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Genetics and Education: Recent Developments in the Context of an Ugly History and an Uncertain Future

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Driven by our recent mapping of the human genome, genetics research is increasingly prominent and beginning to reintersect with education research. We describe previous intersections of these fields, focusing on the ways that they were harmful. We then discuss novel features of genetics research in the current era, with an emphasis on possibilities deriving from the availability of molecular genetic data and the proliferation of genome-wide association studies. We discuss both the promises and potential pitfalls resulting from the convergence of molecular genetic research and education research. The floodgates of genetic data have opened. Collaboration between those in the social and biomedical sciences; open conversation among policy makers, educators, and researchers; and public engagement will all prove critical for enacting regulations and research designs that emphasize equity.

Keywords: *genetics, education research, adversarial collaboration, equity, molecular genetics, polygenic score*

Suppose it's the year 2025. You are a school administrator responsible for making decisions regarding the allocation of educational resources. Two parents come to your office concerned about their kindergartener; their family doctor has suggested that the child has a genetic makeup that indicates a high risk for developing dyslexia in a few years' time. The parents worry that their child will start falling behind in reading soon; indeed, dyslexia diagnoses typically occur too late for optimal intervention (Ozernov-Palchik & Gaab, 2016). Thus, the parents request that learning supports be put into place immediately (e.g., one-on-one reading coaching with a teacher's aide). Resources are scarce, but you want to ensure that every student has the best opportunity for learning. Is this a reasonable request? How well do genes predict dyslexia? Is prediction of equal quality for children from marginalized groups? What do you do?

While research into appropriate answers to these questions is still underway, we think that it is important for educators to begin to contemplate them. The field of genetics is going to affect education and, as a consequence, education research. Given the sudden ubiquity of genetic data and the great public interest that genetics has garnered, we believe that this is inevitable. The described scenario—the diagnosis of learning disabilities—seems a likely candidate for the intersection between the fields given that many learning disabilities involve a medical diagnosis. However, as we discuss, there are other potential points of intersection, including the use of genetic predictors to study a range of nonmedicalized human behaviors and conditions.

Discourses involving genetics are not altogether new to education. Arguments about genes, cognition, and group differences, for example, were prominent in the latter half of the 20th century—for instance, the debate surrounding "The Bell Curve" (Devlin, Fienberg, Resnick, & Roeder, 2013; Heckman, 1995; Herrnstein & Murray, 2010; Jencks & Phillips, 2011; Neisser et al., 1996)—and they have resurfaced recently in popular media (Harris, 2017; Kahn et al., 2018; Klein, 2018; Reich, 2018; Saletan, 2018; Turkheimer, Harden, & Nisbett, 2017). Much of the recent interest is driven by our rapid accumulation of vast amounts of molecular genetic data and the possibilities associated with such data. Whether the reemergence of genetics as an issue in education makes one optimistic, worried, or downright nauseated, it is important to understand the historical contexts of this debate and the present reality that, we argue, makes the return of genetics to education imminent.

We address both these issues herein, starting with the ugly history of genetics in education research before turning to the current wave of molecular genetics research. Whether this iteration of research will produce positive or negative effects on the lives of children and whether it will lead to better opportunities and outcomes for all students, these are

difficult questions. Indeed, we have divergent views on these issues. We consider this article to be a form of "adversarial collaboration" (Kahneman, 2003), driven by a desire to leverage our internal disagreements into a dialogue that can help inform the broader field. Such adversarial collaboration—in which individuals trained in different, even opposing, research traditions partake in a joint research effort—may yield benefits, as it requires skeptics to engage with each other. In this spirit, our overarching goal is to help build an avenue for constructive conversation between the biomedical and social sciences rather than to further contentious debate between the sides. We think that the subject of genetically informed research in education is of sufficient importance that more of the education research community should be aware of the historical precedents and contemporary realities of this branch of scientific and social inquiry. This article is an attempt to cover such ground.

We focus on the availability of molecular genetic data and the proliferation of genome-wide association studies (GWASs). Given the centrality that prediction from molecular genetic data plays in this article, we note at the outset key caveats to bear in mind. Genetic effects on educationally relevant outcomes or behaviors need to be relatively large to have practical relevance. Currently, the fraction of variation explained by polygenic prediction in holdout samples is modest but growing (Cesarini & Visscher, 2017). We write under the assumption that genetic predictors are sufficiently predictive to be useful for scientific inquiry but not necessarily for "clinical" use; we argue that this is reasonable given the predictive power of recent work (Lee et al., 2018). Genetic effects of this size will likely entail questions about genetic determinism, essentialism, racism, and/or classism with respect to their application. We spend a great deal of time on these issues and pay special attention to the particulars of molecular genetic data. This focus is warranted given the sudden proliferation of this type of data and the attendant public interest. However, it is not meant to minimize research in related fields that utilize alternative forms of genetic data, such as twin studies (Asbury, Almeida, Hibel, Harlaar, & Plomin, 2008; Asbury, Dunn, & Plomin, 2006), or even other types of biological data, such as epigenetic studies (Gulson & Webb, 2018; Linnér et al., 2017; Pickersgill, Niewöhner, Müller, Martin, & Cunningham-Burley, 2013).

We proceed as follows. In the next section, we describe the ugly history of how bigoted ideologies combined with genetically informed research to bolster prejudiced policies in the United States (repugnant views can, of course, still be found today; Rosa & Bonilla, 2017). We then turn to the emergence of molecular genetic data and discuss their use in education research. In the final two sections, we discuss ethical and practical problems in this rapidly growing field, noting some of the most challenging issues, and end by providing actionable recommendations.

Genetics and Education Prior to the Molecular Age

We focus on two crucial features of earlier intersections between education and genetics. First, we highlight the eugenic and essentialist discourses that surrounded genetics, intelligence, race, and class in the 19th and 20th centuries. We focus on the pernicious implications that people drew from specious equating of genotype (an individual's unique set of genes) with phenotype (an observable trait or behavior), focusing on arguments involving the supposed normative superiority of certain groups. Second, we discuss scholarship from more recent eras, including the limitations of heritability estimates and the problems of a first wave of studies that used small quantities of molecular genetic data to advance bold claims.

Genetics and Group Differences

The use of genetic language to describe racial and socioeconomic differences in cognitive ability and academic performance was commonplace in the 19th (Galton, 1869; Hunt, 1864) and 20th (Jenkins, 1939; Jensen, 1968, 1970; Shockley, 1971) centuries and continues today (Wade, 2014). Intelligence testing was a frequent locus for such discourse. Between 1890 and 1920, dozens of intelligence tests were developed in Europe and the United States that claimed to offer robust measures of intelligence (Binet, 1913; Terman, 1916). The observation that individuals from different racial and socioeconomic groups tended to perform differently on intelligence tests has caused great controversy (Rushton & Jensen, 2006).

Many hypotheses for these findings have been advanced. One hypothesis has minimized the salience of such findings by pointing to the stark socioeconomic disparities among groups (Heckman, 2011) as well as questioning whether such tests are valid across cultures (Greenfield, Ward, & Jacobs, 1997; Sternberg & Grigorenko, 2004). An alternative hypothesis suggests that differences are largely due to differences in biology across the relevant groups (Jensen, 1969; Shockley, 1971). This latter view is unsettling for a number of reasons, including its potential echo of old arguments that such biological differences will undermine attempts to improve human well-being through social policy—or, even worse, that such differences justify punitive policies. Ability testing was used directly to resist desegregation (Mayo, 1913) and immigration (Brigham, 1922) and generally validate socioeconomic (Galton, 1891) and racial (Shockley, 1972) inequalities. A return to such views would be the most distressing outcome of the increased salience of genetics in popular and scientific discourse; some argue that it is already happening (Gillborn, 2016).

The Study of Heritability

Dating back to the late 19th century (Galton, 1869), many discussions of genetics have revolved around the concept of

heritability: the proportion of observed variation in a trait associated with genetic variation. Heritability can be estimated by comparing a trait's correlation between identical twins with its correlations between fraternal twins (Visscher, Hill, & Wray, 2008), since identical twins are genetic copies of each other while fraternal twins are biological siblings that share only about half of their genes. Strikingly, identical twins are far more similar than fraternal twins on practically every observable characteristic, ranging from height to more complex traits, such as educational attainment (Polderman et al., 2015); this is taken as evidence for the pervasive heritability of nearly all traits, the "first law" of behavioral genetics (Turkheimer, 2000). Outcomes of interest to education researchers are no exception: cognitive ability (Polderman et al., 2015), attention-deficit/hyperactivity disorder (ADHD; Dalsgaard, Østergaard, Leckman, Mortensen, & Pedersen, 2015; Franke et al., 2012), and dyslexia (Byrne et al., 2009; Soden Hensler, Schatschneider, Taylor, & Wagner, 2010) are all highly heritable, with meta-analysis showing that genes explain roughly half the variation among individuals. However, from the perspective of education research, a key limitation of heritability findings is that they have relatively little to say about the effects of educational environments (Turkheimer, 1991)—the foundation of education research. This is an important caveat. That said, others (e.g., Harden, 2018) have argued that genetic studies could offer valuable information to education research that may be lost if genetic research is prematurely dismissed; much of the remainder of this article is an attempt to describe why this might be, as well as the problems associated with such research.

As a general rule, heritability need not be constant across time and place (Feldman & Lewontin, 1975) and may in fact be intimately linked to environmental context. A particularly salient example for our purposes involves the heritability of cognitive functioning. It has been argued that its heritability is larger in households of high socioeconomic status than in those of low socioeconomic status in the United States (Scarr-Salapatek, 1971; Turkheimer, Haley, Waldron, D'Onofrio, & Gottesman, 2003). While the empirical evidence for this argument has been mixed (Figlio, Freese, Karbownik, & Roth, 2017; Tucker-Drob & Bates, 2016), we note that the possibility of such interplay between genetics and environments emphasizes the importance of accounting for environmental context when attempts are made to understand genetic influences. Such concerns are at the fore in contemporary thinking about study designs that include genetic data (Boardman, Daw, & Freese, 2013).

Although studies of heritability have demonstrated that nearly all human characteristics are influenced by a person's genetics, heritability estimates leave much to be desired in terms of the information that they provide regarding social policy. Decomposing the variation of a trait into its "genetic" and "environmental" components provides almost no relevant information with regard to the efficacy and efficiency of different interventions. In fact, many highly heritable traits are readily influenced by policy. As the economist Arthur Goldberger (1979) famously pointed out, distributing eyeglasses to treat myopia would likely pass a cost-benefit analysis with flying colors, even if myopia were 100% heritable. In contrast, many traits with relatively low heritability estimates, such as religiosity (Polderman et al., 2015), would not appear to be particularly actionable as targets of social policy. Thus, findings from research focusing on heritability estimation may have limited practical utility. The study of human genetics leaves undiminished the need for well-crafted social policy.

The Candidate Gene Era

The social sciences were previously limited in their ability to engage with human biology due to one hugely important limitation. Genes, the fundamental biological building block, were largely invisible to scientists until the end of 20th century. Concordant with the completion of the Human Genome Project (Lander et al., 2001), relatively limited quantities of genetic information began to be available for social scientific inquiry. Hoping to move beyond simple heritability estimates and toward exploration of relationships between specific genetic variants and a variety of outcomes, scientists began conducting what have come to be known as "candidate gene" studies based on these limited amounts of molecular genetic data. These studies involve selecting a small set of genetic variants, typically <10, a priori based on their presumed biological function (hence, "candidate genes") and examining their association with a particular trait.

From the late 1990s and into the 21st century, scientists linked candidate genes to outcomes ranging from antisocial behavior (Caspi et al., 2002) and ADHD (Payton et al., 2001) to music aptitude (Ukkola, Onkamo, Raijas, Karma, & Järvelä, 2009) and political participation (Fowler & Dawes, 2008). Due to the high cost of processing genetic information during the candidate gene era, these studies largely relied on samples of a few hundred participants. As a consequence of the small samples and other methodological failings that were not well understood at the time, research linking candidate genes to human behavior was plagued by false positives and replication failures. Although many peer-reviewed studies described statistically significant associations between candidate genes and a variety of traits, the majority of these associations failed replication tests (L. E. Duncan & Keller, 2011; Gizer, Ficks, & Waldman, 2009; Ioannidis, Ntzani, Trikalinos, & Contopoulos-Ioannidis, 2001) leading, in at least one case, to heightened editorial scrutiny for such work (Hewitt, 2012). For example, of 12 genetic variants with published associations with general intelligence, none replicated in follow-up work (Chabris et al., 2012). As a result of these

problems, newer methods have emphasized replication and statistical power in attempting to link individual genetic variants to phenotypes of interest.

The Genomic Era

Today, we are witnessing a new phase of biological inquiry into human behavior. The cost of DNA sequencing is decreasing at breakneck speed (National Human Genome Research Institute, 2016), and great advances have been made in analytic methods for the processing of large amounts of genetic data. Perhaps the most impactful development in recent years is the GWAS. A GWAS probes the relationship between a trait and regions of the genome via large data sets containing individual-level information on genotype and phenotype (Pearson & Manolio, 2008). GWAS relies on the recent availability of DNA from tens to hundreds of thousands of individuals and attempts to identify variants of single-nucleotide polymorphisms (SNPs) that are more common in people exhibiting a given trait of interest. SNPs are the most common form of human genetic variation and represent a mutation at a single locus in the genome; a typical GWAS will involve analysis of millions of SNPs.

We emphasize one key theme from this first decade of the GWAS literature (Visscher, Brown, McCarthy, & Yang, 2012; Visscher et al., 2017). This approach has started to reveal a core similarity across many traits. It has become clear that many traits are affected by a large number of SNPs, with each SNP having only a tiny effect on the trait (Boyle, Li, & Pritchard, 2017; Chabris, Lee, Cesarini, Benjamin, & Laibson, 2015). Put another way, the heritability of most behavioral outcomes is due to a large number of genes rather than a small number or even just one gene. Traits that have this quality—including anthropometric and behavioral outcomes as well as many common diseases—are known as "complex traits" to differentiate them from simpler Mendelian traits, such as cystic fibrosis and Huntington's disease. As one consequence, findings from GWAS of such complex traits are frequently used to generate a single predictor, a "polygenic score" (Dudbridge, 2013), meant to summarize all the identified genetic information pertaining to a particular trait given that the genetic influence on a trait is dispersed so widely throughout the genome. Much of the following section involves discussion of studies that utilized such scores.

Molecular Genetics and Education

So, what do these recent developments have to do with education? We are not alone in trying to answer this question. The past 5 years have seen increased calls for incorporation of genetic information into education (Asbury & Plomin, 2013; Kovas, Tikhomirova, Selita, Tosto, & Malykh, 2016), leading to debate over the relevance of this research to educators (Asbury, 2015; Panofsky, 2015; Sabatello, 2018; Thomas, Kovas, Meaburn, & Tolmie, 2015). Similar discussions are occurring in related disciplines (Conley, 2016; Freese, 2018). Those advocating for the incorporation of genetically informed research into educational practice discuss the promise of "personalized" education (Asbury & Plomin, 2013) and see integrating genetics into education research as a way to optimize educational processes (Kovas et al., 2016). An alternative perspective focuses on the broader possibilities of "biosocial education" (Gulson & Baker, 2018; Gulson & Webb, 2017, 2018; Youdell, 2017)—a framework for education practice focusing on the potential inclusion of biological information from fields such as epigenetics (Youdell, 2017, 2018) and neuroscience (Immordino-Yang, Darling-Hammond, & Krone, 2018; Williamson, Pykett, & Nemorin, 2018)—in an attempt to enrich understandings of students and their learning.

We focus on the implications of increased availability of molecular genetic data for education and education research. In the following sections, we briefly discuss what we have learned about the genetics of education-related phenotypes via GWASs, how these genetics were followed up in polygenic score studies, and potential techniques through which researchers argue such data may be used to improve the practice of education. We do not attempt a comprehensive review; rather, we aim to provide a concise overview of the relevant findings and methods.

GWAS of Education-Related Traits

Twin studies have long suggested that educational attainment, defined as the years of schooling that a person receives, is heritable (Branigan, McCallum, & Freese, 2013). The first GWAS probing the genetic influences of educational attainment was published in 2013 (Rietveld et al., 2013). Three years later, the same core team of researchers (Okbay et al., 2016) increased their sample to roughly 300,000 individuals and published a follow-up GWAS identifying 74 genetic loci significantly related to years of schooling. A third-generation educational attainment GWAS, based on >1 million individuals, recently identified >1,000 genetic loci associated with years of schooling (Lee et al., 2018). The genetic variants identified in these studies are associated with plausible biological mechanisms (e.g., a variety of processes in the central nervous system). In a similar vein, several studies have examined the genetics of cognition (Hill, Davies, McIntosh, Gale, & Deary, 2017; Sniekers et al., 2017; Trampush et al., 2017; Zabaneh et al., 2017).

Researchers have also learned about the genetics of traits whose development is highly salient to educators, such as cognitive ability (Sniekers et al., 2017) and ADHD (Demontis et al., 2017). Follow-up work focusing on individual genetic variants may be of interest in some cases, but we suspect that genetic predictors that aggregate information, such as

polygenic scores, will be of greater interest given the small predictive utility of each variant. Polygenic scores are beginning to have sizable predictive power. For example, the polygenic score derived from the most recent educational attainment GWAS (Lee et al., 2018) explains roughly 12% of the variation in years of schooling and 9% of the variation in cognitive ability. By way of comparison, this is on par with that of parental education or individual cognition—two widely used predictors instrumental to our understanding of educational processes in the social and psychological sciences.

GWAS Follow-Up

What, precisely, are genetic discoveries related to educational attainment capturing, and in what contexts do they apply? How is it that new polygenic scores predict educational attainment roughly as well as our best existing social and psychological measures? Are these studies identifying genes that influence cognition? Presumably so, but evidence suggests other influences as well (Krapohl et al., 2014). What about appearance? Personality and socioemotional skills? Or, more distressingly, are these findings driven by genes that simply map onto existing patterns of social stratification? Work on these questions is ongoing. In the following, we offer a brief summary of what we know thus far (for an alternative perspective, see Cesarini & Visscher, 2017).

A large number of genetic variants identified in these studies play a role in various stages of brain development, both prenatally and over the life course (Okbay et al., 2016). Educational attainment polygenic scores have been shown to associate with phenotypes linked with educational processes, including school performance (Selzam et al., 2017), increased verbal ability in childhood (Belsky et al., 2016), personality (Mõttus, Realo, Vainik, Allik, & Esko, 2017), and learning disabilities (de Zeeuw et al., 2014). They are consistently predictive of educational and occupational attainments across a variety of school contexts (Trejo et al., 2018). They are also increasingly being tied to more distal phenotypes, such as longevity (Marioni et al., 2016) and smoking (Wedow et al., 2018).

While follow-up studies have given us some sense of people's characteristics that are associated with the educational attainment polygenic score, a more fundamental question is whether these studies merely detected genetic variants associated with social class. Polygenic scores constructed from these GWAS results are indeed associated with family home environment (Belsky et al., 2016; Conley et al., 2015; Krapohl & Plomin, 2016) and neighborhood socioeconomic status (Belsky, Caspi, et al., 2018; Domingue, Belsky, Conley, Harris, & Boardman, 2015). However, even after controlling for socioeconomic origin (which we know to be associated with educational attainment), these polygenic scores predict changes in an individual's socioeconomic standing over the life course (Belsky, Domingue, et al., 2018). Moreover, individuals with higher scores tend to accrue more years of educational attainment than their siblings, suggesting that the polygenic score is not entirely confounded by family background (Belsky, Domingue, et al., 2018; Domingue et al., 2015). These findings suggest that such scores may be useful in future research as indicators of individual difference; we discuss this in detail in the following section.

Although the evidence suggests that polygenic scores are potentially useful indicators of individual-level characteristics, they need to be used and interpreted with care. Consider recent findings of "social genetic effects" (Domingue & Belsky, 2017). In a study of friends and schoolmates, the genetics of social peers correlated with a focal individual's own genetics and were also predictive of the focal individual's outcomes net of their own genes (Domingue et al., 2018). A related example comes from a study of parental genetics. A mother's genotype is associated with an offspring's attainment (Bates et al., 2018; Belsky, Domingue, et al., 2018; Kong et al., 2018) net of the offspring's genes. Such findings make it hard to separate "nature" from "nurture." These associations between genes and environments complicate simple interpretations of results involving this genetic predictor.

Using Molecular Genetic Studies to Improve Education Research

Now that evidence has begun to accumulate suggesting that polygenic scores are valid predictors of individual difference, how might such scores be utilized in education research? We focus on discussions of several approaches that are methodologically tractable for nongeneticists and consistent with existing analytic approaches in quantitative education research. In particular, we discuss utility in understanding individual development as well as the design and analysis of interventions (or other types of exogenous shocks). Crucially, the possible applications that we discuss here do not involve "precision education" (i.e., the use of individual genotype to tailor educational services to a child); instead, they involve using genetic information to form a better understanding of how educational processes, within both an individual and a society, might contribute to positive educational outcomes.

Given that an individual's genotype is established at fertilization, a polygenic score can be used as a fixed point from which to observe child development (Belsky & Israel, 2014). This design has been used to show that individuals with higher polygenic scores begin to differentiate themselves early in the life course from lower-scored peers on dimensions related to language ability but not other important developmental milestones (Belsky et al., 2016). Information obtained along these lines may ultimately be useful for the design of interventions to improve learning for

all students (Belsky, Moffitt, & Caspi, 2013), as they can help us identify the specific processes that are most germane to downstream outcomes of interest. Additionally, the use of polygenic scores may improve our understanding of intervention pathways by reducing confounding. Biological and social endowments are both passed down from parent to child. By using polygenic scores as a control variable in work studying intergenerational processes, researchers could be better able to understand the causal relationship between social factors and educational attainment.

Polygenic scores may offer a useful mechanism for better understanding responses to educational interventions. For example, recent work used the polygenic score for educational attainment to emphasize changes in association between genotype and phenotype after the decline of Soviet rule in Estonia (Rimfeld et al., 2018), in different retirement saving regimes (Barth, Papageorge, & Thom, 2018), and to demonstrate the effect of mandatory schooling on health (with a polygenic score for body mass index; Barcellos, Carvalho, & Turley, 2018). Findings from these studies support the concept that social policies that reduce choice—in the case of mandatory schooling laws in the United Kingdom, for example—also reduce the salience of genotype. They may also be useful in the study of heterogeneous response; polygenic scores can be used to test hypotheses related to why otherwise similar people respond differently to interventions. Genetic predictors have already been used to understand differences in literacy skills and response to intervention (Kegel, Bus, & van IJzendoorn, 2011): as their predictive power increases, so might their utility in this regard. Finally, others noted that the availability of genetic predictors may increase the power associated with randomized controlled trials, potentially shrinking the costs associated with such research (Rietveld et al., 2013, see p. 28 of their supplemental information).

Focal Issues

While the previous section considered some possible avenues through which molecular genetic data may advance education research, a variety of issues complicate the degree to which such advances will be equity promoting. In the following sections, we outline specific foci that merit attention as molecular genetic data become increasingly relevant in the scientific and public spheres.

Human History and Genetic Diversity

Human history is deeply intertwined with our genome. Examples abound: genetics can provide us information about patterns of immigration in the United States (Han et al., 2017), the relative isolation of indigenous groups in pre-Columbus Mexico (Moreno-Estrada et al., 2014), and even the possibility of interbreeding between humans and other humanoid groups such as Neandertals (Sankararaman, Patterson, Li, Pääbo, & Reich, 2012). Indeed, individual interest in one's "genetic history" is presumably a key driver in the market success of direct-to-consumer genetics testing. This genetic diversity is a scientific treasure of the highest order, but it will require extremely careful study given that genetics and history are so intertwined.

In certain cases, the study of genetic differences can yield useful information regarding why the life trajectories of otherwise similar people diverge. Genetic differences may be a viable means for understanding divergent outcomes among individuals who have comparable starting points, such as siblings (although, even in this relatively simple case, there is complexity; Dunn & Plomin, 1990). In contrast, we argue that to use genetic differences to explain variation in complex traits among individuals or groups who experience manifestly unequal environments is a fraught endeavor. Such an enterprise is, at the very least, technically challenging (Martin et al., 2017), and population geneticists have advised toward caution in this regard ("Letters," 2014). This is not to deny the existence of genetic differences. Human genetic variation undoubtedly exists, and genetic differences do occur among those from different ancestral backgrounds (The 1000 Genomes Project Consortium, 2012). That said, it will be nearly impossible to isolate the effects of genetic differences from the effects of environmental differences, given the severe levels of socioeconomic stratification that we observe in most societies across groups and the fact that many of the key group differences (e.g., among racial groups) are associated with dramatic differences in the ways that we experience our environments (e.g., Gaddis, 2014).

Further complicating matters, ancestral differences should not be conflated with race. *Ancestry*, as geneticists use the term, refers to an individual's place in the many branching lines of genealogic descent. While humans largely share the same expansive family tree, ancestry captures genetic similarities of individuals due to more recent common forebearers. Ancestry is thus an individual characteristic that is captured in a person's DNA, while *race* refers to a complex social process that ascribes individuals to socially constructed groups or certain geographic areas (Yudell, Roberts, DeSalle, & Tishkoff, 2016). Critically, the correspondence between racial and ancestral groups is dynamic: social processes perpetually redefine racial identities within and across generations (B. Duncan & Trejo, 2011), while lines of genetic ancestry remain fixed. The increase in intermarriage (Wang, 2012) will further complicate questions of race and ancestry and the difficulties that these issues pose to genetic analysis.

While genetics offers a fascinating lens from which to observe human history (Han et al., 2017; Moreno-Estrada et al., 2014), it is just one lens. Context matters. Using genetic differences as mechanisms for explaining group differences in traits that are highly contextualized—such as

educational attainment—is inflammatory and stretches existing empirical evidence quite thin. Genetic differences among ancestral groups are likely small relative to the differences in environmental exposures, which we know to be sizable (Baradaran, 2017; Browning et al., 2017; Clark, Millet, & Marshall, 2014). Furthermore, adequate study designs would be incredibly difficult to actually implement (Conley & Fletcher, 2017, chap. 5). In the case of complex traits, we are highly sympathetic to the disquiet that many social scientists experience for genetic explanations of trait differences among ancestral groups or, worse yet, racial groups. In particular, we see little value in pursuing such lines of inquiry pertaining to cognition and educational attainment. That said, others may not be dissuaded; racist and deterministic interpretations of genetics research into human behavior have existed for some time and remain a concern.

Unequal Access to Precision Services

If personalization of medicine or education becomes precise only for certain groups of people, it runs the risk of becoming a driver of inequality rather than a systemic means to improve public health. Although this is slowly changing (Wojcik et al., 2017), minority and indigenous populations are underrepresented in research samples and data sets (Bustamante, Francisco, & Burchard, 2011; L. Duncan et al., 2018; Knerr, Wayman, & Bonham, 2011). We emphasize two key points. First, individuals of European ancestry capture only a small amount of the total genetic diversity that exists in humans. Northern Europe, for example, is quite genetically homogeneous, meaning that an individual from Denmark (in terms of ancestry) and one from Norway are likely to be more genetically similar than two Nigerians living a few miles from each other (Li et al., 2008; Rosenberg & Kang, 2015). These collections of genetically homogeneous data have limited methodological strengths for some purposes, but they do not offer information that necessarily generalizes to all humans. Second, misdeeds of previous generations may have led to certain populations being cautious of engagement with biomedical research. For example, the Tuskegee experiment led to substantial mistrust of the medical community (Alsan & Wanamaker, 2017). Perhaps as a consequence of such experiences, there is reduced enrollment in genotyping efforts among African Americans (Bogner et al., 2004; McQuillan, Pan, & Porter, 2006).

The relative homogeneity of the samples from whom most genetic information is drawn leads to a risk that any benefits of genotyping, should there be any (e.g., personalized medicine), will accrue to already privileged groups (Popejoy & Fullerton, 2016). For example, there are concerns that prescription drug dosage guidelines may need to vary across ancestral groups, partially as a function of differences in certain allele frequencies (Burroughs, Maxey, & Levy, 2002; Evans, 1999; "Genes, Drugs and Race," 2001). This is not a simple issue, and the lack of diverse genetic data will hamper our ability to make decisions about where such refinements are needed. An additional concern is that, at present, predictive performance of polygenic scores is typically maximal for those of European ancestry (L. Duncan et al., 2018), which is to be expected given the composition of discovery samples (Scutari, Mackay, & Balding, 2016). Going back to the original motivating example, genetic tests for early identification of learning disabilities that have clinical relevance only for European-descent individuals would exacerbate existing disparities in issues associated with identification of those entitled to special education services—an issue that we discuss in more detail below.

Even if equivalent information can be derived from genetic data for all people, there are additional reasons for concern. As the commercialization of genetics advances, policy makers and educators will have to consider the implications of genetic testing (conducted inside and outside of schools) for equity. Higher-income people generally tend to respond more quickly to new health-related information (Link, Northridge, Phelan, & Ganz, 1998). Decreasing costs have made genetic information accessible to the everyday American, resulting in a market for consumer genetics. Getting genotyped has quickly become a popular way for individuals to discover more about themselves and their family history in a relatively inexpensive manner. Such access to consumer genetics has the potential to widen class and race disparities in education if information derived from genotyping becomes available largely to families with sufficient means. Or, such information may be actionable only in schools that have the proper resources to tailor interventions. If this is the case, consumer genetics could further divide the opportunities available to students from different social and economic backgrounds.

Inequality due to differential access to genetic screening is particularly unsettling, as prenatal genetic screening has the potential to translate social inequality into genetic differences. It is already common practice for families to conduct genetic testing in utero to detect disorders such as Down syndrome, cystic fibrosis, and Tay-Sachs disease (Péter, 2015). Moreover, parents utilizing in vitro fertilization can choose to select for specific attributes, such as the sex of their child (Baruch, Kaufman, & Hudson, 2008). Perhaps this will evolve such that parents with the means and resources go beyond simply screening their children for learning disabilities and choose to also screen unborn children for socially valued traits, such as cognitive functioning or athleticism. As we begin to better understand the genetic basis for a wider range of characteristics, differential access to such screening practices could create new gaps in the genetic risks for a variety of valued life outcomes across social strata. Socioeconomic gaps in genetic risk could serve to strain the role that the public education system plays in equalizing opportunities across individuals.

An alternative concern is the potential for discrimination based on genotype. Consider the possibility of insurance rate setting as a function of genotype. This already happens to a certain extent in some countries (e.g., United Kingdom; Godard et al., 2004). In the United States, the Genetic Information Nondiscrimination Act of 2008 makes it currently illegal to discriminate for health insurance based on genotype ("The Genetic Information Nondiscrimination Act," 2009). However, the law does not offer protections for long-term care, disability, or life insurance, creating a loophole for genetic discrimination. As scientific and technological advancements continue, researchers and policy makers will have to proactively collaborate to prevent genetic discrimination in access to not only health care but possibly educational environments too. An overreliance on genetic information could create systems that constrict rather than expand educational opportunity.

Learning Disabilities

An increased capacity for inexpensive identification of developmental disorders at younger ages could be transformative for children who have learning disabilities. Genetics are one component in the etiology of many of these conditions, such as dyslexia (Carrion-Castillo, Franke, & Fisher, 2013), ADHD (Middeldorp et al., 2016), and autism (de la Torre-Ubieta, Won, Stein, & Geschwind, 2016). Due to the plummeting cost of genotyping and the increasing predictive power of polygenic scores, the implementation of a genetic screening system could transform our approach to managing learning disabilities from reactive to proactive. In the most optimistic scenario, children with preclinical symptoms that might have gone unnoticed could receive the extra help that they need sooner, or those who have been misdiagnosed might be placed in an environment to which they are better suited. Such systems would require resolution of a variety of challenges. For example, there are arguments regarding the degree to which genetic influences associated with learning disabilities are general rather than disease specific (Plomin & Kovas, 2005), thus raising questions about the viability of disease-specific genetic screenings. However, even if individual-level screening remains impractical, it is also possible that genetics may be a useful tool for refinement of disease nosology; work in this arena is beginning to occur with respect to psychiatric conditions (Anttila et al., 2018; S. H. Lee et al., 2013) and may ultimately be of interest in studies of learning disability. We anticipate this to be an active area of research given the prospect of clinical utility of genetic prediction for other medical conditions (Torkamani, Wineinger, & Topol, 2018).

Aside from clinical prediction, a better understanding of the distribution of various genetic risks across schools could be used to study inequities in the current ways that the educational system under- and overdiagnoses students. For example, research could use polygenic scores to compare the relationship between genetic risk and diagnosis for neurodevelopmental disorders across school-age individuals in a population, thereby identifying differential diagnoses and treatment across groups. Such screenings may add useful data—specifically, indicators with some degree of objectivity—to the existing debate regarding whether children from marginalized groups are overrepresented in special education (e.g., economically disadvantaged students [Sullivan & Bal, 2013] and English language learners [Sullivan, 2011]). Should genetics provide actionable information—which, we stress, is an open question given the difficulties associated with constructing clinically relevant genetic predictors in diverse samples—school systems might be better able to determine which students would benefit from certain education support services and interventions.

Specific Recommendations

In this section, we provide two actionable recommendations for researchers with interest and concerns in genetics and education research that we think might serve to minimize the negative consequences for equity.

Refrain From Overly Broad Claims

In most cases, scientific discovery leads to a gradual accumulation of knowledge, and preliminary findings can be contradicted by later work. One does not have to go far afield to observe this phenomenon, given the candidate gene era's failure to identify replicable genetic variants associated with characteristics such as intelligence (Chabris et al., 2012). Due to its uniquely sensitive role in discourses regarding social inequality and individual differences, the field of genetics must avoid the repetition of previous mistakes by responsibly tempering claims as they pertain to education. In particular, research needs be attentive to the structural realities that underlie many observed educational differences among groups (Callier & Bonham, 2015; Parens & Appelbaum, 2015): findings should be grounded in the appropriate contexts, and interpretations that acknowledge these realities should be favored.

However, it may be that such well-grounded research is not enough. As education is a topic relevant to nearly all Americans, such responsible research should be reliably disseminated to the media and the general public. One potential exemplar in this regard is the work of the Social Science Genetic Association Consortium, which brings together social scientists, molecular geneticists, and bioethicists. Their papers, especially their discovery work on the genetics of educational attainment (Okbay et al., 2016; Rietveld et al., 2013), are all accompanied by carefully worded online FAQs that offer context and clarity for interpreting their findings. This practice has been framed as "the best example

of prophylaxis against hyperbole" (Parens & Appelbaum, 2015). They give clear guidance against overly simplistic interpretations of their findings: "Did you find 'the gene' for cognitive performance? No" (Social Science Genetic Association Consortium, n.d.). Researchers at the intersection of genetics and education would do well to work hard to explicitly spell out what their results do and do not entail—to both their academic peers and the public at large.

Encourage Adversarial Collaboration

Conversations regarding the role of genetics in education are ongoing in the biomedical and social sciences. However, thus far, little has been done to foster a conversation between them. We are talking past, instead of with, each other. Now is the time for collaborative interdisciplinary research. We argue, with others (Rose, 2013), that researchers should aim for critical engagement in place of the existing critical distance between these research communities. Those interested in bringing genetic information into education ought to think critically about how to conduct socially responsible work that recognizes the socioeconomic and racial inequity inherent within the United States. Without consideration of the contextual factors, implanting genetics research into education runs the risk of normalizing group differences in educational outcomes. Collaboration with social scientists studying systemic inequality from a qualitative-oriented perspective may help foster interdisciplinary approaches to genetically informed research. Participants in this form of "adversarial collaboration" are engaging with disciplines that are frequently seen as being at odds with each other and will presumably continue to have differences in opinion (Kahneman, 2003). Such collaborations are not driven by a focus on short-term results; rather, the goal is to encourage processes that lead to a richer understanding of a particular subject or issue.

Conclusion

Let's return to the scenario posed at the beginning of this article: you are a school administrator grappling with a request for early reading support for a child whose parents claim is at heightened genetic risk for dyslexia. It is too early for any authoritative answer to the central question—what do you do?—but we have attempted to point educators to a more tractable question: What will you want to know? In particular, we have tried to sketch out the relevant issues that one must consider to answer this question by focusing on the possibilities and limitations of research utilizing molecular genetics.

To be clear, we do not advocate for any specific usage of molecular data in schools. Rather, we hope that this review of the growing body of molecular genetics findings relevant to education may begin to orient people toward key points in this rapidly evolving field. We offer a quick reiteration of some of the most important questions, focusing on genetic predictors derived from molecular genetic data. How predictive are genetics for the question at hand, and how consistent is prediction across the kinds of groups that typically co-occur with educational inequality? What specific features of the learner in question are being predicted? At present, the available genetic predictors are fairly broad, but more targeted genetic predictions may become available over time. Finally, what are the implications of using genetic predictors for equity? Can all children take advantage of any useful diagnostic information that becomes available? To further complicate matters, there will be continuous need for monitoring the consequences of including such information in research and practice.

We close by focusing on the question of equity. As genetics increases in salience across scientific domains and public life, we advocate for critical and open conversation among policy makers, educators, and researchers. To ensure that genetics research benefits all and not just some, regulation meant to safeguard privacy and equal treatment will be increasingly important. Spaces for academic debate and engagement with the American public on issues pertaining to genetically informed research are already opening (Columbia University, 2013; Emanuel, 1998; Personal Genetics Education Project, n.d.; University of California San Francisco, n.d.). Expanding the conversation to encourage adversarial collaboration and public awareness will prove critical for enacting regulations that keep equity in mind.

The floodgates of genetic data have opened. It is our opinion that education will undoubtedly be affected. When should genetic data be used? What regulations should be put in place? These are challenging questions that demand informed engagement. How we as researchers engage with these new developments to proactively combat the use of genetically informed research for racist, classist, or inequitable purposes will be of the utmost importance.

Authors' Note

Authors contributed equally.

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