improve causal conclusions on how genes and environment interact to affect behavior. As has been observed with both genome- and brain-wide association studies, bigger is not always better, and an increased focus on smaller, more thoroughly characterized populations with functional genetic data will lead to stronger conclusions. A critical factor that needs to be considered in all studies is the growing awareness of the plasticity of genetic mechanisms of behavior, particularly the role of epigenetics.

The line between what was traditionally seen as genetic and environmental effects is increasingly blurred. Rather than environmental confounding, these may be epigenetic effects, and the discussion of PGSs in social science would be informed by a greater understanding of and appreciation for animal studies of behavioral genetics, where the bar for causal conclusions may be much higher. This is an especially important consideration in discussions of using PGSs, or any other type of genetic data, to control for genetic effects and focus on environmental factors. This is a problematic notion at the very least. Even if other types of genetic data are beyond the primary focus of the target article, we argue that consideration of functional genetic outputs is critical for future genetic studies in the social sciences, whether or not these data are collected in a particular PGS study.

Financial support. This research received no specific grant from any funding agency, commercial, or not-for-profit sectors.

Competing interest. None.

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Cognitive traits are more appropriate for genetic analysis than social outcomes

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doi:10.1017/S0140525X22002515, e224

Abstract

The critique of the genetics of complex social outcomes is partly well-founded, insofar as social outcomes sometimes have unreliable relations with cognitive traits. But the correct conclusion is not to dismiss the entire field altogether. Rather, the implication is to redirect geneticists' attention to the stable cognitive phenotypes that are natural candidates for genetic analysis.

Burt's point that heritability estimates and polygenic scores are context- and population-dependent is well-taken and widely appreciated. However, it should not be overstated as implying that all genetic analyses are irremediably socially contingent, varying widely depending on period, culture, and context, thereby shunning any hope of identifying stable, meaningful genetic associations.

One can of course tell stories about education being something very different in a remote hunter–gather society or in the distant future, but this should not obscure the fact that the notion of educational achievement in the twenty-first century that is the current focus of genetic analysis is a well-defined and circumscribed concept that is essentially the same all over the world except for some extremely isolated cultures where schools don't exist. Even if it is true that the personality traits that were likely to attract a young woman to higher education in the 1870s and in the 2020s United States may differ to some extent, the cognitive traits (detailed further below) that would have been important for her to succeed at university in 1870 are very likely to be the same as those important in 2020, and they are also the same in the United States, in Saudi Arabia, or in Thailand, thus providing a stable basis for the genetic analysis of educational achievement. When some of these factors differ between countries or periods, this should not be cause for despair or rejection of genetic approaches, as the issue is perfectly empirically tractable: This should rather be welcomed as an opportunity to describe interesting gene–environment interactions.

Nevertheless, Burt's critique has the merit of highlighting the potential gaps between the social outcomes that are currently subjected to genetic analysis, and their cognitive basis. One should recall that social outcomes such as educational achievement or income have been genetically studied mainly because they were conveniently available in very large databases. In every genetics project, every participant answers one question about their highest obtained degree, regardless of the initial goal of the research. Thus, pooling across many projects has enabled researchers to gather the millions of participants required to compute reliable educational achievement polygenic scores (Okbay et al., 2022).

But to the cognitive scientist, this may seem a temporary distraction: These complex social outcomes are not phenotypes that

are under direct natural selection and that should naturally be the focus of genetic analysis. The phenotypes of interest for genetic analysis are situated at the cognitive level, where stable traits can be defined and can be the target of selection. For educational achievement, these are specific cognitive abilities: Not just general intelligence (which is itself a complex emerging property; Ramus, 2017), but its underlying components: Verbal ability, abstract reasoning, working memory, and also more specific cognitive skills such as phonological awareness (which contributes to reading acquisition) or number sense. One should not forget the popular but ill-named "noncognitive skills" (Ramus, 2022) such as conscientiousness, self-control, intrinsic motivation, grit, which do explain part of the educational achievement variance and which are also genetically influenced (Demange et al., 2021). These traits reliably underlie educational achievement regardless of time, culture, and gender of the learner, and there is every reason to think that they have a stable neural and genetic basis, which may be to a large extent similar in all populations.

Similarly, the answer to the question "have you ever had sex with someone of the same sex? Yes/No" has never been a valid phenotype for genetic analysis, but it is the one that was available for UK Biobank and 23andMe participants (Ganna et al., 2019). These authors are of course well aware that the stable cognitive trait of interest is sexual orientation, that it is continuous (e.g., as on the Kinsey scale), and that its relationship with actual sexual behaviour is imperfect, subject to social norms, to opportunities, and to many life circumstances. Genome-wide research on the genetics of sexual orientation will have to wait until an appropriate scale is rated by a sufficiently large number of participants.

An additional difficulty that may be less widely appreciated is that the cognitive functions that are under genetic influence are latent, unobservable variables, that cannot simply be equated with performance in one behavioural test. This is because any test, no matter how elementary it seems, inevitably recruits several cognitive functions. For instance, even the simplest reaction time test involves not only processing speed but also vision (or audition, to perceive the signal), sustained attention, language skills (to understand instructions), and motor skills (to produce a response). Therefore, there never is a one-to-one mapping between cognitive functions and behavioural tests. Any cognitive function can only be inferred by triangulating across several behavioural tests involving it in different ways.

This implies that research into the genetics of cognitive functions is going to be much more difficult than running a genome-wide association study (GWAS) on an answer to a single question or on a single test score. It will require administering well-designed, comprehensive test batteries to very large populations.

The conclusion is that the critique of the genetics of complex social outcomes is partly well-founded, insofar as social outcomes sometimes have unsystematic relations with cognitive traits. But the correct conclusion is not to dismiss the entire field altogether. Rather, the implication of this critique is to redirect geneticists' attention to the stable cognitive phenotypes that are natural candidates for genetic analysis. Unfortunately, studying the genetics of specific cognitive functions will take greater efforts and a longer time until the necessary test results are collected in sufficiently large genotyped populations.

Financial support. This work has received support by grants ANR-17-EURE-0017 and ANR-10-IDEX-0001-02.

Competing interest. None.

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Misguided model of human behavior: Comment on C. H. Burt: "Challenging the utility of polygenic scores for social science…"

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doi:10.1017/S0140525X22002333, e225

Abstract

This commentary emphasizes two problem areas mentioned by Burt. First, that within-family designs do not eradicate stratification confounds. Second, that the linear/additive model of genetic causes of form and variation is not supported by recent progress in molecular biology. It concludes with an appeal for a (biologically and psychologically) more realistic model of such causes.

Behavior geneticists tend to think that their field is unfairly controversial because of past associations with racism and eugenics. But there's more to it than that. Over the history of BG many scholars have commented on its seeming existence in a parallel universe, demanding relaxed scientific standards, building castles in the air with much reliance on "promissory notes," as Burt puts it. Regarding BG's grounding in unlikely assumptions, Kempthorne (1978, p. 18) asked "How naive can you get?" An illustration is how variations in cognition, educational attainment (EA), height, weight, and so on, are considered to be equally "complex," with similar causal patterns of form and variation, as if eons of evolution and gulfs of biological necessity had never happened.

Another example, of course, is how genome-wide association studies/polygenic scores (GWASs/PGSs) appeal to vague "phenotypes," using poorly validated measures, "surrogates" and "proxies," inferring causes from mountains of correlations that largely wash-out over time (Richardson & Norgate, 2015). Noting such thin evidential gruel Fletcher (2021, p. 256) refers to the "sleights of hand and folk wisdom from behavioral genetics." Burt expertly

https://doi.org/10.1017/S0140525X22001145 Published online by Cambridge University Press