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Title: The Dubious Precision and Utility of Heritability Estimates

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## Abstract

Uchiyama et al. question heritability estimates in a convincing manner. We offer additional arguments to further bolster their claims, highlighting methodological issues in heritability coefficients' derivation, their misuse in various contexts, and their potential contributions to exacerbating common erroneous intuitions that have been shown to lead to deleterious social phenomena. We conclude that science should move away from using them.

We are largely in agreement with the convincing, important arguments of Uchiyama et al. As they cogently explain, culture plays an oversized role in human phenotypes, and this has been largely neglected in behavioral genetics research to date. It is not surprising that it has taken a while for researchers to appreciate the key ways in which culture is implicated in our phenotypes, as culture so often remains invisible to observers. People rarely notice culture until they encounter exotic others who are doing things differently, and still this often just leads people to appreciate how culture shapes other people, as opposed to themselves (Causadias et al., 2018). This culture-blindness has affected commonplace approaches in behavior genetics, but also has been exacerbated by its predominant methodological approaches and the conclusions they introduce. For example, both comparisons of monozygotic and dizygotic twins, and comparisons of adopted versus biological siblings, are conducted almost entirely within cultures due to the availability of such samples. These foundational methods of behavioral genetics have thus precluded the ability to detect the influence of culture in heritability, leading to a systemic neglect of culture in that field.

We argue that when one considers the arguments of Uchiyama et al., the accuracy of heritability estimates becomes deeply questionable, as a major contributor to the variability explained is not only neglected but is often erroneously attributed to a different source – genes. For example, consider the heritability of self-esteem (see Darnimrod & Heine, 2011a). Self-esteem's heritability was estimated to be around .5, with shared environmental effects explaining negligible amount of the variance (e.g., Roy et al., 1995). These analyses neglected the substantial cultural variability in the construct (e.g., a meta-analysis estimated the magnitude of cultural differences in self-esteem

between Westerners and East Asians to be  $d = 0.91$ : Heine & Hamamura, 2007). The neglect of this large cultural component of self-esteem surely must contribute to an overestimation of the heritability.

Heritability estimates are often inappropriately used to establish a purported hierarchy of the degree to which genetics affects different phenotypes; for example, the estimated heritability of schizophrenia has been found to be higher than it is for depression (e.g., Wray & Gottesman, 2012). However, Uchiyama et al.'s arguments suggest that these contrasting heritability values may reflect instead that the uniformity of a culture contributes more to schizophrenia risk than it does for depression, undermining the utility of these comparisons across traits.

Another way that heritability estimates are commonly used is to provide an estimate of the ceiling of genetic variability that polygenic scores can be used to account for, often terming the residual unexplained variability that is attributed to the genes as “missing heritability.” For example, a paper may conclude that because a given trait is 40% heritable, and that polygenic scores can predict 20% of variability in that trait, then this means that the polygenic estimate is accounting for half of genetic variability (e.g., Derringer et al., 2010; Schunkert et al., 2011). However, this would also seem to be a dubious conclusion given that Uchiyama et al. make the case that the absolute value of heritability for a given sample can never be known until cultural factors are fully accounted for. Moreover, it is important to note that people do not just belong to a single monolithic cultural group, but rather belong to many overlapping subcultures that include their religion, social class, ethnic group, geographic region, etc. (e.g., Cohen, 2009).

Hence, it will rarely be straightforward to identify all of a given individual's cultural influences, and thus heritability estimates will remain imprecise.

Heritability estimates may not only be inaccurate, as discussed above, but may also introduce societal costs. People have essentialist intuitions that are particularly accessible whenever genetic contributions to phenotypes are discussed (Dar-Nimrod & Heine, 2011; Heine, 2017). Essentialist intuitions lead people to assume that the ultimate cause of any natural phenomenon is the result of some invisible forces that lie deep within it (Gelman, 2003); we also seem to treat many social categories like we treat natural categories (Rothbart & Taylor, 1992). Hence, people are tempted to assume that whenever you see differences between two groups, the most likely cause of those differences lies inside them, such as in their respective genomes. In contrast, whereas it requires more cognitive effort to consider other potential causes, such as in their cultures, their life histories, or their social environments. These intuitions can become especially problematic when we reflect on the heritability of desirable traits, which are often undergirding discussions of racism, sexism, and eugenics (e.g., Heine et al., 2017). The unwarranted air of scientific confidence in the precision of heritability estimates may have contributed to these deleterious intuitions, as research indicates that those intuitions are magnified by common media portrayals of scientific findings (Dar-Nimrod et al., 2021). We are hopeful that Uchiyama et al.'s clear-eyed questioning of heritability estimates may also contribute to dampening people's reflexive urges to turn to simple genetic essentialist accounts and the harms associated with them.

The combination of the questionable practices at the basis of the derivation of heritability estimates, their misuse in some contexts (e.g., the missing heritability), and

their potential contributions to sustaining erroneous, deleterious intuitions, leads us to call for discarding this metric under most circumstances. We acknowledge the potential utility for it when one restricts their heritability estimates to a specific homogeneous population from which a large enough sample has been assessed (with potential use for medical research), but we contend that, as it is used today, it brings about more damage and less precision to the scientific endeavor it was meant to serve. With growing technological capabilities and better ability to derive useful metrics, such as polygenetic scores and penetrance, we will benefit from moving away from the mirage of accurate heritability estimates.

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