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Introduction to IDEA Special Issue

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GUEST EDITORIAL

Introduction to IDEA Special Issue

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Starting with Francis Galton's 1875 study of British twins sampled from the "upper and professional classes" (Burbridge 2001), quantitative genetic studies have typically represented individuals of European ancestry from middle and upper-middle class backgrounds. Even now, 86% of genome-wide association studies (GWAS) involve individuals of European descent (Fatumo et al. 2022). This special issue of *Behavior Genetics*, devoted to topics of inclusion, diversity, equity, and access, is intended to highlight why this lack of diversity is a problem, to identify some solutions, and to showcase studies that include diverse samples and describe methodological innovations to analyze data from diverse groups. Before turning to these papers, we briefly review why the lack of diversity is a problem for the field.

Researchers in the social and medical sciences have long recognized the implications of this lack of diversity. Over 20 years ago, Stoolmiller measured the restricted range of environments in studies of adoptees growing up in predominantly White, middle-class families and identified it as a potential source of downward bias in estimates of the shared environment (Stoolmiller 1999). There is ample evidence that social determinants of health and social outcomes are not equally distributed across sub-populations, their effects may differ across subpopulations, and their effects may vary as a function of other social determinants and genomic determinants (Kolak et al. 2020). More recently, researchers have recognized that polygenic scores based on samples from one ancestral group are not portable to other ancestral groups and that risk prediction models and personalized interventions involving these scores are likely to perpetuate health and social disparities (Martin et al. 2019).

This lack of diversity, both with respect to genetic diversity and diversity of experience, hampers our ability to develop accurate risk prediction models, to generate unbiased estimates of genetic and environmental factors, and to comprehensively characterize the range of environments, exposures, and experiences that impact complex human traits. Recruiting samples that reflect both genetic diversity and diversity of experience will require researchers to study groups who have, historically, been under-represented in research and to change how we study them, both in terms of the kinds of questions we ask and in terms of how we facilitate and incentivize their participation. Here, we provide some examples of how to achieve these changes. The studies included in the special issue, which we describe in greater detail below, describe some additional strategies. Finally, we acknowledge efforts like those of the National Human Genome Research Institute to develop a more diverse genomics workforce by increasing exposure and access to genomics research and to supporting training programs and networks that connect undergraduate and graduate students to careers in genomics and that foster independent research and clinical careers (https://www.genome.gov/sites/default/files/media/files/2021-01/NHGRI_DiversityActionAgenda.pdf).

A common approach to increasing genetic diversity is to collect genetic data from people across the globe. Many countries, across multiple continents, have established biobanks for this purpose. Genetic diversity within countries may also be substantial and, in such countries, another approach is to recruit nationally representative samples representing hundreds of thousands of participants. Examples of this include the All of Us Research program, sponsored by the National Institutes of Health and designed to collect biospecimens from one million adults in the United States (The All of Us Research Program Investigators 2019). In theory, such large samples have the advantage of being sufficiently well-powered for sub-population analyses of genetic effects and of genotype x environment interactions.

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A potential downside is that the protocols designed to assess people's environments and experiences may query a relatively homogeneous set of experiences that are broadly applicable to all respondents. One way to address this challenge is to recruit large and well-powered samples that are homogeneous in key respects and diverse in others. This is a strategy employed by researchers who have recruited large samples of self-identified Hispanic or Latino participants, or large samples of Non-Hispanic Black participants that are diverse with respect to socioeconomic status, immigration status, national origin, acculturation status, and other salient experiences that, crucially, may be unique to those groups (Sorlie et al. 2010). In the United States, these sampling approaches are complicated (in some respects) and enriched (in others) by the growing number of individuals who identify as multiracial – a category that grew 276% between 2010 and 2020 according to US census data. Genetic diversity is common within other continental ancestral groups as well, underscoring the need for methodological approaches that adequately address genetic admixture (Kachuri et al. 2023).

Efforts to make samples more diverse will benefit from the involvement of potential participants in the research design and implementation process. This is the approach taken by Whole Communities-Whole Health. Whole Communities–Whole Health is a highly interdisciplinary effort at UT Austin to design a 5-year cohort study to understand how physical and emotional adversity, biology, and the environment affect the health of families facing systemic injustice (https://bridgingbarriers.utexas.edu/whole-communities-whole-health). The Whole Communities-Whole Health team has taken steps to increase the value and ease of participation for potential participants and to reflect their priorities and experiences. They have surveyed community members about what they perceive to be the major problems in their community, and they are collecting data about those issues. They have made it easier for individuals to participate by introducing wearable technology and sensor-based approaches to measuring things like air quality. They have refined their measurement protocol, by piloting the study with "ambassador families" who provide feedback on the various measures and assessments. Finally, they are sharing data with participants so participants can learn about their own health and have access to information about their community that they can use to advocate for change.

Contents of the Special Issue

The articles included in this first of issue of Behavior Genetics devoted to topics of inclusion, diversity, equity, and access offer additional discussion of and solutions to the challenges around making quantitative genetic studies and the genomics workforce more diverse. The issue is organized into three categories: methods for diversifying behavior genetics programs, methodological issues in conducting behavior genetic research in diverse populations, and presentations of behavior genetic research incorporating aspects of diversity. *Garrison, et al.* emphasize that to improve diversity among researchers in behavior genetics it is vital to improve diversity in the pipeline of students interested in the field. They provide specific strategies that faculty can implement to cultivate supportive and inclusive undergraduate research environments that are crucial for fostering the next generation of behavior genetic researchers. For students who have opted into the field, *Paulich et al.*. highlight the need for Diversity, Equity, and Inclusion committees integrated within behavior genetic programs that can actively confront misuse of behavioral genetic results and promote anti-racism.

The next set of articles focuses on methodological issues. Genome wide association studies (GWAS) and polygenic scores (PGS) have become the new standard in behavior genetic research; however, *Non et al.* discuss the methodological, theoretical, and ethical concerns that lead to misinterpretation, particularly for minoritized groups. Behavior genetic research in underrepresented groups, minoritized groups, and low- and middle- income countries (LMIC) is currently lacking. *Oginni et al.* discuss the challenges and opportunities of conducting twin research in Nigeria, where higher rates of twinning make the twin design highly feasible and suitable. Although 25% of the world population is from South Asia, South Asians represent only 2% of participants in genetic studies. *Dokuru et al.* discuss the vast cultural and genetic diversity of the region and suggest strategies for future studies in the area. As an example, *Dissanayake et al.*, present their pilot study of collecting twin and children-of-twin data in Sri Lanka as part of the Colombo Twin and Singleton study (COTASS). All four papers emphasize the role that participant engagement in the research will play in successful behavior genetic studies in diverse and underrepresented populations.

The final group of papers presents behavior genetic research that incorporates diversity in some form: country of origin, socioeconomic adversity, racial/ethnic background. Rapid urbanization in many LMICs is associated with dramatic changes in demography and health behaviors. *Zavos et al.*, investigated the etiology of nutrition and cardio-metabolic phenotypes in COTASS: a population-based twin and singleton sample in Colombo, Sri Lanka. The remaining papers examine emotional health and resilience in adolescents and the possible moderating role of family environment. Using data from the Adolescent Cognitive Brain Development Study (ABCD), *Elam et al.* examined

differences in genetic influences on depression trajectories across Black/African American, White/European American, and Hispanic/Latinx adolescents. Associations with subsequent substance use also differed across groups. In their investigation of the role of parenting and family conflict on externalizing behaviors in adolescents in the ABCD study, *Trevino et al.* found complex interactions among racial/ethnic background, polygenic score for alcohol use disorder, and parenting style. *Rea-Sandin et al.* focused particularly on family values in the ABCD study using the Mexican American Cultural Values Scale. Results suggested that family cultural values like loyalty, support, and obligation modified genetic and environmental influences on internalizing and externalizing behaviors. Finally, *Vazquez et al.* focused on the role of parental behavior as a modifier of genetic and environmental influences on youth resilience in Twin Study of Behavioral and Emotional Development in Children. Children experiencing high levels of parental nurturance were more resilient to disadvantage, regardless of their genetic predisposition towards resilience.

Conclusions

Behavior genetics has a history of both eugenic thinkers (e.g., Francis Galton, often referred to as the father of behavior genetics) and adamant anti-eugenicists (e.g., Theodosius Dobzhansky, the first present of the Behavior Genetics Association). Dobzhansky emphasized that natural variation is an essential resource for any organism: without sufficient genetic diversity an organism might eventually lose its capacity to evolve. Behavior genetics as a field has evolved over time, but it will only continue to adapt and respond to new innovations, new discoveries, and new challenges if we ensure that the field has a deep reserve of diversity in researchers, samples, and methods. We hope this is only the first of many issues of the journal to be devoted to methodological issues and research outcomes that highlight inclusion, diversity, equity, and access in behavior genetics.

References

Burbridge D (2001) Francis Galton on twins, heredity and social class. Br J Hist Sci 34:323–340

Fatumo S, Chikowore T, Choudhury A, Ayub M, Martin AR, Kuchenbaecker K (2022) A roadmap to increase diversity in genomic studies. Nat Med 28(2). https://doi.org/10.1038/s41591-021-01672-4

Kachuri L, Chatterjee N, Hirbo J, Schaid DJ, Martin I, Kullo IJ, Kenny EE, Pasaniuc B, Witte JS, Ge T (2023) Principles and methods for transferring polygenic risk scores across global populations. Nat Rev Genet 1–18. https://doi.org/10.1038/s41576-023-00637-2

Kolak M, Bhatt J, Park YH, Padrón NA, Molefe A (2020) Quantification of Neighborhood-Level Social Determinants of Health in the Continental United States. JAMA Netw Open 3(1):e1919928. https://doi.org/10.1001/jamanetworkopen.2019.19928

Martin AR, Kanai M, Kamatani Y, Okada Y, Neale BM, Daly MJ (2019) Clinical use of current polygenic risk scores may exacerbate health disparities. Nat Genet 51(4). https://doi.org/10.1038/s41588-019-0379-x

Sorlie PD, Avilés-Santa LM, Wassertheil-Smoller S, Kaplan RC, Daviglus ML, Giachello AL, Schneiderman N, Raij L, Talavera G, Allison M, LaVange L, Chambless LE, Heiss G (2010) Design and implementation of the Hispanic Community Health Study/Study of latinos. Ann Epidemiol 20(8):629–641. https://doi.org/10.1016/j.annepidem.2010.03.015

Stoolmiller M (1999) Implications of the restricted range of family environments for estimates of heritability and nonshared environment in behavior-genetic adoption studies. Psychol Bull 125(4):392–409

The all of Us Research Program Investigators (2019) The all of Us Research Program. N Engl J Med 381(7):668–676. https://doi.org/10.1056/NEJMsr1809937