CHILD DEVELOPMENT PERSPECTIVES

Genetics and Child Development: Recent Advances and Their Implications for Developmental Research

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ABSTRACT—***Recent genetic discoveries offer a new lens through which to study cognitive, emotional, behavioral, and social processes that are foundational to children's development. In this article, we review the latest advances in genomics—genome-wide association studies and the polygenic scores that have come out of them—and discuss how these techniques can be leveraged to shed light on developmental research questions. Then, we describe how developmental scientists might apply these methods in their own lines of work—for example, in investigations of individual differences in developmental trajectories, intergenerational transmission, peer relationships, and processes of resilience and positive adaptation. Finally, we discuss ethical concerns and limitations of genetics research as they pertain to developmental science.***

KEYWORDS—*child development; education; genetics; individual differences; polygenic scores*

Developmental psychologists have grappled with several key questions for decades: Which factors shape individual differences in children's developmental trajectories? How do parents influence children and transmit traits across generations? How can environments be modified to promote children's positive adaptation and reduce inequalities? Recent methodological advances in genetics—namely, *polygenic scores*—offer a new lens through which to study these developmental processes by shedding light on the cognitive, emotional, behavioral, and social processes that underlie children's development.

In this article, we review how polygenic scores can be integrated into developmental science to study questions about children's and adolescents' development. Building on other recent reviews about polygenic scores (Belsky & Harden, 2019; Harden & Koellinger, 2020), we provide an overview tailored to developmental scientists by focusing on child and adolescent development before age 18 and discuss how genetic methods can be applied to questions uniquely relevant to developmental scientists. First, we review recent research that has created and used polygenic scores to study social science outcomes. Then, we describe how developmental psychologists across diverse subspecialties might apply polygenic-score methods in their own lines of work. We conclude by discussing the limitations and ethical concerns in this emerging area of research.

NEW DISCOVERIES IN BEHAVIORAL GENETICS

Studies of twins and children who have been adopted have a long history in developmental psychology, and provided initial evidence that virtually all traits are partially influenced by genes (Matthews & Turkheimer, 2019; Plomin, 2019; Silventoinen et al., 2020). These studies compare individuals who differ in genetic relatedness (e.g., identical versus fraternal twins) to investigate the relative influence of genes versus environments. More recently, the plummeting cost of genotyping has made it possible to study genetic influences by directly measuring DNA. It is now feasible to measure (i.e., to *genotype*) millions of genetic variants in a few hours for less than $100.

In psychological research, genotyping was initially used to investigate associations between specific candidate genes and traits of interest. However, focusing on a limited set of candidate genes has proved largely ill-advised, with many findings failing to replicate. This replication failure occurred in part because

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most human traits are influenced by thousands of genes simultaneously (i.e., they are *polygenic)*, each of which has a small effect size (Plomin, 2019). To detect these small effects, studies of candidate genes require very large samples, but research has relied on small studies that were underpowered, yielding results that were in many cases probably false positives (Plomin, 2019).

A different approach leverages genome-wide association studies (GWAS) to improve upon candidate gene research. GWAS use genetic information from large numbers of people (e.g., 1.1 million; Lee et al., 2018), and scan the *entire* genome for associations between genetic variants and human phenotypes (Visscher et al., 2017). Initial GWAS examined diseases (e.g., diabetes) and anthropometric traits (e.g., height; Visscher et al., 2017). However, GWAS are increasingly being used to search for genetic associations with outcomes integral to developmental science, such as educational attainment (Lee et al., 2018), personality (Penke & Jokela, 2016), and risk-taking behavior (Linnér et al., 2019).

Polygenic Scores

Since most complex human traits are highly polygenic (Plomin, 2019), associations between single genetic variants and traits identified in GWAS tend to be negligible. However, the effects of variants across the entire genome can be combined into a *polygenic score*, which represents the weighted sum of genetic variants associated with a trait (Plomin, 2019). In 2013, this technique was applied in a genome-wide association study of educational attainment, the first of its kind, to identify several genetic variants robustly associated with a social science outcome—specifically, how many years of schooling individuals completed (Rietveld et al., 2013). Follow-up GWAS, most recently a study of 1.1 million people, revealed more than 1,000 genetic variants associated with educational attainment (Lee et al., 2018). Following the pattern of other complex traits, these GWAS have demonstrated that educational attainment is associated with many genetic variants scattered across the entire genome. Individually, these variants have negligible effects, but collectively they show larger associations, with the most recent education polygenic score accounting for 10% of individual differences in attainment. More investigations in independent samples have revealed that this translates to an effect of more than a half a year of school per one-standard-deviation increase in education polygenic score (Trejo et al., 2018).

Associations between the polygenic score and attainment are evident even for siblings growing up in the same family who differ in their polygenic scores (e.g., Belsky et al., 2018), providing strong evidence that associations are not simply the result of confounders, such as environmental differences that systematically covary with genetics (Harden et al., 2020). Although it is impossible to draw conclusions about an individual's education based on his or her polygenic score (because these are average-level associations; Harden & Koellinger, 2020), at a population level, these associations approach effect sizes of traditional predictors of attainment, such as parental education (Lee et al., 2018). The GWAS for other outcomes (e.g., internalizing problems, externalizing, and risk-taking behavior; Linnér et al., 2019) are increasing in size, but have not yielded genetic predictors of similar effect size.

Using published results of GWAS as a scoring algorithm, researchers can calculate the same polygenic score in their own samples, independent of the GWAS sample in which the score was first developed. These independent samples need not be enormous. For example, assuming correlations between the polygenic score and outcomes between $r = 0.015–0.30$ (based on correlations between the most recent education polygenic score with educational outcomes, cognitive, and socioemotional skills; Demange et al., in press; Lee et al., 2018), studies with samples of 100–400 would be sufficiently powered to detect associations. See Figure 1 for a conceptual pathway for this process.

Polygenic Scores for One Trait Also Predict Related Traits

Polygenic scores often predict outcomes beyond the trait initially targeted (Harden & Koellinger, 2020). This finding has been striking in research using the education polygenic score. As might be expected, children and adolescents with higher education polygenic scores perform better than their peers on academic tests (de Zeeuw et al., 2014; Krapohl & Plomin, 2016); they also improve more in academic performance across the teenage years (Ayorech, Plomin, & von Stumm, 2019), and have higher IQs (Belsky et al., 2016; Wertz et al., 2018), compared to their peers. However, perhaps more surprisingly, these children also tend to exhibit fewer attention problems (de Zeeuw et al., 2014), and have higher levels of self-regulation, self-awareness, interpersonal skills, and positive peer relationships (Armstrong-Carter et al., 2020; Belsky et al., 2016; Wertz et al., 2018). Similarly, adolescents with higher education polygenic scores report more self-efficacy, optimism, and perseverance, and less depression, antisocial behavior, and peer conflict (Krapohl et al., 2014) than their peers.

As another example, polygenic scores from GWAS of schizophrenia predict trajectories of alcohol and drug use during late adolescence (Mallard, Harden, & Fromme, 2019). The broad predictions of the polygenic score occur because GWAS capture associations between genetic variants and an outcome that is itself embedded in a network of correlated phenotypes (Belsky & Harden, 2019). One implication of these findings is that the polygenic scores for GWAS of a specific outcome (e.g., educational attainment) are not relevant just to researchers interested in that outcome (e.g., education) per se but also to researchers studying children's development in other related domains. It follows that to select a polygenic score to use in their own work, developmental psychologists may consider not only scores from GWAS of the particular trait they are interested in, but also from GWAS of traits that are *related* to their trait of interest.

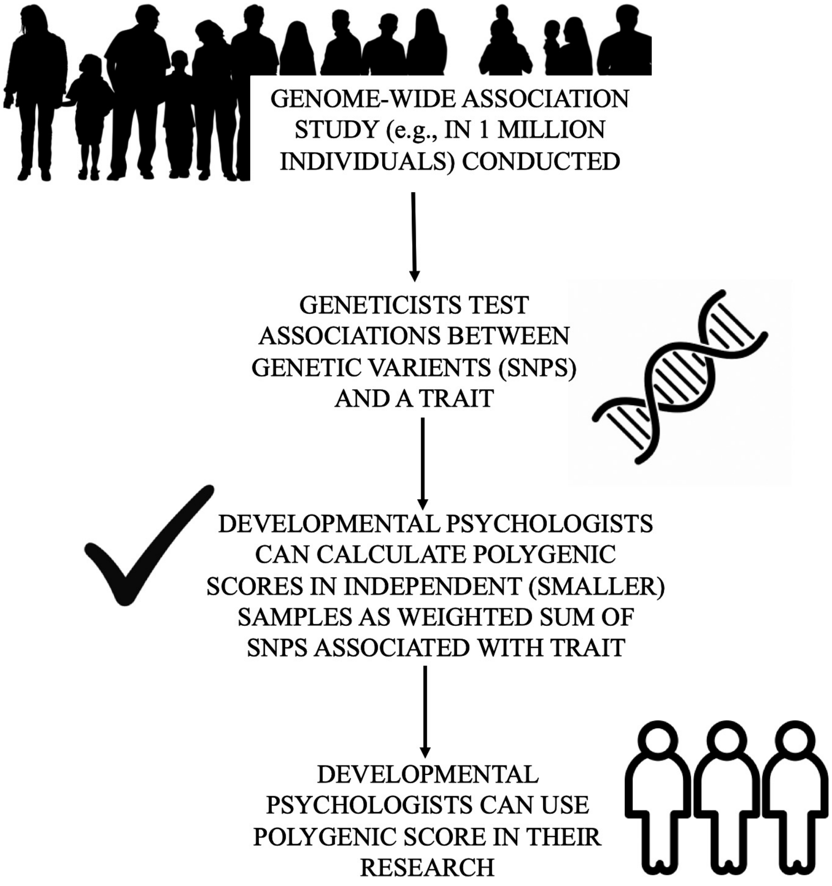

Figure 1. Process for identifying genetic variants and using polygenic scores in subsequent studies. Genome-wide association studies (GWAS) with large samples are used to test associations between millions of genetic variants across the entire genome and a particular trait of interest. For each tested genetic variant (or single-nucleotide polymorphisms), GWAS report an effect size of the association between the genetic variant and the outcome of interest. Developmental psychologists can use these estimated weights as a scoring algorithm to construct a polygenic score (i.e., a weighted sum of genome-wide associations with the trait) in their smaller, independent samples of children, adolescents, and adults for whom genetic data are available. This polygenic score indexes genetic associations with that trait on average across the population. (For more information, see Plomin, 2019.)

Polygenic Scores Partially Capture Influences of Children's Environments

Perhaps surprisingly, genetic variation identified in GWAS partially captures environmental influences. Some researchers may have expected genetic variants identified in GWAS to influence individual development directly; for example, perhaps variants identified in the GWAS for educational attainment relate to brain development. However, emerging evidence—from studies of genotyped parents and children—indicates that genetic variants can also have *indirect effects* that occur via an individual's environment. In these studies, even genes that were *not* passed from parents to children still affected children's outcomes (Bates et al., 2018; Kong et al., 2018). As shown in Figure 2, genetic variants partially shape parental behavior and in turn, children's outcomes. For instance, mothers with higher education polygenic scores had higher socioeconomic status and more optimal health during pregnancy, which in turn partially explained their children's greater academic performance at ages 4–6 years (Armstrong-Carter et al., 2020). Similarly, mothers with higher education polygenic scores displayed more cognitively stimulating parenting behaviors (e.g., book reading), which in turn contributed to their children's academic performance at age 18, over and above genetics they directly transmitted to their children (Wertz et al., 2019). These studies reveal an environmentally mediated genetic effect—*genetic nurture* (Kong et al., 2018)—that is consistent with theory and evidence of gene–environment correlation that emerged in developmental psychology more than 30 years ago (e.g., Scarr, 1992).

POLYGENIC SCORES AS A TOOL FOR DEVELOPMENTAL PSYCHOLOGISTS

We now describe how polygenic scores could be incorporated into developmental research to help advance understanding of child development.

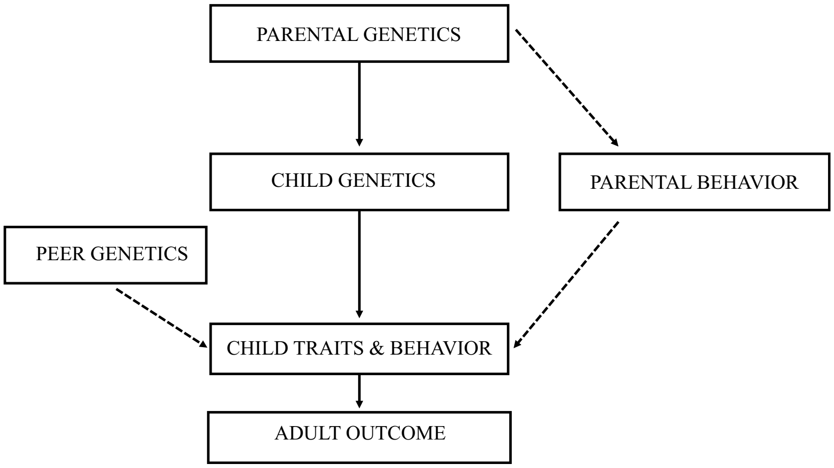

Figure 2. **Conceptual model linking genetics and child outcomes through direct (i.e., via child genetics) and indirect (i.e., via child environment) pathways. Children's genetics are inherited from parents and influence children's outcomes through processes that occur in the child (e.g., behavior, biological processes). Parent and peer genetics influence child outcomes through parent and peer behavior that shapes children's environments, such as parental caregiving or peer interactions with the child.**

Individual Differences in Developmental Trajectories

Why do behaviors and traits persist across life for some individuals but change for others? Thirty years ago, it was hypothesized that individuals with stable trajectories of behaviors might have a greater genetic predisposition for these behaviors (Scarr, 1992). Polygenic scores offer new opportunities to directly test this hypothesis—by comparing the scores of children who follow different developmental trajectories (Rimfeld et al., 2018). For example, children with lower education polygenic scores were more likely to follow a life-course persistent pattern of antisocial behavior than to have less persistent patterns of behavior (Wertz et al., 2018). Similarly, children's genetic risk for attention difficulties is associated with the course of these difficulties across development (Agnew-Blais et al., 2019). Using polygenic scores, researchers could shed light on individual variability in developmental trajectories of other traits, such as emotional difficulties and social skills. This research could help elucidate contributors to individual differences in the life-course trajectories of these behaviors.

Intergenerational Transmission

Why do behaviors, traits, and environmental circumstances repeat across generations? For example, highly educated parents tend to have children who are successful in school and children of anxious parents tend to be more anxious. While intergenerational transmission of wealth and institutional barriers account for a large portion of these phenomena, researchers still do not understand much about how experiences are passed from parents to children (Teti, Cole, Cabrera, Goodman, & McLoyd, 2017). Polygenic scores can help shed light on intergenerational transmission in two ways. First, they can help determine how genetic and environmental mechanisms shape intergenerational (dis)continuity. As mentioned earlier, parents' genetics contribute to intergenerational transmission not only directly—via the passage of genes from parent to child—but also indirectly—via parental genes that influence parents' behaviors in ways that influence children's outcomes. For instance, parental genetics are linked to parents' feeding practices, such as breastfeeding, which in turn predicts children's academic achievement (Krapohl et al., 2017), and to limiting food or encouraging eating, which predicts children's body mass index (Selzam et al., 2018).

Second, polygenic scores can help clarify at what point in development familial influences begin to shape children's development. For example, children who inherit higher education polygenic scores experience different prenatal environments than their peers—their mothers tend to be healthier during pregnancy—and are born into more advantageous socioeconomic circumstances (Armstrong-Carter et al., 2020; Belsky et al., 2016). These findings add to evidence that interventions to reduce inequalities must address multigenerational processes from before birth (Noble & Giebler, 2020). Children with higher education polygenic scores further diverge from their peers at an early age—for example, in their developmental milestones by age 4 (Armstrong-Carter et al., 2020), speech and reading skills by age 7 (Belsky et al., 2016), and attention skills by age 8 (de Zeeuw et al., 2020). Researchers could expand this work by investigating how polygenic scores are associated with other developmental markers across time—such as social behaviors, risk taking, and cognitive skills—to clarify when processes of intergenerational transmission are set in motion. This requires longitudinal designs that measure the same phenotypes at different ages. Such information could help highlight critical periods for targeting interventions to reduce inequalities in children's experiences and outcomes that could otherwise persist across generations (Caspi et al., 2017).

Understanding Children's Resilience

Why do children who experience similar events adapt differently? Among children who grow up in contexts of disadvantage (e.g., poverty, maltreatment), some exhibit better-than-expected psychological and social outcomes—a phenomenon termed *resiliency* (Choi, Stein, Dunn, Koenen, & Smoller, 2019). Polygenic scores could be used to test hypotheses about children's characteristics (e.g., cognitive or social skills) that might influence resilience (Choi et al., 2019). For example, children with higher education polygenic scores were more likely to break cycles of low educational attainment within families (Belsky et al., 2018) and to parent their children more positively than the parenting they experienced when they were young (Wertz et al., 2019). Researchers could build on this work by comparing the polygenic scores of children who display resilience across multiple domains of social, emotional, and academic adaptation. For example, children with higher polygenic scores for education show a constellation of positive socioemotional skills, which are believed to protect in contexts of adversity (Demange et al., 2020). Follow-up studies could directly investigate whether higher polygenic scores and associated traits are protective (i.e., moderators of environmental influences) in contexts of environmental disadvantage. Such research should be approached and interpreted with caution: Identifying and estimating statistical interactions comes with several analytic and inferential challenges that may have contributed to the poor replication record of this work in the past (Domingue, 2020).

Peer Influences on Children's Outcomes

Why do children often find themselves in social environments that match and reinforce their dispositions? A challenge in research on peer groups is to disentangle processes of selection (i.e., children choosing their peer groups because of shared experiences or traits) from processes of socialization (i.e., peers influencing children's experiences and traits; Prinstein & Giletta, 2020). Polygenic scores can help separate these processes. For example, children with more education-associated genes are more likely to have friends who also have more education-associated genes, and those friends' genes, in turn, predict children's own higher levels of educational attainment, even after controlling for selection (Domingue et al., 2018). Similarly, children in elementary school are more likely to smoke if they have peers with higher polygenic scores for smoking; in one study, a few children with higher polygenic scores for smoking influenced the smoking behavior of an entire class (Sotoudeh, Harris, & Conley, 2019). This research could be extended to investigate the extent to which genetic similarities account for the positive correlation among children's aggression, risk-taking, self-regulation, prosocial behavior, and learning disabilities and those of their peers.

Moreover, polygenic scores could shed light on reciprocal influences among children in shared environments. For instance, nongenetic research has shown that elementary school children's improvements in cognitive skills across the school year were associated with their classmates' cognitive skills across the school year, suggesting that peers' cognitive development may influence children's own cognitive development (Finch, Garcia, Sulik, & Obradović, 2019). Polygenic scores could be integrated into this type of research to consider selection effects and to test whether genetic similarity among children modulates reciprocal influences. Such research could shed light on the mechanisms through which youth influence each other's development across school and neighborhood environments.

Supporting Children's Positive Development

Perhaps counterintuitively, genetics research can help illuminate how environments can be changed to accommodate children with different needs. One way to do this is to study how children with similar polygenic scores fare in different environments. Using this approach, recent work has demonstrated that children with low polygenic scores were less likely to disenroll from math courses in high school if they attended well-resourced schools than their peers in under-resourced schools (Harden et al., 2020). This work adds new evidence that high-quality educational environments protect youth at risk for lower attainment. Researchers could build on this by investigating how interventions or natural experiments (e.g., leveraging policy changes or the COVID-19 pandemic) affect children with different polygenic scores (Harden, 2020). For example, polygenic scores could be incorporated into parenting interventions to test hypotheses about why some children benefit more from parenting interventions than others (Belsky & van IJzendoorn, 2017). Polygenic scores and the traits with which they are associated may index key individual differences among children that affect how they respond to environmental exposures and interventions. We are not suggesting that genetic information should be used to assign interventions, but rather that genetic information may provide insight into how children's characteristics shape their response to changes in their environment. This could inform efforts to widen children's access to stimulating opportunities and adequate supports.

CAUTIONS AND LIMITATIONS OF INTEGRATING GENETICS INTO DEVELOPMENTAL PSYCHOLOGY

Current research on polygenic scores has several limitations. First, most GWAS have been conducted in individuals of European ancestry (Martin et al., 2019). This limits the calculation of polygenic scores to samples of individuals with European ancestry because genetic associations vary across populations of different ancestries (Martin et al., 2019). Developing polygenic scores for more diverse samples is crucial for facilitating a more comprehensive and inclusive understanding of the link between genetics and child development across the globe.

Second, polygenic scores that are currently available capture only a portion of the total known heritability of a trait—which has been termed *missing heritability* (Matthews & Turkheimer, 2019). Researchers cannot assume that including polygenic scores in their models fully captures all genetic influences.

Third, because GWAS necessitate large samples, effects are averaged across groups of individuals from different countries and different age cohorts. Although this approach helps secure the large samples needed for genetic discovery, it may obscure interactions between genes and environmental contexts (Tropf et al., 2017). Relatedly, polygenic scores may be naturally biased toward revealing genetic associations with temporally and contextually stable developmental trajectories, whereas genes associated with instability or plasticity are more likely to be missed.

Fourth, polygenic scores are based on simple associations between genes and an outcome; by themselves, they do not imply causality or reveal the mechanisms of how genetics are associated with that outcome (Visscher et al., 2017). These associations may depend on the cultural contexts in which GWAS are conducted, and on social and institutional biases that mediate the link between genetics and different phenotypes (Jackson, 1993). Thus, polygenic scores explain only a portion of variance in the outcome, leaving many additional sources of variance—and underlying mechanisms—unexplained. More research is needed to illuminate the pathways connecting genes to children's outcomes.

ETHICAL CONCERNS AND THE NEED FOR A DEVELOPMENTAL PERSPECTIVE IN GENETIC RESEARCH

The finding that genetic variants are correlated with educational attainment and other complex behaviors has been controversial. Many researchers—and parents and children—are understandably concerned about misuse of genetic information. The violent and discriminatory history of the use of genetic information in psychological research validates these concerns, both in the past and now (Jackson, 1993; Martschenko, Trejo, & Domingue, 2019). To prevent findings from being misinterpreted and misused, it is important to discuss them openly and have clear, proactive guidelines for ethical research practices and interpretation (Martschenko et al., 2019). To reduce misconceptions, it is also important to obtain a better grasp of how genetics revealed in GWAS are associated with outcomes. For example, the recent finding that genetics identified in GWAS partly reflects environments reemphasizes that discoveries made by GWAS are not inimical to socialization theories because they work partly through factors such as the home environment. Furthermore, polygenic-score research shows that genetics influence outcomes such as educational attainment in a nondeterministic, probabilistic fashion, via a long path of earlier-emerging behavioral and environmental mediators.

In addition to contributing to a more nuanced understanding of associations between genes and children's development, these findings highlight the importance of adopting a developmental perspective in genetics research. Thus, as much as we have emphasized how new genomic methods might contribute to developmental research, a greater consideration of developmental science principles will also advance genetics research. Developmental psychologists are in a unique position to promote equitable research practices, and ensure accurate interpretation of research linking genetics and children's development because they have the necessary expertise, data, and theoretical understanding of environmental and social influences on development (Belsky & Harden, 2019; Wertz et al., 2019).

CONCLUSION

Innovations in genetic data collection and analysis are happening rapidly. This provides a promising opportunity for new genetic discoveries to be integrated into developmental psychology to help shed light on core questions in developmental research. Polygenic scores are a convenient way to incorporate genetics in developmental studies because they do not require specialized samples (e.g., twins), and genotyping can be added to a study easily (Harden & Koellinger, 2020; Rietveld et al., 2013).

Integrating polygenic scores can be useful for solving developmental research questions, even for researchers who are not interested in genetics. First, incorporating genetics can provide a clearer understanding of how environments influence behavior—for example, by controlling for genetics in peer studies to disentangle socialization from selection effects or incorporating genetics in parenting research to identify parental influences on children. Second, genetics are a point of origin for developmental cascades in that DNA is present from birth. As such, polygenic scores are useful as *molecular tracers* to help understand how children with different characteristics progress across development (Harden & Koellinger, 2020). Third, since human behavior is shaped by both genetics and environment, any researcher who studies behavior is also inadvertently studying the manifestation of genetic influences. Polygenic scores are a way for developmental researchers to incorporate these genetic influences explicitly.

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