathematics performance should be more affected by environmental factors than that of children with a genetic predisposition for low mathematical ability. In behaviour genetics such a situation is termed *genotype-environment interaction*: the relative importance of environmental influences differs depending on students' genotypic values. To investigate genotype-environment interaction, we analyzed mathematics performance of 2110 Dutch twin pairs on a national achievement test. In the analysis we corrected for error variance heterogeneity in the measurement of mathematics performance through the application of an item response theory (IRT) measurement model. As hypothesized, results indicated that environmental influences are relatively more important in explaining individual differences in students with a genetic predisposition for high mathematical ability.

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## 1. Introduction

While some children find it easy to solve complex mathematical equations, others are struggling to pass their math exams. Dutch teachers usually focus on the latter group: the weakest (Dekker, 2014). Often criticized as a “culture of C-grades”, education in the Netherlands has the reputation of being traditionally less focused on students with high mathematics performance levels. In an ideal school system, however, the talented child should be nurtured to its full potential as well. After all, the brightest students may be the ones who make important contributions to science, find cures for diseases or invent new technologies.

International comparisons such as the Program for International Students Achievement (PISA) and the Trends in International Mathematics and Science Study (TIMSS) show that, in the Netherlands, the average mathematical performance level in primary education is relatively high. This observation can, however, be attributed mainly to the high performance in the left tail of the achievement distribution: the weakest students are performing better than the weakest students from all other countries participating in PISA and TIMSS. The variance of test scores is, however, compared to other countries, very small: the performance levels of lowest- and highest-scoring students are relatively close. In

other words, whereas Netherlands' weakest students perform exceptionally well, the top students are outperformed by the brightest students from Asian and other western countries (see e.g. Meelissen et al., 2012). This appears to be a persistent phenomenon as similar patterns have been found over the years for different age groups (see e.g. Minne, Rensman, Vroomen, & Webbink, 2007). These findings are often presented as underperformance in the high-ability students (see e.g. van der Steeg, Vermeer, & Lanser, 2011) and interpreted as an indication that mathematical education in Dutch schools is better tailored to the weaker students than to the mathematically talented students. However, one cannot draw conclusions on underlying processes based on the test score distribution alone. There are alternative explanations for the relatively poor performance of the top students in the Netherlands, for one that there might indeed be different underlying distributions of talent across countries.

In this article, the underperformance of Dutch mathematically talented students was investigated from a behaviour genetics perspective. A child's genetic mathematical talent was operationalized as the *genotypic value*, a genetic concept representing the sum of the average effects of genes that influence mathematical achievement (Falconer & MacKay, 1995). If the education were ideal for every child (with or without genetic mathematical talent), this would predict that individual differences in scores are mainly explained by genetic differences rather than environmental influences (see Shakeshaft et al., 2013 for a similar argument). That is, differences in children's mathematics performance

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can be explained solely by their different genetic talents and not by random environmental influences such as what friends or teachers they have. This line of reasoning would also imply that, if indeed, in primary education, mathematically talented children are not nurtured to their full potential, their performance should be more affected by random situational factors than the performance of average or weak students for whom the educational program is more appropriate, that is, better tailored to their personal needs. For example, talented students might be at the mercy of random events like having a teacher that is interested in their abilities or a neighbour that is willing and able to help with the more challenging homework assignments. Such a situation induces the presence of *genotype-environment interaction*: conditional on a child's *genotypic value* for mathematical ability, environmental influences can be more or less important (see e.g. Cameron, 1993), or put differently, environmental factors create more variance in test scores of the talented than the less talented children.

One of the methods used in behaviour genetics to estimate the relative influence of genetic and environmental factors is the twin design. Twin pairs are either identical (monozygotic, MZ) or non-identical (dizygotic, DZ). MZ twins (largely) share the same genomic sequence and the same rearing environment, including prenatal environmental conditions. DZ twins also share the same environment but on average only share half of the segregating genes. By using the twin design, the relative contributions of genetic and environmental variability can be estimated, where the heritability is defined as the ratio of genetic variance divided by total variance in a measured trait (phenotypic variance).

Although a considerable number of twin studies have studied the heritability of mathematical ability (see e.g. Alarcon, Knopik & DeFries, 2000; de Zeeuw, de Geus, & Boomsma, 2015), to our knowledge, there is only one twin study that compared the relative contributions of genetic and environmental influences in mathematically high-scoring children and children in the normal range. In a population-based sample of 10-year-old British twins, Petrill, Kovas, Hart, Thompson, and Plomin (2009) defined mathematically high-scoring twins as those who scored at or above the 85th percentile. In the top 15% of students, the heritability estimate was similar to the one obtained across the normal range of ability. Similar results were reported for high cognitive performance and high reading performance (e.g. Boada et al., 2002; Petrill et al., 1998; Ronald, Spinath, & Plomin, 2002), traits that are correlated with mathematical ability (e.g. Davis, Haworth, & Plomin, 2009). These findings seem to argue against the presence of a genotype-environment interaction, at least in the populations studied. If there were indeed genotype-environment interaction, studies focusing on the high extreme of mathematical ability should reveal that environmental influences differ in importance compared to the normal range of ability.

Although the comparison of heritability across high and normal performing twins provides a simple test for a different etiology of extreme performance scores, it does not provide information on heritability along the entire performance continuum (see also Boada et al., 2002). In addition, an often arbitrary cutoff point has to be chosen. Most importantly, comparing the heritability in two separate ranges of ability can be misleading when one does not take into account differences in measurement reliability (van den Berg, Glas, & Boomsma, 2007).

Therefore, instead, here we estimate genotype-environment interaction continuously, letting the size of environmental variance components vary as a function of the genotypic value (see below for details). Thus, rather than studying subgroups, we take advantage of the continuous nature of the scores on mathematical performance. In this approach, we also would like to correct for the increased measurement error in the upper tail of the test score distribution. While most achievement tests show little measurement error for average scores, scoring can become very unreliable for high performing students due to the small amount of information provided by only a few very difficult items, a problem that finds its most extreme form in ceiling effects. In

other words: measurement error is not the same across the ability continuum (heterogeneity). The relative lack of reliability in the upper and lower tails leads to lower correlations among sum scores (attenuation), which leads to bias when estimating genetic and environmental variance components (see van den Berg et al., 2007) and furthermore can lead to the finding of spurious genotype-environment interaction effects or missing them altogether (see Molenaar & Dolan, 2014; Schwabe & van den Berg, 2014). The problem of heterogeneous measurement error can be solved by, instead of focusing on observed test scores, modelling latent variables, and using measurement models (van den Berg et al., 2007). We model genotype-environment interaction continuously, by applying a recently developed method (Molenaar & Dolan, 2014; Schwabe & van den Berg, 2014) that corrects for measurement error through the application of an item response theory (IRT) measurement model. By incorporating an IRT model into the analysis, the results regarding genotype-environment interaction presented here are free of artefacts due to heterogeneous measurement error across the performance continuum. The method was applied to data from 2110 12-year-old Dutch twin pairs on the *Eindtoets Basisonderwijs* test, a Dutch national educational achievement test that assesses what a child has learned during primary education. If the primary educational system in the Netherlands really is better suited for students without much genetic talent (i.e. low genotypic value) for mathematics than for talented students (i.e. high genotypic value), results should show more environmental variation in children genetically predisposed towards high mathematical ability than for children genetically predisposed towards low mathematical ability.

## 2. Method

### 2.1. Data

The sample of twins for this study comes from the Netherlands Twin Register (NTR, Boomsma et al., 2002). Data on the *Eindtoets Basisonderwijs* test of 12-year-old twins from birth cohorts 1998–2000 were analyzed to study genotype-environment interaction in mathematical achievement on the *Eindtoets Basisonderwijs* test. Conducted and analyzed by the testing company Cito, this test consists of 290 multiple choice items in four different subjects (language, arithmetic/mathematics, study skills and world orientation [optional]). For this paper, the 60 dichotomous item scores (coded as 0 = incorrect, 1 = correct) of the mathematics subscale of this test were analyzed. The methods used in this study required item data, whereas at the NTR only total test scores were available. The NTR data on twins for whom signed informed consent forms for database linking were available were therefore linked to item data available at Cito. This was done by an ICT employee at Cito who was not involved in the study. Linking was based on name, sex, birth year, name of the school, and total Cito score, if available, for 7031 twins. The first step was to link the NTR data to a BRIN code, a 6-digit number that is given to educational institutes by the Dutch ministry. Then 12 different queries with a different combination of the BRIN code, birth year, sex, surname and initials of a twin were used to identify the item data associated with an individual. 1017 twins had more than one unique match and 2427 twins could not be matched at all, reducing the dataset to 3587 twins consisting of 2149 families. To link twins with item scores to the NTR data of their co-twin, a unique family ID was used. Excluding triplets ( $N = 63$  individuals), this led to a dataset of 4238 twins (2119 twin pairs). Twin pairs with unknown zygosity ( $N$  pairs = 9) were excluded from the analysis, leading to a total of 4220 twins, forming 581 MZ pairs and 1529 DZ pairs. Of the monozygotic twins, 282 pairs were male and 299 were female; of the dizygotic twins, 360 pairs were male, 309 were female, and 860 were of opposite sex. For 711 twins, item scores were unknown. Scores were missing either because the child had not reached final grade yet ( $N$  twins = 52), the child was attending special education ( $N$  twins = 34), a different test was used at the school the twin was attending ( $N$

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