



Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.

Furthermore, it facilitates future studies exploring the relevance of genetic variants in disease burden among the African populations. An example is the *APOL1* variants (Figure 1) that provide protection against specific *Trypanosoma* species in African populations from endemic regions like West Africa, but also increase susceptibility to nephropathy in populations from non-trypanosomiasis endemic areas in Africa or from the African Diaspora. The study also identifies new evidence for natural selection in 62 genes associated with immune-related functions (for viral and bacterial infection), involved in DNA maintenance and carbohydrate and lipid metabolism. The researchers additionally teased out signals of selection within each population, for example, genes involved in metabolism were under selection among individuals from Botswana. Among the selection signals detected in Botswana, the authors also found evidence for preferential gene-flow from Khoe-San ancestry, highlighting adaptive introgression in Southern Africa.

The study presented by Choudhury *et al.* [3] is also a major milestone in African genomics research capacity, as it was led predominantly by local researchers using local infrastructure and resources for large-scale genomics research in Africa. Collectively, their results refine our current understanding of human migration, patterns of admixture, and strong drivers of selection across the African continent. The study also points out the extent of uncatalogued genomic variation across the continent and the need for future genomic studies of the many diverse under-represented populations in Africa.

Acknowledgements

C.F.-L. and C.S. were funded by the European Research Council (ERC StG AfricanNeo, grant no. 759933 to C.S.). C.F.-L. was funded by the Marcus Borgström Foundation for Genetic Research, the Sven and Lilly Lawski's Foundation, and the Royal Physiographic Society of Lund (Nilsson-Ehle Endowments).

Resources

<https://h3africa.org/>

¹Human Evolution, Department of Organismal Biology, Evolutionary Biology Centre, Uppsala, Sweden
²Palaeo-Research Institute, University of Johannesburg, Johannesburg, South Africa
³SciLifeLab, Uppsala, Sweden

*Correspondence:
cesar.fortes-lima@ebc.uu.se (C. Fortes-Lima) and
carina.schlebusch@ebc.uu.se (C. Schlebusch).
<https://doi.org/10.1016/j.tig.2020.11.005>

© 2020 The Author(s). Published by Elsevier Ltd. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

References

- Schlebusch, C.M. and Jakobsson, M. (2018) Tales of human migration, admixture, and selection in Africa. *Annu. Rev. Genomics Hum. Genet.* 19, 405–428
- Sirugo, G. *et al.* (2019) The missing diversity in human genetic studies. *Cell* 177, 1080
- Choudhury, A. *et al.* (2020) High-depth African genomes inform human migration and health. *Nature* 586, 741–748
- H3Africa Consortium *et al.* (2014) Research capacity. Enabling the genomic revolution in Africa. *Science* 344, 1346–1348
- Gurdasani, D. *et al.* (2019) Uganda genome resource enables insights into population history and genomic discovery in Africa. *Cell* 179, 984–1002
- Bergström, A. *et al.* (2020) Insights into human genetic variation and population history from 929 diverse genomes. *Science* 367, eaay5012
- Schlebusch, C.M. *et al.* (2020) Khoe-San genomes reveal unique variation and confirm the deepest population divergence in *Homo sapiens*. *Mol. Biol. Evol.* 37, 2944–2954
- Fan, S. *et al.* (2019) African evolutionary history inferred from whole genome sequence data of 44 indigenous African populations. *Genome Biol.* 20, 82
- Patin, E. *et al.* (2017) Dispersals and genetic adaptation of Bantu-speaking populations in Africa and North America. *Science* 356, 543–546
- Semo, A. *et al.* (2020) Along the Indian Ocean coast: genomic variation in Mozambique provides new insights into the Bantu expansion. *Mol. Biol. Evol.* 37, 406–416

Science & Society

Genetics and COVID-19: How to Protect the Susceptible

Robert I. Field,¹
 Anthony W. Orlando ^{2,*} and
 Arnold J. Rosoff³



Along with the potential for breakthroughs in care and prevention, the search for genetic mechanisms

underlying the spread and severity of coronavirus disease 2019 (COVID-19) introduces the risk of discrimination against those found to have markers for susceptibility. We propose new legal protections to mitigate gaps in protections under existing laws.

Genetic research holds the promise of unlocking secrets of COVID-19 and opening new avenues for mitigation [1]. Among suggestive findings to date is a possible correlation between disease severity and DNA polymorphisms in the virus host factors *ACE2* and *TMPRSS2* [2]. Findings on genetic correlates of COVID-19 progression may lead to better understanding of the cellular mechanisms of susceptibility and resistance and may enable predictions of individual risk for severe disease progression.

Discrimination Risks

However, such advances come with a significant social risk in the potential for a new form of discrimination. Until a vaccine or effective treatment is available, those whose genomes make them especially vulnerable might be considered ill-suited for exposure-prone jobs, especially in health care. They might also face resistance in other spheres, such as health-related insurance, apartment leases, nursing home placements, and even bank loans. Conversely, those found to have genetic resistance may be treated more favorably in these regards.

Governments would also face incentives to favor those with genetic resistance to COVID-19 in disease mitigation strategies. ‘Genetic passports’ exempting genetically resistant individuals from strict social distancing restrictions would enable states to avoid more widespread lockdowns. Those with genetic markers for susceptibility would face stronger restrictions.

A similar mechanism has been proposed for ‘immunity passports’, which assume that an individual has acquired immunity to the disease based on a serologic test. This idea has already raised concerns of a number of negative social effects. For example, they would erode privacy, disadvantage marginalized groups, advantage those with better access to tests, create new forms of social stratification, and facilitate new forms of discrimination [3]. Genetic markers raise even greater concern in this regard, as they are immutable. Those born with genetic susceptibility will always have it, while those who lack immunity because they have not been exposed to the virus can later acquire it. Moreover, those with known genetic susceptibility would be less likely to acquire antibody-building exposure because of their heightened need to avoid the disease.

Inadequacy of Current Legal Protections

Current legal protections and their ethical foundation are ill-suited for this challenge. The four principal federal statutes that address genetic privacy and discrimination contain significant gaps. The Health Insurance Portability and Accountability Act (HIPAA), through its Privacy Rule, restricts the use and disclosure of ‘Protected Health Information’, which includes the results of genetic tests along with other patient medical information. However, there is an exception for the sharing of data in deidentified form for research, which is concerning because it is becoming increasingly easy to reidentify anonymous genomes [4]. The Common Rule, formally known as the Federal Policy for the Protection of Human Subjects, applies to research funded by several federal agencies and requires researchers to communicate risks and benefits of research to human subjects and to obtain their written consent. However, it does not apply to research funded by nongovernmental entities, and isolated genetic biospecimens do not ordinarily qualify as ‘human subjects’ [5].

The Genetic Information Nondiscrimination Act (GINA) prohibits employers and health insurers from using genetic information in hiring or promotion and in underwriting and setting health insurance premiums, although the Affordable Care Act has made the insurance protection irrelevant. However, the law does not extend beyond these two contexts, leaving it possible to discriminate with regard to life insurance, disability insurance, long-term care insurance, housing, and consumer finance [6]. The Americans with Disabilities Act (ADA) prohibits discrimination in employment and public services based on a disability, a history of having had one, or a perception of having one. However, the law’s protection applies only to disabilities that have already manifested, so susceptibility to a condition is not covered before symptoms appear.

The Need for an Updated Ethical Framework

The ethical framework underlying these laws is similarly obsolete. It places primary emphasis on autonomy in protecting privacy and on beneficence in protecting those found to have genetic vulnerabilities. The seriousness of the COVID-19 pandemic elevates the crucial importance of research in the face of a global crisis; thus, a fresh consideration of the relative value of individual protection and research promotion is needed.

To honor beneficence, we must weigh the vulnerability of those who are most genetically susceptible to the disease against that of those most likely to suffer the burden of indiscriminate social distancing restrictions. To honor autonomy, we must protect the privacy of genetic findings, but would we permit those who are genetically susceptible to ignore their heightened risk and possibly expose others to infection? Alternatively, we might ground new legal protections in utilitarianism, seeking the greatest good for the greatest number of people, but doing this requires an inherently controversial and subjective

balancing of social harm from genetic discrimination against the loss of health and life from the disease.

Avenues for Reform

There are opportunities for legal reforms through regulations that embody a broadened ethical foundation and more effectively balance individual rights and research progress. As a start, the Privacy Rule could add narrower limits on sharing identified genetic information, except in the context of clinical need and then only in the most compelling circumstances. It might also require that genetic information be stored separately from the rest of the medical record. The Common Rule could set stricter parameters for collecting, storing, and sharing genetic information, including requirements for encrypting data and restricting access, coupled with more vigorous oversight by institutional review boards (IRBs). Implementing regulations under GINA could add COVID-19 susceptibility as an explicit example of the kinds of genetic tests that are subject to the law. Implementing regulations under the ADA could characterize COVID-19 susceptibility as a covered disability that is protected from discrimination. A disability under the Act is defined as an impairment of an essential life activity, and COVID-19 susceptibility could restrict the ability to socialize freely. Regulations could also define the kinds of measures, defined in the law as ‘reasonable accommodations’, that are appropriate for susceptible individuals to balance costs against risks.

In the longer term, new legislation might designate a single federal agency as the lead in regulating genetic risks, including those from COVID-19 susceptibility, to reduce inconsistencies and gaps in coverage and enforcement. Of course, the creation of such a body would require political consensus, which may be difficult in the current political environment.

None of these changes would unreasonably burden genetic investigations concerning COVID-19. Identified information could still be exchanged as needed for clinical care and for research. However, the risk of unauthorized disclosure and discrimination would be diminished, albeit not wholly eliminated. In the longer term, an effective vaccine would greatly mitigate both sets of concerns, but even if it were readily available, questions would still arise as to access, allocation, and acceptance.

COVID-19 has already forced us to confront ethical challenges for which we were unprepared, such as allocating scarce

equipment and medications and limiting civil liberties to control disease spread. The sooner we consider responses to the legal and ethical challenges of genetic research, the better prepared we will be.

Author Contributions

All authors contributed equally to the preparation of the manuscript.

¹Dornsife School of Public Health and Kline School of Law, Drexel University, Philadelphia, PA, USA

²College of Business Administration, California State Polytechnic University, Pomona, CA, USA

³The Wharton School, University of Pennsylvania, Philadelphia, PA, USA

*Correspondence:

aworlando@cpp.edu (A.W. Orlando).

<https://doi.org/10.1016/j.tig.2020.08.019>

© 2020 Elsevier Ltd. All rights reserved.

References

1. COVID-19 Host Genetics Initiative (2020) The COVID-19 Host Genetics Initiative, a global initiative to elucidate the role of host genetic factors in susceptibility and severity of the SARS-CoC-2 virus pandemic. *Eur. J. Hum. Genet.* 8, 715–718
2. Hou, Y. *et al.* (2020) New insights into genetic susceptibility of COVID-19: an *ACE2* and *TMPRSS2* polymorphism analysis. *BMC Med.* 18, 216
3. Kofler, N. and Baylis, F. (2020) Comment: ten reasons why immunity passports are a bad idea. *Nature* 581, 379–381
4. Drabiak, K. (2017) Caveat emptor: how the intersection of big data and consumer genomics exponentially increases information privacy risks. *Health Matrix* 27, 143–228
5. Koch, V.G. and Todd, K. (2018) Research revolution or status quo? The new Common Rule and research arising from direct-to-consumer genetic testing. *Hous. L. Rev.* 56, 81–121
6. Roberts, J.L. (2011) The Genetic Information Nondiscrimination Act as an antidiscrimination law. *Notre Dame L. Rev.* 86, 597–648