



The nature-nurture of academic achievement at the intersection between gender, family background, and school context

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ABSTRACT

We investigate the role of gender, family SES, school SES, and their intersection in educational achievement using a twin design. Drawing on theories of gene-environment interaction, we test whether high-SES environments compensate genetic risks or enhance genetic potential, and its dependency on gender. Using data on 37,000 Danish twin and sibling pairs from population-wide administrative registers, we report three main findings. First, for family SES, but not for school SES, we find that genetic influences play a slightly smaller role in high-SES environments. Second, this relationship is moderated by child gender: in high-SES families, the genetic influence is considerably lower for boys than for girls. Third, the moderating effect of family SES for boys is almost entirely driven by children attending low-SES schools. Our findings thus point to significant heterogeneity in gene-environment interactions, highlighting the importance of considering the multiplicity of social contexts.

1. Introduction

Academic achievement has consequences for economic, social, and health outcomes. Therefore, ample research has focused on the question of why some students perform better than others. Children differ from one another in many different ways, including their gender, the family they are raised in, and the school they attend. An additional source of individual differences that received less attention in the sociological literature is genetic influences. Twin studies show that differences in children's educational performance can also be explained by genetic differences between them (e.g., [de Zeeuw et al., 2015](#)). However, genetic influences do not operate in a vacuum but are influenced by broader environments, including historical contexts, institutions, and local communities ([Elder and Shanahan, 2006](#); [Herd et al., 2019](#)). Therefore, the extent to which genes play a role in academic achievement can be expected to depend on key socializing contexts in children's lives, including their family and school environment.

There are competing expectations on how genes and environmental contexts interact in shaping children's academic achievement. On the one hand, genetic influences may be larger in more advantageous environments. According to the bioecological model, genetic potential is enhanced in more stable and resourceful environments, such as provided by high-SES families ([Bronfenbrenner, 1992](#); [Rowe et al., 1999](#); [Scarr-Salapatek, 1971](#)). On the other hand, genetic influences may be smaller in such advantageous environments. This pattern follows from the diathesis-stress model that states that the realization of genetic risks is less likely to be encouraged if levels of environmental risks and stressors are lower ([Rende and Plomin, 1992](#)), but also from the idea that an advantageous

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environment may compensate for negative endowments (Bernardi, 2014; Shanahan and Hofer, 2005).

Twin studies provide a way to investigate gene-environment interactions in children's educational outcomes. Previous research has examined interactions in educational outcomes with family SES (Baier et al., 2022; Baier and Lang, 2019; Figlio et al., 2017; Tucker-Drob and Bates, 2016) and, to a lesser degree, the school environment (Hart et al., 2013; Haughbrook et al., 2017; Taylor et al., 2010, 2020). Yet, so far family and school environments have been studied as independent contexts. Moreover, gender differences in these gene-environment interactions have not been examined. Research suggests that boys' academic outcomes are more strongly affected by environmental factors than girls', as the gender gap appears to be larger in disadvantaged families and schools (e.g., Autor et al., 2019; Legewie and DiPrete, 2012). For example, boys may be more sensitive to school contexts, whereas the achievement of girls is less responsive to the extent to which the school environment is learning-oriented, disruptive, or disorganized (Legewie and DiPrete, 2012; Van Hek et al., 2017). Therefore, if the family and school environment moderate genetic and environmental influences, this moderation could be more pronounced among boys than girls. Providing insight into this is of interest to both researchers and policymakers in light of the reversal of the gender gap in education (Buchmann and DiPrete, 2006) and the emergence of a public discourse dictating that boys suffer from a "feminine" culture in primary schools (Epstein et al., 1998; Sommers, 2000).

In this paper, we examine gene-environment interactions across family and school environments and investigate whether these interactions differ by gender. Thus we effectively study the genetic influence on achievement at the intersection between gender, family background, and school context. By considering the multiplicity of contexts, we advance existing research in this area, which examines families and schools as separate environments, thus potentially neglecting that individuals are simultaneously embedded in both family and school environments. Adding gender as an extra layer to the interaction allows us to examine whether these interactions play out differently for boys and girls.

We analyze high-quality data on about 37,000 Danish twin and sibling pairs from population-wide administrative registers. These registers comprise information on children's compulsory school grade-point-average (GPA), their parents' socioeconomic standing, the schools they attend, and child's gender. One significant advantage of our register data is that they provide us with many cases, yielding sufficient statistical power to detect the different interactions, something that is not possible in relatively small twin samples. However, our data do not comprise information on zygosity. Therefore, we rely on the comparison of same-sex twins and siblings. We follow previous studies and estimate the genetic relatedness of same-sex twins (e.g., Figlio et al., 2017; Rodgers et al., 1994). By comparing same-sex twins with an assumed average genetic relatedness of 75%, with same-sex siblings who share 50% of their genetic makeup, we decompose the variance in GPA into genetic variance (A), shared environmental variance (C), and non-shared environmental variance (E). We subsequently break down these components by groups defined by family SES, school SES, and gender.

We report three main findings. First, the genetic influences are moderated by family, but not school, SES. Although genetic influences play a relatively large role in both low-SES and high-SES families, they play a slightly larger role in the former. Second, this relationship is moderated by child gender. In high-SES families, the genetic influence is considerably lower for boys than for girls, while in low-SES families it is the same for both genders. Third, the moderating effect of family SES for boys is almost entirely driven by children attending low-SES schools. Genetic influences play a much smaller role among high-SES boys who attend low-SES schools (and common environmental influences play a comparably larger role for this group of children). We discuss how these findings can be interpreted in light of existing theoretical models and empirical evidence.

2. Theoretical background

2.1. Gene-environment interactions in educational performance

Today scholars realize that genetic and environmental influences are not additive but interdependent explanations for educational performance (Conley and Fletcher, 2017; Freese, 2008). This interdependency is apparent in gene-environment interactions; that is, when environmental characteristics moderate genetic influences (Shanahan and Hofer, 2005). Theories on how genes and the environment interact are dominated by two competing interaction patterns (Asbury et al., 2005). On the one hand, a social context could *enhance* the actualization of genetic endowment for education (Shanahan and Hofer, 2005). Such an interaction pattern can be derived from the bioecological model (Bronfenbrenner, 1992; Bronfenbrenner and Ceci, 1994), which poses that enriched environments exacerbate the influence of genetic potential. Enriched environments have higher levels of positive proximal processes (i.e., enduring forms of interaction characterized by increasing complexity) that promote the actualization of genetic potential. Simultaneously, these environments are also thought to buffer against environmental differences in developmental outcomes. Under this model, more advantageous environments will therefore increase genetic variance and decrease shared environmental variance.

On the other hand, a social context could *compensate* for genetic vulnerabilities in educational performance (Shanahan and Hofer, 2005). The diathesis-stress model states that the realization of a diathesis (i.e., a genetic vulnerability) is more likely when the level of environmental risks and stressors is higher (Paris, 1999; Rende and Plomin, 1992). The absence of these stressors and/or the presence of positive features in the environment can neutralize or compensate the realization of genetic vulnerability. This model implies an interaction pattern in opposite direction from the bioecological model, namely less genetic variance in advantageous environments. Although the diathesis-stress model has mostly been applied to psychopathological outcomes such as depression and ADHD, it can also be considered for "positive" developmental outcomes such as cognitive ability and educational performance. For example, a child with genetic risks for poor reading may become a good reader because of a favorable literacy environment (Pennington et al., 2009).

2.2. Family background and school SES

2.2.1. Gene-SES enhancement interaction

When investigating gene-environment interactions in cognitive and educational outcomes, studies often examine the family SES environment as an enhancing social context (Hart et al., 2013). The bioecological model predicts that genetic potential for educational outcomes is more fully realized in high-SES families, while in low-SES families the importance of shared environmental influences is larger (Bronfenbrenner and Ceci, 1994; Scarr-Salapatek, 1971).¹ In high-SES families, the home environment is not only more resourced and stable but also thought to be more adapted to children's genetic potential. High-SES parents' parenting style is more active, and focused on planned interactions and cognitively and emotionally stimulating activities with their children (Lareau, 2003). This implies that high-SES parents actively foster children's specific talents (Baier and Lang, 2019).

Apart from family SES, the type of school in terms of SES composition that children attend can also be expected to play a role in the gene-environment interplay. School SES could have an effect beyond the family, as it relates to peer group influences, the quantity and quality of resources and teachers, and organizational and management processes within the school, amongst others (Caldas and Bankston, 1997; Sykes and Kuyper, 2013). Low-SES schools are characterized by more instability and disorganization than high-SES schools. For example, students in low-SES schools may experience higher levels of classroom disorder (Van Hek et al., 2017) and teacher shortage and turnover (Ingersoll, 2001). If we follow the bioecological model, such unstable and less resourceful environments reduce the extent to which genetic potential is realized because in such environments proximal processes are less powerful in enhancing children's potential for greater academic achievement (Bronfenbrenner and Ceci, 1994). High-SES schools, on the other hand, may provide a more stable and resourceful environment with teacher-child interactions that are more responsive to children's potential. A high SES composition is also positively associated with school characteristics that contribute to better learning outcomes such as teacher quality, school resources, peer group processes, and academic culture (Rumberger and Palardy, 2005; Sykes and Kuyper, 2013). Therefore, it can be expected that in high-SES schools children's specific talents are more easily discovered (e.g., via more experienced teachers) and that these schools are better equipped to further develop children's talents (via, e.g., the availability of challenging materials or high-achievement norms). This pattern may be less prevalent in low-SES schools, and thus genetic potential may more often be left unrealized in these schools.

2.2.2. Gene-SES compensation interaction

In contrast to the interaction pattern of enhancement, a compensation interaction implies that genetic variance is *lower* in high-SES contexts. Under the diathesis-stress model, genetic differences associated with negative outcomes are more likely to be realized when the level of environmental risks and stressors is high (Rende and Plomin, 1992). Such risks and stressors more often appear in low-SES families, which more often are single-parent families, have financial problems, experience stress, and are characterized by home disorganization and unpredictability (Bradley and Corwyn, 2002; Dumas et al., 2005). Many of the characteristics that pertain to low-SES families also pertain to low-SES schools in that they have more environmental risk factors. As mentioned earlier, these schools are more often unstable and disorganized than high-SES schools. In high-SES schools, genetic variance in educational performance can be expected to be lower, simply because risk factors and stressors appear less often, discouraging the realization of genetic risks.

Moreover, in addition to fewer risk factors, high-SES environments are characterized by more protective factors. The protective factors in high-SES families and schools may neutralize or compensate against low genetic endowment (or negative genetic risk) for educational performance. For example, in supportive educational environments at home or in school, children with reading disabilities receive adequate support, and the negative consequences of genetic susceptibilities for reading disabilities can be avoided (Friend et al., 2008). This idea is consistent with the notion of compensatory advantage, a situation in which prior negative outcomes (e.g., health and cognitive endowments at birth, poor school performance) entail fewer negative consequences for children from higher SES backgrounds (Bernardi, 2014). To the extent that the negative outcomes are genetically influenced, this notion could be expanded to include the compensation of genetic risks.

Although the bioecological model is the dominant framework in studies investigating gene-environment interplay in education, the empirical evidence for the enhancement interaction is mixed. A meta-analysis of gene-environment interactions of family SES in educational achievement and cognitive ability found that there was an enhancement interaction supporting the bioecological model in the United States but not in other countries (Tucker-Drob and Bates, 2016). Especially in studies on countries other than the United States, no interaction or a compensation interaction pattern has been found (Asbury et al., 2005; Baier et al., 2022; de Zeeuw et al., 2019; de Zeeuw and Boomsma, 2017; Figlio et al., 2017; Ruks, 2022). Compared to the family environment, the school environment is much less studied. Also here the results are inconclusive. Genetic influences on reading achievement and general academic achievement were both found to be larger (Haughbrook et al., 2017; Taylor et al., 2010, 2020) and smaller (Hart et al., 2013) in more advantageous school environments, as measured by (proxies for) school quality, teacher quality, and school SES.

2.2.3. The interplay between family SES and school SES

The roles of family SES and school SES are not necessarily independent and could interact. To our knowledge, such interaction has not yet been considered in gene-environment studies of educational performance. However, sociologists pay substantial attention to the interplay between family and school environments. On the one hand, family and school influences could act as *substitutes* in

¹ The gene-family SES interaction in cognitive ability has also become known as the Scarr-Rowe hypothesis. This hypothesis can be seen as a specific case of the more general gene-environment enhancement interaction of the bioecological model.

predicting educational outcomes. Higher levels of parental resources could substitute for poorer learning opportunities at low-SES schools by providing, e.g., supplemental educational investments such as private tutoring (Hanselman, 2018). Similarly, low-SES children may benefit more from high-SES schools because these schools provide environmental inputs (e.g., resources, academic climate, higher levels of motivation and aspiration) that these children are less likely to find at home (Coleman et al., 1966; Kahlenberg, 2001). On the other hand, family and school influences might also *amplify* each other. In this case, children from high-SES families would have a cumulative advantage and reap greater rewards from the learning opportunities in high-SES schools. High-SES children enter the school better academically prepared and may therefore benefit more from school opportunities (Hanselman, 2018). Moreover, the cultural overlap between family and school environments may play a role. From a cultural reproduction perspective, high-SES students are more positively evaluated by teachers and they experience a greater sense of belonging at school, all leading to improved educational outcomes (Bourdieu and Passeron, 1977; de Graaf et al., 2000). Applied to gene-environment interactions in education, a substitution effect of families and schools would imply that the gene-family SES interaction is stronger in low-SES schools than in high-SES schools. If families and schools amplify each other's influence in the enhancement of genetic potential or compensation of genetic risk, then the gene-family SES interaction would be stronger in high-SES schools.

2.3. Gender differences

Boys tend to perform better in math, whereas girls outperform boys on most other educational outcomes (Downey and Vogt Yuan, 2005). Boys and girls also differ in the dispersion of educational performance: boys show greater variance in educational performance irrespective of area (reading, mathematics, and science) and educational level (primary or secondary school) (Baye and Monseur, 2016; Gray et al., 2019). We expect that the moderating role of family and school SES on genetic and environmental influences differs between boys and girls. Studies suggest that environmental factors have a larger impact on boys' academic outcomes than girls, as the gender gap appears to be larger in disadvantaged families and schools (Autor et al., 2019; Legewie and DiPrete, 2012). Thus, insofar as the environment moderates genetic and environmental influences, this moderation would be more pronounced among boys than girls.

Two interrelated mechanisms may account for SES disparities in the gender gap: investments in boys relative to girls could depend on SES (i.e., differential investment) and boys could be more affected by investments and circumstances associated with SES (i.e., differential sensitivity) (Autor et al., 2019). First, concerning differential investments, high-SES parents are argued to invest more in boys, and low-SES parents more in girls (Freese and Powell, 1999). Parents may spend less time monitoring and interacting with boys than girls in low-SES families, a pattern that could be related to traditional gender-role attitudes and a higher level of single-mothers among low-SES families (e.g., Bertrand and Pan, 2013; Buchmann and DiPrete, 2006). In contrast, high-SES parents may provide more compensatory investments in boys than girls (Autor et al., 2019). Parents may invest more resources to improve boys' education because boys are expected to have a lower likelihood to earn a college degree (Quadlin, 2019). Especially high-SES parents may compensate since they have a larger pool of resources (Conley, 2008). Still, empirical evidence for differential investments by child gender and its dependency on family SES is mixed (Autor et al., 2019; Buchmann et al., 2008). The notion of differential investment also applies to the school context. It could be that aspects of higher-quality school environments, such as teacher involvement and attention, are more beneficial for boys than girls simply because they are more exposed to such teacher interactions (Opdenakker, 2021). Teachers seek to give equal treatment to girls and boys and believe they do so (Younger et al., 1999). Yet, they may still (unconsciously) favor one gender over the other, although the direction is not entirely clear (Buchmann et al., 2008). For example, some studies suggest that boys receive more questions and feedback from the teacher, while others found that teachers' attitudes, expectations, and the broader learning environments favor girls (Meece et al., 2006).

Second, even if inputs from the family or school environment are qualitatively and quantitatively similar for boys and girls, they may be more influential for boys' educational performance given boys' greater sensitivity to their environment.² One reason for this greater sensitivity is related to boys' lower levels of intrinsic motivation (Opdenakker, 2021; Vantieghem and Van Houtte, 2018). If boys are more often externally motivated, they may also be more triggered by environmental factors such as the encouragement of the teacher (Opdenakker, 2021). Another reason is provided by the gender-role socialization perspective, according to which mothers are more important for the development of girls' educational aspirations and attainments, and fathers more for boys (Buchmann et al., 2008). Therefore, in single-mother families or in families with little father contact—which is more prevalent in low-SES families—boys may be more vulnerable to the absence of a male role model and lower levels of paternal time and resources (Buchmann and DiPrete, 2006; Lei and Lundberg, 2020).

² Disentangling whether the underlying causes of boys' greater environmental sensitivity are genetic or environmental in origin is difficult. Environmental sensitivity is a characteristic that can be genetically influenced (Pluess and Belsky, 2013), but to our knowledge there is no research investigating gender differences in this relationship. Therefore, we focus on the (largely environmental) explanations that are available in the literature. Still, one should be aware that the actual mechanisms are probably more complex than what is suggested here (including genetic and environmental influences, and their interplay).

The third reason for boys' greater sensitivity is that boys may be particularly sensitive to how gendered identities are constructed in schools. Masculinity tends to be associated with disruptive behavior and opposition to school authority, not with educational effort and performance, which more often is labeled as feminine and thereby stigmatized (Legewie and DiPrete, 2012; Van de Gaer et al., 2006). For this reason, boys may be more likely to develop an anti-school subculture, whereas for girls femininity is not associated with disengagement from school. These gendered patterns are reinforced by peer pressure to conform to (gender-stereotypical) norms of the peer group, which is experienced stronger for boys than girls (Warrington et al., 2000). These processes may be especially prevalent in schools lacking academically-oriented learning climates such as schools with lower school quality and less motivated and lower performing students (e.g., low-SES schools). In such schools, there may be a stronger oppositional culture in male than female peer groups. Disengagement from school could increase boys' peer group status in such schools (Legewie and DiPrete, 2012). Conversely, a school context that is more academically oriented promotes academic competition as an aspect of masculinity and thereby provides a different way of 'doing gender' (Legewie and DiPrete, 2012). Therefore, boys are argued to benefit more from aspects that contribute to this learning-oriented culture, such as high-quality teachers, and a larger proportion of high-SES students and girls in the classroom (Legewie and DiPrete, 2012; Van Hek et al., 2017; Van Houtte, 2004).

2.4. Summary and expectations

Previous research points to different expectations regarding the gene-environment interplay in education. On the one hand, an enhancement interaction can be expected based on the bioecological model. More stable and resourceful environments such as those provided by high-SES families and schools could increase the realization of genetic potential. Genetic influences would then be larger (and shared environmental influences smaller) in high-SES families and high-SES schools. On the other hand, a compensation interaction can be expected according to the diathesis-stress model and sociological notion of compensatory advantage. High-SES families and schools may be compensating against genetic risk or lower genetic potential to perform well in school. Genetic influences would then be smaller (and shared environmental influences larger) in low-SES contexts.

Moreover, the literature on the role of family and school environments in explaining gender differences in educational performance suggests that boys are more sensitive to environmental factors. Combining these perspectives, we expect to see boys' greater sensitivity reflected in the genetic and environmental influences on educational performance and its interplay with the family and school environment. More specifically, we expect that (i) environmental influences on educational achievement would be larger for boys than for girls, and (ii) the family and school environments have a stronger moderating effect for boys than for girls. As boys and girls are embedded in both the family and school context, we take this into account by exploring gender differences at the intersection of family SES and school SES. Given the competing ideas (i.e., substitution vs. amplification) of how family SES and school SES influences are related, we expect to see both a stronger gene-family SES interaction in low-SES schools and high-SES schools. We present an overview of the different interactions in Table 1.

3. Data and methods

3.1. Data

We analyze data from the Danish administrative registers, which are annually updated databases comprising a range of information on all members of the population. The register data are of exceptional quality, containing highly reliable variables and only very few missing observations (Jensen and Rasmussen, 2011). We restrict our analyses to all Danish children completing compulsory school between 2003 and 2014 (with the vast majority being born between 1986 and 1998).³ Moreover, given our twin study design, we only

Table 1
Overview of the expected gene-environment interaction patterns.

Moderator	Enhancement		Compensation	
Family SES	(+)	genes \times family SES	(-)	genes \times family SES
School SES	(+)	genes \times school SES	(-)	genes \times school SES
Family SES \times School SES				
Substitution				
Low-SES school	(++)	genes \times family SES	(--)	genes \times family SES
High-SES school	(+)	genes \times family SES	(-)	genes \times family SES
Amplification				
Low-SES school	(+)	genes \times family SES	(-)	genes \times family SES
High-SES school	(++)	genes \times family SES	(--)	genes \times family SES
Gender	(++)	all of the above stronger for boys	(++)	all of the above stronger for boys

Note. (+) indicates a positive gene-environment interaction where A is higher and C is lower with increased levels of SES, (-) indicates a negative gene-environment interaction where A is lower and C is higher with increased levels of SES. A double sign (++) or (--) indicates that the interaction is expected to be stronger.

³ We choose these cohorts as 2003 is the first cohort for which GPA is observed in the administrative registers.

Table 2

Descriptive statistics for the analytical sample.

	Male twins	Male siblings	Female twins	Female siblings
No. of pairs	2,459	16,974	2,551	15,309
Average GPA	6.33	6.38	6.85	7.06
SD GPA	2.31	2.22	2.24	2.15
Percent with college-educated parents	40%	43%	38%	41%
Percent in high-SES schools	53%	54%	52%	53%

consider (i) same-sex twins and siblings, (ii) siblings who are spaced by no more than three years, and (iii) twins and siblings that attend the same school type.⁴ Our final sample comprises 5010 twin pairs and 32,283 sibling pairs.

For the cohorts we analyze, children attend compulsory school from grades 1 through 9; that is, primary and lower secondary schools which children attend from approximately ages 6 through 16. These grades are completely untracked, and students typically follow their classmates through grade 9. As a result of how schools are funded in Denmark and the fact that all school-level teachers are college-educated, there is less variation in school quality compared to many other countries. Thus Denmark presents itself as a best-case scenario in that if we can detect interaction effects between genetic influences, family SES, and school SES, they will likely exist in other systems too.⁵

3.2. Variables

Our dependent variable is *compulsory school grade-point-average (GPA)*, which covers grades from a wide range of courses at the end of lower secondary school.⁶ It includes grades awarded by the teacher during the school year and grades on final exams awarded by teachers and external examiners. Grades are measured on a 7-point scale ranging from –3 to 12 and include the values –3 (ECTS equivalent: F), 00 (Fx), 02 (E), 4 (D), 7 (C), 10 (B), 12 (A). According to Table 2, girls have higher GPAs on average and slightly lower dispersion than boys. Moreover, female siblings have on average a slightly higher GPA than female twins in the full sample.

Our two focal variables are *parental SES* and *school SES composition*. We measure SES by whether at least one parent has obtained a college degree (i.e., the equivalent of a bachelor's degree or higher). We construct the school SES composition measure using the full population of children completing compulsory school between 2003 and 2014. We calculate by school and graduation cohort the share of children with college-educated parents and then divide this measure into two equally sized groups (cut at the median). As Table 2 shows, both the school SES composition variable and parental college variable are well balanced across the four groups.

3.3. Methods

We apply the Classical Twin Design (CTD) to sibling and twin data to separate genetic and environmental sources of variance in educational performance. In the CTD, the similarity in an outcome among MZ twins is compared with the similarity among DZ twins. MZ twins are genetically identical while DZ twins share on average 50% of their segregating genes. Based on this information and additional assumptions,⁷ the variance in an outcome can be decomposed into three components: genetic (A), shared environmental (C), and non-shared environmental variance (E) (Knopik et al., 2016). The genetic component includes additive genetic influences on educational performance, which include genetically influenced characteristics such as cognitive skills and non-cognitive skills (Demange et al., 2021; Krapohl et al., 2014). The genetic component may also capture more complex processes such as gene-environment correlations and interactions if these are present but unmodeled (Rijsdijk and Sham, 2002). Shared environmental variance includes all non-genetic sources of twin similarity in educational performance, including parental SES, shared school experiences, and neighborhood characteristics (Engelhardt et al., 2019). Non-shared environmental variance captures non-genetic sources of twin dissimilarity, including distinct events (e.g., differential treatment by parents or teachers, peer influence, illness) or events that twins experience differently. It also includes variance due to random measurement error (although such errors are very small in administrative data). Measured environmental characteristics, in our case family SES and school SES, are always shared between siblings and therefore explain shared environmental variance (Turkheimer et al., 2005). This means that the shared environmental variance that is left after taking into account the environmental measures refers to shared environmental variance not

⁴ Not all siblings go to the same schools, nor twins for that matter. In our sample, 75 percent attend the same type of school (as defined by family SES composition), and 67 percent attend the same school.

⁵ In Denmark, children are as a general rule allocated to schools based on their school district. Districts usually span different neighborhoods with different socioeconomic compositions, and this creates variation in the parental SES composition of schools. Although variation in school quality is comparably low in Denmark, there is still significant differences across and recent studies also show that teachers in Denmark sort into schools in ways that lead high-SES schools to have higher-quality teachers on average (Gensowski et al., 2020). Moreover, school SES composition reflects differences in peer environments and culture, also likely producing differences in learning environments.

⁶ The GPA covers grades in reading, writing, grammar, and oral abilities, English (oral), mathematics, and physics/chemistry.

⁷ Assumptions that are made include: MZ and DZ twins share their shared environment to the same extent (i.e., equal environment assumption), there is no assortative mating, twins are generalizable to the general population, and there are minimal gene-environment correlations and interactions (Rijsdijk and Sham, 2002).

related to our family SES and school SES measures.

Our data do not contain information on twin zygosity. Therefore, we rely on data on same-sex twins and same-sex non-twin siblings. Previous studies used twins' sex composition to approximate their zygosity (e.g., Erola et al., 2021; Figlio et al., 2017; Pokropek and Sikora, 2015; Rodgers et al. 1994). Opposite-sex twin pairs are always DZ and share, just as non-twin sibling pairs, on average half of their genes.⁸ Same-sex twin pairs are a mixture of DZ and MZ twin pairs and thus genetically more similar. It is often assumed that this mixture is fifty-fifty (e.g., Rodgers et al., 1994) Rodgers et al., 1994. Therefore, the average genetic relatedness of same-sex twins can be assumed to be the average of MZ and DZ twins' genetic relatedness, that is, 75%. We performed several robustness analyses to check this assumption. Importantly, while the assumed genetic relatedness could affect the levels of the ACE-components, it cannot affect the gender gaps in these components.

We use structural equation models using full information maximum likelihood estimation in Stata to decompose the total variance in educational performance into *A*, *C*, and *E*. The twin and sibling pairs differ in their (assumed) genetic correlation (0.75 vs. 0.50, respectively). The shared environment is assumed to be perfectly correlated between twins and between siblings, while the non-shared environment is uncorrelated between twins and between siblings as it only contributes to within-pair differences. Based on this parameterization, the expected covariance in the educational performance of same-sex twins is $\text{cov}_{(\text{ss twins})} = 0.75A + C$. For same-sex siblings, it is $\text{cov}_{(\text{ss siblings})} = 0.50A + C$. Therefore, *A* can be estimated by $(\text{cov}_{(\text{ss twin})} - \text{cov}_{(\text{ss sibling})}) / (0.75 - 0.50)$. Shared environmental variance is the residual of the twin or sibling covariance not accounted for by *A*, that is, $\text{cov}_{(\text{ss twin})} - 0.75A$ for same-sex twins, or $\text{cov}_{(\text{ss sibling})} - 0.50A$ for same-sex siblings. Variance unexplained by *A* and *C* results from non-shared (or unique) environmental influences including measurement error (*E*).

We estimate the covariances and resulting variance components by different subgroups, also known as non-parametric gene-environment interaction analyses. The subgroups include family SES (low vs. high), school SES (low vs. high), gender (boys vs. girls), and their intersections. The means and variances of educational performance were constrained to be equal between twins and siblings and allowed to differ between the different subgroups (i.e., family SES, school SES, and gender). We report both standardized and unstandardized variance components. We performed several checks to test whether our results are robust to different modeling specifications, which we report at the end of the results (see section 4.4.).

4. Results

4.1. ACE decomposition by family SES and school SES

In the full sample, the proportional genetic contribution (i.e., heritability) is 68.6% for boys and 76.3% for girls, but this difference is not statistically significant at a five percent level ($p = .082$). Both environmental sources of variance are larger for boys than for girls, but only the difference in non-shared environmental variance is statistically significant ($p = .002$), implying that the overall sibling correlation is slightly larger for girls than for boys.

To examine general (non-gender specific) patterns of a gene-environment interplay in the Danish student population, we break down the ACE-decomposition by family SES and school SES pooled over both genders (see Table 3). For family SES, we find that the heritability is 86% in low-SES families and 75% in high-SES families. Additionally, we find larger contributions of the shared and non-shared environment in high-SES families than in low-SES families (see Table 3). These results are consistent with the compensation interaction pattern. However, only the difference in the genetic component is statistically significant at a five percent level ($p = .033$). The unstandardized components show that the finding of lower genetic variance in high-SES compared to low-SES families results from both smaller absolute genetic variance and larger environmental variance (see Table 3). The decrease in genetic variance is stronger than the increase in environmental variance, leading to the less total variance in educational performance in high-SES families.

For school SES, the minor (and non-significant) differences in genetic and environmental influences are in the same direction as family SES (see Table 3). Although we find some differences by school SES, the genetic and environmental influences are largely similar between low-SES and high-SES schools. Thus we find no support for a general gene-environment interaction for school SES.

4.2. Gene \times SES interactions by gender

To examine how gene-environment interactions depend on gender, we further break down the variance decompositions by gender. We do this for two separate models, one for family SES and one for school SES. Fig. 1 shows the results, and we refer to Table A1 in Appendix A for more details including standardized and unstandardized ACE-estimates, total variances, and means.

We find that the gene-family SES interaction differs by gender. For boys, but not for girls, *A* is statistically significantly lower in high-SES families (difference = 21.25, $se = 7.73$, $p = .006$), while both *C* (difference = 10.91, $se = 4.53$, $p = .016$) and *E* (difference = 10.33, $se = 3.45$, $p = .003$) are significantly higher. This direction of the interaction is consistent with the compensation pattern. We observe this interaction for boys because we find no gender differences in the ACE-decomposition in low-SES families, while we do find these differences in high-SES families. In high-SES families, *A* is considerably lower for boys than for girls. For boys in high-SES

⁸ We do not use opposite-sex twins (nor opposite-sex siblings). Comparing same-sex and opposite-sex twins with unknown zygosity provides insufficient information to identify a model in which both ACE-components and sex differences are separately identified. Additionally, using opposite-sex twins requires the assumption that they have only lower similarity in educational performance than same-sex twins because they are less genetically similar, not because they differ in sex (Figlio et al., 2017).

Table 3
ACE decomposition for GPA separately by family SES and school SES.

	1. Family SES						2. School SES					
	Low-SES (<i>N</i> = 21,734)		High-SES (<i>N</i> = 15,559)		Difference		Low-SES (<i>N</i> = 17,373)		High-SES (<i>N</i> = 19,920)		Difference	
Mean	6.04***	(0.01)	7.60***	(0.01)	1.57***	(0.02)	6.10 ***	(0.02)	7.20 ***	(0.01)	1.10***	(0.02)
Variance	4.68***	(0.04)	3.89***	(0.04)	−0.79***	(0.05)	4.92 ***	(0.04)	4.41 ***	(0.04)	−0.51***	(0.06)
% <i>A</i>	85.74***	(3.05)	74.94***	(4.05)	−10.80*	(5.07)	77.77 ***	(3.37)	74.79 ***	(3.12)	−2.99	(4.59)
% <i>C</i>	11.47***	(1.87)	16.23***	(2.39)	4.77	(3.03)	17.68 ***	(2.04)	20.16 ***	(1.88)	2.48	(2.78)
% <i>E</i>	2.80*	(1.30)	8.83***	(1.79)	6.03	(2.21)	4.55 ***	(1.46)	5.05 ***	(1.35)	0.50	(1.99)
<i>A</i>	4.01		2.91				3.83		3.30			
<i>C</i>	0.54		0.63				0.87		0.89			
<i>E</i>	0.13		0.34				0.22		0.22			

Notes: **p* < .05, ***p* < .01, ****p* < .001 (two-tailed). Estimates with standard errors in parentheses. *A*, *C*, and *E* refer to genetic, shared environmental, and non-shared environmental variance, respectively. *N* refers to the number of twin/sibling pairs.

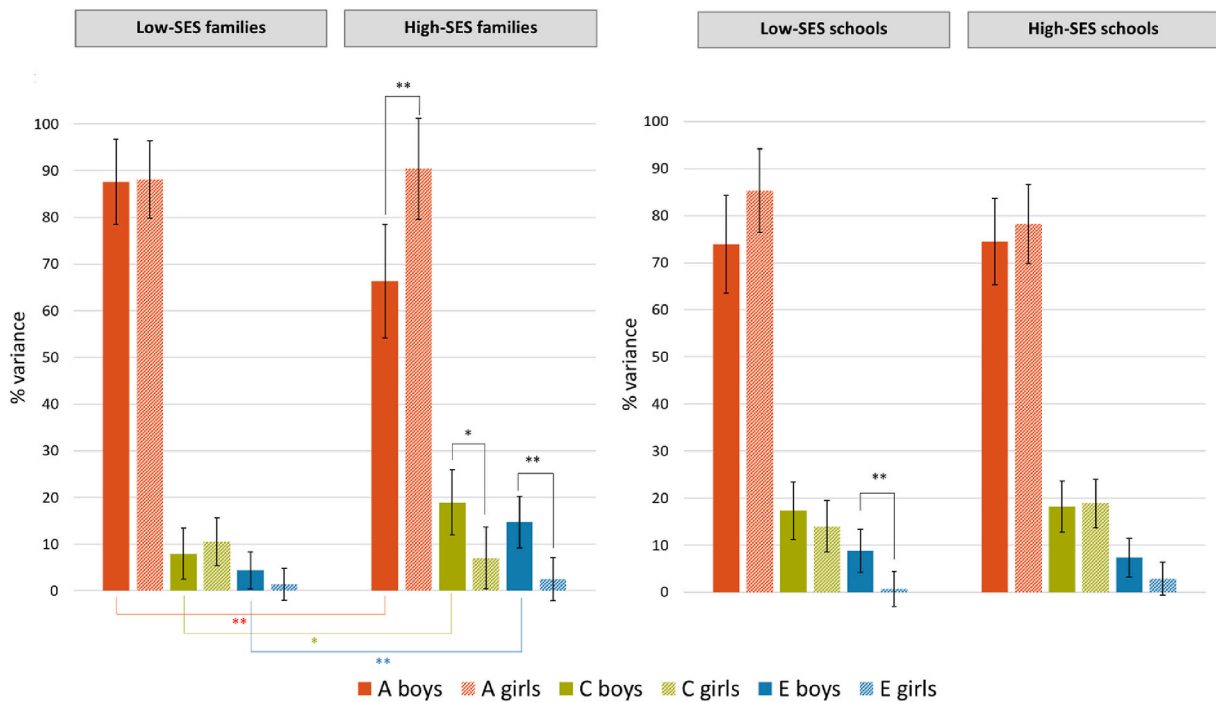


Fig. 1. ACE decomposition for boys and girls by family SES and school SES.

Notes: * $p < .05$, ** $p < .01$, *** $p < .001$ (two-tailed). Standardized genetic (A), shared environmental (C), and non-shared environmental (E) variance including 95% CI.

families, 66% of the variance in educational performance can be attributed to genetic variance; for girls, 90%. Boys in these families are thus more dependent on environmental influences. This result holds for both the shared environment and the unique environment (see Fig. 1).

For school SES, however, there are barely any gender differences (see Fig. 1). We do not find any gene-environment interaction with the school SES environment: A, C, and E do not significantly differ between low- and high-SES schools among both boys and girls. In low-SES schools, the non-shared environmental contribution to boys' education performance ($E = 8.82\%$, $se = 2.35$, $p < .001$) is significantly larger ($p = .007$) than for girls ($E = 0.70\%$, $se = 1.89$, $p = .710$), pointing to that the sibling correlation is larger among girls than boys in these schools. Other than that, there are no statistically significant gender differences in the genetic and environmental sources of variance for children attending low- and high-SES schools.

4.3. Gene \times family SES \times school SES interactions by gender

Although high-SES children more often attend high-SES schools, this relationship is far from perfect. In our data, 25% of high-SES children attend low-SES schools, whereas 38% of low-SES children attend high-SES schools. In Fig. 2 (and Table A2 in Appendix A), we report the ACE decomposition for boys and girls for the interaction between school and family SES.

We find that the moderating effect of family SES that we found for boys is almost entirely driven by children attending low-SES schools. For boys attending low-SES schools, A is significantly lower in high-SES families compared to low-SES families (difference = 36.29, $se = 14.37$, $p = .011$), while both C (difference = 21.56, $se = 8.19$, $p = .009$) and E (difference = 14.74, $se = 6.57$, $p = .025$) are significantly larger in high-SES families. For boys in high-SES schools, on the other hand, we do not find such interaction for family SES. Here we only find that boys' non-shared environmental variance is significantly larger in high-SES families than in low-SES families (difference = 10.61, $se = 4.46$, $p = .018$).

4.4. Robustness checks

To test the robustness of our findings, we perform five auxiliary analyses (reported in Appendix B). First, we estimate the interactions by gender, school, family SES, and their intersections based on the Intraclass Correlation Coefficients (ICCs) of twins and siblings. The interaction between genes and the SES environment involves changes in the twin and sibling (dis)similarities as a function of SES. Parameterizing these (dis)similarities in ICCs instead of ACE components has the advantage that the assumptions that are needed to fit the ACE-model can be relaxed, although it provides less precise information on the sources of (dis)similarities (Turkheimer and Horn, 2014). Results based on the ICCs are similar to those we report based on the ACE-model. Second, we take into account that the genetic similarity of twins may not be exactly 0.75 and the environmental similarity of siblings may be lower than 1.

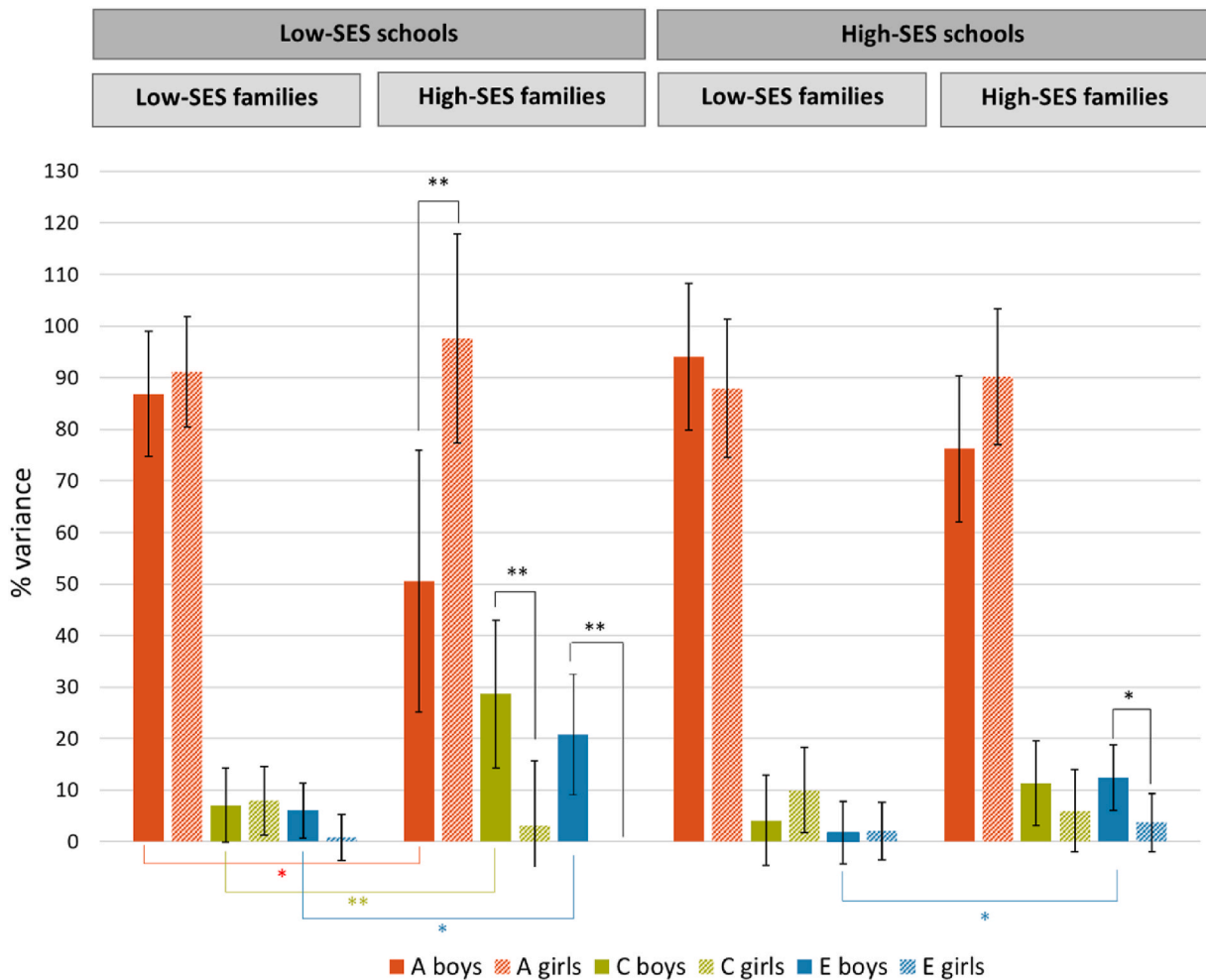


Fig. 2. ACE decomposition for boys and girls by school SES x family SES.

Notes: * $p < .05$, ** $p < .01$, *** $p < .001$ (two-tailed). Standardized genetic (A), shared environmental (C), and non-shared environmental (E) variance including 95% CI.

To reflect both sources of uncertainties, we performed analyses with 0.70 and 0.80 as an estimate for the average genetic relatedness among same-sex twins. The gender differences and interactions by family and school SES are similar, pointing to that the substantive conclusions in the main analyses hold up. Third, we use alternative birth spacing among siblings (two instead of three years) to check if the potentially smaller environmental relatedness among them compared to twins influences our results. The gender differences and interactions by family and school SES are substantively similar, but we have a harder time detecting significant interaction terms stemming from the loss of statistical power. Fourth, controlling for cohort fixed effects in our structural equation models does not change any of our results. Fifth, we test whether our results are robust against coding SES into terciles. We only do this for school SES, because splitting both school and family SES into more than two groups would lead to a significant loss of statistical power. Our conclusions remain the same as those reported in the results section.

5. Discussion

Children differ in their educational achievement and one reason for this lies in genetic differences between them. Other common explanations include differences concerning family background, school environment, and gender. These influences are not independent. The importance of genetic influences on education depends on the social context, including the family and school context (Shanahan and Hofer, 2005). Also, non-genetic research suggests that boys' educational achievement is more dependent on the school and family environment than that of girls (Autor et al., 2019; Legewie and DiPrete, 2012). We add to these strands of literature by considering gene-environment interactions at the intersection between family background, school SES context, and gender. Our empirical analyses on the educational achievement of about 37,000 Danish twin and sibling pairs from population-wide administrative registers reveal three main findings.

First, we find a gene-environment interaction for family SES, but not for school SES. In both low-SES and high-SES families, genetic influences play a large role in explaining children's educational achievement, but they do so to a greater extent in low-SES families. This compensation pattern is in line with the diathesis-stress model and suggests that the lower genetic influence in high-SES families results from the neutralization or compensation of genetic vulnerabilities (Paris, 1999; Rende and Plomin, 1992; Shanahan and Hofer, 2005). This finding contradicts the bioecological model, in which case we would have found an enhancement pattern with more genetic variance in high-SES families as genetic potential would be more fully realized in such environments (Bronfenbrenner, 1992; Bronfenbrenner and Ceci, 1994; Rowe et al., 1999; Scarr-Salapatek, 1971).

Second, we find that the gene-family SES interaction is further moderated by the child's gender. In high-SES families, the genetic influence is considerably lower for boys than for girls. Additionally, shared and non-shared environmental influences are larger for boys than girls in these families. We thus find a gene-family SES compensation interaction for boys but not for girls. This result is consistent with the idea that environmental factors have a larger impact on boys, due to differential investments and/or differential sensitivity (see, e.g., Autor et al., 2019). One interpretation of this finding is that high-SES parents provide more compensatory investments in boys, investments that eventually reduce their genetic risk toward lower educational performance.

Third, the moderating effect of family SES for boys is almost entirely driven by low-SES schools. In low-SES schools, but not in high-SES schools, genetic influences play a much smaller role and shared and non-shared environmental influences a larger role for high-SES boys. In other words, for boys in low-SES schools, our findings are in line with the compensation interaction pattern, suggesting that genetic risks are more actualized in low-SES families and neutralized or compensated in high-SES families. One explanation for this finding is that especially the genetic risks towards lower school performance of boys in low-SES schools may be compensated by parental SES. Especially for boys, low-SES schools may provide a disadvantageous context, as boys are more responsive to an environment that is less learning-orientated and more disruptive (e.g., Legewie and DiPrete, 2012). It may be that especially with such school circumstances, a high-SES family environment contributes to hampering the realization of genetic risks of boys. This also corresponds with the idea that family and school influences substitute each other's influence, leading to a more pronounced gene-family SES interaction in lower-SES schools. However, although differences in *ACE* in low-SES schools are consistent with such an interpretation, the mean differences do not follow what you would expect based on the idea of compensation. If high-SES parents would compensate boys in low-SES schools, we would expect a smaller gender gap in average performance. Instead, the gender gap is similar among low- and high-SES families in low-SES schools.

Our finding of greater genetic variance in low-SES families contributes to the evidence pointing towards no or reversed interactions in countries other than the United States (e.g., De Zeeuw and Boomsma, 2017; Tucker-Drob and Bates, 2016). It also contributes to the increasing empirical studies into gene-environment interactions in education within Europe. A recent cross-national study by Baier et al. (2022) find no significant gene-family SES interactions in GPA in Germany and Norway, but a significant gene-environment compensation interaction in Sweden. We likewise find a significant compensation interaction in Denmark. Country-specific welfare state arrangements and features of educational systems may play a role, but more comparative research is needed to understand how such contextual characteristics affect gene-environment interactions in education.

Furthermore, while we find that genetic influences play a larger role in low-SES families, this pattern does not extend to school SES. In contrast to the United States (Hart et al., 2013) where larger genetic variance in low-SES schools is found, we do not find such an interaction in Denmark. This could be due to the fact that there is less variation in the school environment in Denmark than in the United States, partly as a result of the public funding of schools and relatively uniform teacher quality (all teachers are college-educated) in Denmark. Still, this does not mean that school SES does not play a role in Denmark. The gene-family SES interaction appears to be heterogeneous, as it is largely concentrated among boys attending low-SES schools. This finding highlights the importance of investigating the intersection of gender, family SES, and school SES. Thus, future gene-environment interaction studies could benefit from considering the multiplicity of contexts for complex outcomes such as educational achievement (Seabrook and Avison, 2010).

Most prior twin studies likely did not investigate multiple interactions as it requires large and socioeconomic diverse twin samples. Twin samples with known zygosity often lack the power to detect (multiple) interaction effects. Moreover, twin samples are more likely to suffer from self-selection bias (Trejo et al., 2018). Relying on twin-sibling analyses based on population-wide register data, as we do, has the advantage that it comprises all socioeconomic strata and provides us with many cases to investigate the gene-environment interactions. A trade-off here is that these data do not contain zygosity information. While analyses with unknown zygosity also reduce statistical power (Eaves and Jinks, 1972), the sample size provided by population data can offset such issues.

Although the twin design applied to twin and sibling register data allows us to investigate the complex interplay between genes, gender, and family and school SES, it also comes with some disadvantages. First, we relied on comparing same-sex sibling types that differ in genetic relatedness: twins and non-twin siblings. This design relies on two assumptions: (i) twins' genetic relatedness is 0.75 and (ii) siblings' shared environmental relatedness is 1. Violation of these assumptions may influence the *ACE*-decomposition. For example, if the genetic relatedness of twins is lower than 0.75, this results in larger genetic variance and smaller shared environmental variance. And if siblings do not share their shared environment to the same extent as twins, this leads to a smaller genetic variance and larger shared environmental variance. However, we do not find that these assumptions affect our conclusions. We provide several robustness checks that relax these assumptions, and the results are largely similar. Moreover, possible violations of the assumptions do not influence gender differences in *ACE*.

Second, our *ACE*-moderation models do not allow for causal interpretations. The environmental moderators that we use, family SES and school SES, are endogenous (Schmitz and Conley, 2017). Such endogeneity may arise from gene-environment (and environment-environment) correlations involving family and/or school SES. For example, children with more genetic risks towards poor educational performance may be selected into low-SES schools (cf. Smith-Woolley et al., 2018). Therefore, the gene-environment

interactions as reported in our study can be related to the effects of genetic risks that are weaker in high-SES families, but could also reflect environmental constraints placed on the (genetic) variation in educational performance making the high-SES subgroup more homogenous. Although both may be related to inequality, we are interested in the first interpretation. Yet, drawing such conclusion requires other research designs such as applying quasi-natural experimental approaches to gene-environment interaction models (e.g., regression discontinuity design) (Schmitz and Conley, 2017).

In conclusion, our study suggests that the importance of genetic and environmental influences on educational achievement differs by (the intersections between) family SES, school SES, and gender. For boys, but not for girls, genetic influences play a considerably smaller role in high-SES families than in low-SES families. This interaction appears to mainly take place among high-SES boys attending low-SES schools. These results suggest that high-SES families compensate for the realization of genetic risks towards lower educational performance of boys, particularly when boys are attending low-SES schools as these schools may be especially disadvantageous to them. Whether these gene-environment interaction patterns reflect causal pathways remains a question for future research. In any case, we show that such pathways likely depend on several individual and environmental characteristics including but not limited to gender, family SES, and school SES.

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Declaration of competing interest

None.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.ssresearch.2023.102870>.

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