

Large-scale GWAS Investigating Genetic Contributions to Queerness Will Decrease Stigma Against LGBTQ+ Communities

Authors : Paul J. McKay

Abstract : Large-scale genome-wide association studies (GWAS) investigating genetic contributions to sexual orientation and gender identity are largely lacking and may reduce stigma experienced in the LGBTQ+ community by providing an underlying biological explanation for queerness. While there is a growing consensus within the scientific community that genetic makeup contributes – at least in part – to sexual orientation and gender identity, there is a marked lack of genomics research exploring polygenic contributions to queerness. Based on recent (2019) findings from a large-scale GWAS investigating the genetic architecture of same-sex sexual behavior, and various additional peer-reviewed publications detailing novel insights into the molecular mechanisms of sexual orientation and gender identity, we hypothesize that sexual orientation and gender identity are complex, multifactorial, and polygenic; meaning that many genetic factors contribute to these phenomena, and environmental factors play a possible role through epigenetic modulation. In recent years, large-scale GWAS studies have been paramount to our modern understanding of many other complex human traits, such as in the case of autism spectrum disorder (ASD). Despite possible benefits of such research, including reduced stigma towards queer people, improved outcomes for LGBTQ+ in familial, socio-cultural, and political contexts, and improved access to healthcare (particularly for trans populations); important risks and considerations remain surrounding this type of research. To mitigate possibilities such as invalidation of the queer identities of existing LGBTQ+ individuals, genetic discrimination, or the possibility of euthanasia of embryos with a genetic predisposition to queerness (through reproductive technologies like IVF and/or gene-editing in utero), we propose a community-engaged research (CER) framework which emphasizes the privacy and confidentiality of research participants. Importantly, the historical legacy of scientific research attempting to pathologize queerness (in particular, falsely equating gender variance to mental illness) must be acknowledged to ensure any future research conducted in this realm does not propagate notions of homophobia, transphobia or stigma against queer people. Ultimately, in a world where same-sex sexual activity is criminalized in 69 UN member states, with 67 of these states imposing imprisonment, 8 imposing public flogging, 6 (Brunei, Iran, Mauritania, Nigeria, Saudi Arabia, Yemen) invoking the death penalty, and another 5 (Afghanistan, Pakistan, Qatar, Somalia, United Arab Emirates) possibly invoking the death penalty, the importance of this research cannot be understated, as finding a biological basis for queerness would directly oppose the harmful rhetoric that “being LGBTQ+ is a choice.” Anti-trans legislation is similarly widespread: In the United States in 2022 alone (as of Oct. 13), 155 anti-trans bills have been introduced preventing trans girls and women from playing on female sports teams, barring trans youth from using bathrooms and locker rooms that align with their gender identity, banning access to gender affirming medical care (e.g., hormone-replacement therapy, gender-affirming surgeries), and imposing legal restrictions on name changes. Understanding that a general lack of knowledge about the biological basis of queerness may be a contributing factor to the societal stigma faced by gender and sexual orientation minorities, we propose the initiation of large-scale GWAS studies investigating the genetic basis of gender identity and sexual orientation.

Keywords : genome-wide association studies (GWAS), sexual and gender minorities (SGM), polygenicity, community-engaged research (CER)

Conference Title : ICQBSOGI 2022 : International Conference on Queer Bioethics, Sexual Orientation and Gender Identity

Conference Location : New York, United States

Conference Dates : December 09-10, 2022