ge²p² global foundation
governance, ethics, evidence, policy, practice

Center for Genomic Medicine Governance, Ethics & Policy

Genomic Medicine Governance, Ethics, Policy: A Quarterly Review

May 2022 Number 01

This inaugural edition begins our exploration of a quarterly digest intended to aggregate and distill key content addressing genomic sciences and genomic medicine.

To curate this digest, we will directly review a broad spectrum of peer-reviewed journals and grey literature, as well as announcements and strategic actions from various practice domains and organization types including international agencies, INGOs, governments/regulatory bodies, academic and research institutions, consortiums and collaborations, foundations, and commercial organizations. More broadly, we will utilize *Google Scholar* to scan the literature. We acknowledge that this scope yields an indicative and not an exhaustive digest product.

This digest is a service of the GE2P2 Global Foundation and its newly-formed Center for Genomic Medicine Governance, Ethics & Policy. The Foundation is solely responsible for its content. Comments and suggestions should be directed to:

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GE2P2 Global Foundation
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We will organize digest content in each edition using subject categories to help readers navigate. We expect that these categories will evolve over time. Active subject areas in this edition include:

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REGULATORY GUIDANCE/CALL FOR PUBLIC COMMENT/CONSULTATION

FDA - Human Gene Therapy Products Incorporating Human Genome Editing; Draft Guidance for Industry

March 2022 [Docket No. FDA-2021-D-0398]

In this guidance, we, FDA, are providing recommendations to sponsors developing human gene therapy products incorporating genome editing (GE) of human somatic cells. Specifically, this guidance provides recommendations regarding information that should be provided in an Investigational New Drug (IND) application in order to assess the safety and quality of the investigational GE product, as required in Title 21 of the Code of Federal Regulations 312.23 (21 CFR 312.23). This includes information on product design, product manufacturing, product testing, preclinical safety assessment, and clinical trial design.

FDA - Considerations for the Development of Chimeric Antigen Receptor (CAR) T Cell Products; Draft Guidance for Industry.

March 2022 [Docket Number: FDA-2021-D-0404]

Chimeric antigen receptor (CAR) T cell products are human gene therapy products in which the T cell specificity is genetically modified to enable recognition of a desired target antigen for therapeutic purposes. This guidance is intended to assist sponsors, including industry and academic sponsors, developing CAR T cell products. In this guidance, we, FDA, provide CAR T cell specific recommendations regarding chemistry, manufacturing, and control (CMC), pharmacology and toxicology, and clinical study design. Recommendations specific to autologous or allogeneic CAR T cell products are noted in this guidance. This guidance also provides recommendations for analytical comparability studies for CAR T cell products. While this guidance specifically focuses on CAR T cell products, much of the information and recommendations provided will also be applicable to other genetically modified lymphocyte products, such as CAR Natural Killer (NK) cells or T cell receptor (TCR) modified T cells. These related product types can be highly specialized, and in many cases, considerations beyond those recommended in this guidance would depend on the specific product and manufacturing process. To discuss considerations specific to these related products, we recommend sponsors communicate with the Office of Tissues and Advanced Therapies (OTAT) in the Center for Biologics Evaluation and Research (CBER) before submitting an Investigational New Drug Application (IND) (e.g., by requesting a pre-IND meeting (Ref. 1))..

New guideline will enhance oversight of research in frontier fields

Zhang Zhihao

China Daily Updated: Mar 24,2022 10:20

[ENG.GOV.EN The State Council - The People's Republic of China]

[Editor's Note: We have not identified a full English translation of this guideline as of 10 May 2022. We have added text bolding for emphasis.]

A new national guideline on research ethics and governance will enhance China's oversight of projects in frontier fields, including life sciences, medicine and artificial intelligence, aiming to ensure that scientific and technological progress serves the greater good of humankind, officials and experts said.

The guideline also demands that international research projects abide by the regulations of the participants' home countries and pass ethical reviews. **Chinese authorities can organize experts to reevaluate international projects that have high ethical risks**, it said.

On March 27, the general offices of the Communist Party of China Central Committee and the State Council, China's Cabinet, issued the country's first comprehensive guideline on enhancing governance over ethics in science and technology.

Xiang Libin, vice-minister of science and technology, said the current ethic governance system cannot keep up with China's rapid sci-tech growth, given how some of the country's cutting-edge scientific endeavors are exploring unchartered territories with many uncertainties. "Science and technology is a double-edged sword," Xiang said. "Therefore, the guideline plays a key role in building consensus, improving public awareness on the importance of research ethics and governance, and mitigating ethical risks in scientific undertakings."

A key requirement of the guideline is that **research ethics should be emphasized and upheld throughout the entire process of scientific research and technological development**, Xiang said. Managing sci-tech ethics in accordance with laws and regulations, swiftly and properly handling emerging ethical challenges, **establishing a system of ethical standards based on Chinese characteristics,** and enhancing international cooperation in sci-tech governance are also among the top objectives, he added.

Scientific activities should serve the greater good of humankind, respect human and animal rights, treat social groups from different backgrounds fairly and equally, properly prevent and manage ethical risks, and maintain openness and transparency during research, according to the guideline.

"No agency, organization or individual can conduct scientific activities that damage social, public, biological and ecological security, nor can they undermine the safety and well-being of people's lives, health and dignity," it said.

Universities are encouraged to bolster education about research ethics in undergraduate and graduate studies. **Chinese authorities should guide universities, research institutions, medical agencies, social groups and companies to optimize their monitoring and early warning mechanisms to spot ethical risks.**

Violators of research ethics will be investigated and punished in accordance with relevant laws and regulations, with measures ranging from revoking research grants and titles to banning offenders from conducting future studies.

In regard to ethical review of high-risk research, Dai Guoqing, director of the Department of Supervision and Scientific Integrity at the Ministry of Science and Technology, said there will be a multilayered review mechanism in which a proposal is not only required to pass a review by the ethical committee of the researchers' institution, but also several rounds of reviews by local regulatory agencies.

Zhai Xiaomei, a member of the National Science and Technology Ethics Committee, said the profound respect for the right to life and personal dignity highlighted in the guideline is in the same spirit that led to the creation of China's first Civil Code, which went into effect in January last year.

In the medical experiments, the rights of trial participants should be fully protected, including their right to privacy and the right to make informed decisions, Zhai said. "They should be treated fairly and justly, and not be forced to make a compromise due to their circumstances."…

A major takeaway from the guideline for Zeng is the **requirement for international projects to pass ethical reviews in the participants' home countries.** "This is a big deal because foreign researchers can no longer carry out studies in China that are deemed too ethically risky in their home countries," he added.

The release of the new guideline, along with the country's efforts to improve research ethics and governance in recent years, show that China has begun a systematic building of ethics in scientific activities, which will benefit the country's sci-tech development and open new areas for international cooperation, Zeng said.

Editor's Note:
We are not aware that an official translation of this guidance into English has been released at this writing. We note the translation/analysis completed by the Institute of Automation, Chinese Academy of Sciences. at https://ai-ethics-and-governance.institute/2022/03/22/china-released-opinion-on-strengthening-the-ethics-and-governance-in-science-and-technology/. Further, we note the news item from *Nature* below.

> **China focuses on ethics to deter another 'CRISPR babies' scandal**
> *But some question whether a statement from the government will deter scientists from carrying out research that violates ethical norms.*
> NEWS
> **Nature,** 27 April 2022

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PROFESSIONAL CONDUCT

Standards of Conducts for Biostatisticians and Stem Cell Researchers: A Call for Self-formulated Aspirational Ethics Over Built-in Prohibitive Ethics

Keiko Sato & Mika Suzuki
Original Research/Scholarship - Open Access
Science and Engineering Ethics
Volume 28, issue 2, April 2022
Published: 17 March 2022
Abstract
We proposed the Standards of Conducts to provide a general framework that will serve as the basis for guiding each biostatistician and stem cell researcher to formulate their personal standards, rather than as rules with which they are required to comply. Given the responsibility and characteristics of their work, they are expected to maintain independence and work autonomously as professionals. Each of the Standards of Conducts comprises a preamble, mission and values to uphold, Standards of Conducts (10 items), and background. When one internalizes "self-formulated" standards, to make excuses for oneself would be akin to a self-betrayal; responsible actions can be anticipated. If one begins and continues to consider "who I am and what do I work for," this will become their inner energy, and a source of motivation and pride to inspire oneself. In addition, this aspirational style might help citizens to recognize the autonomous stance of the professional body and that they share the same values.

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CROSS-CUTTING ISSUES

Getting genetic ancestry right for science and society

We must embrace a multidimensional, continuous view of ancestry and move away from continental ancestry categories
Anna C. F. Lewis, et al.
Policy Forum

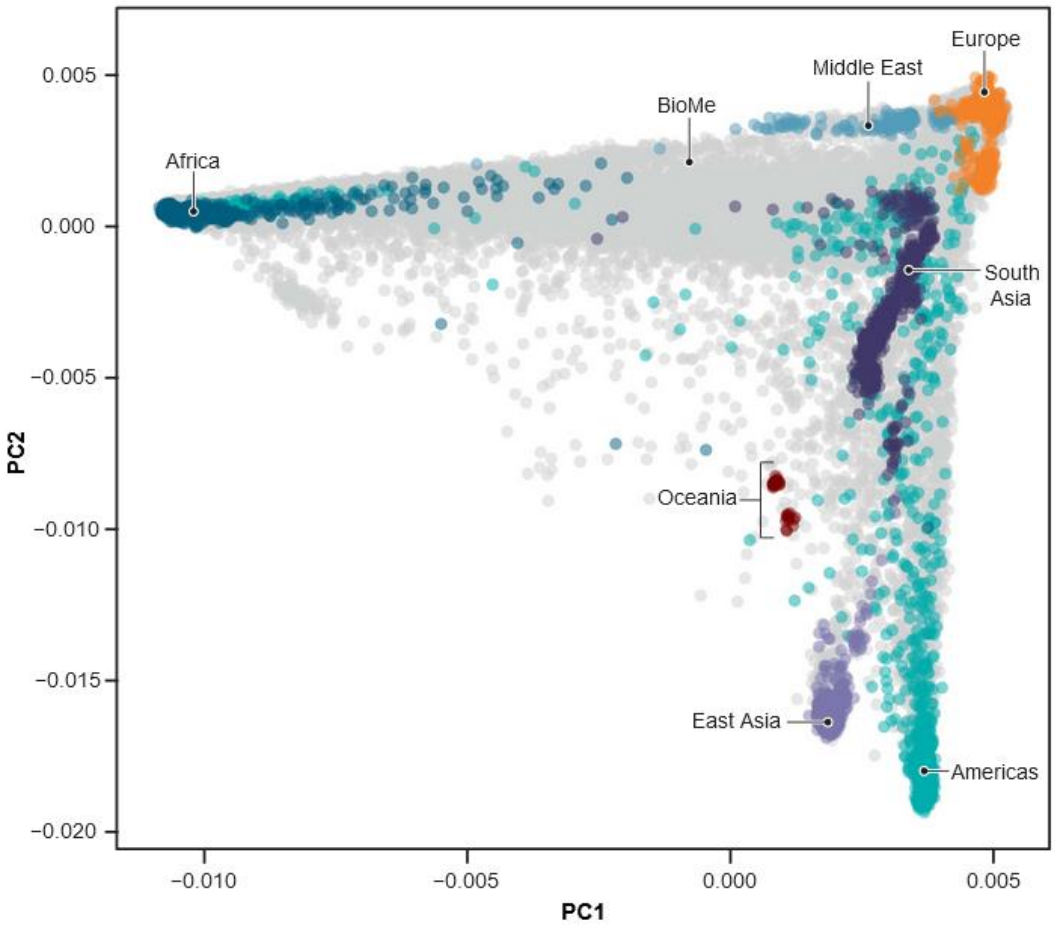
Science, Volume 376| Issue 6591| 22 Apr 2022

Abstract

Glaring health disparities have reinvigorated debate about the relevance of race to health, including how race should and should not be used as a variable in research and biomedicine (1). After a long history of race being treated as a biological variable, there is now broad agreement that racial classifications are a product of historically contingent social, economic, and political processes. Many institutions have thus been reexamining their use of race and racism and stating intentions about how race should be used going forward. One common proposal is to use genetic concepts—in particular, genetic ancestry and population categories—as a replacement for race (2). However, the use of ancestry categories has technical limitations, fails to adequately capture human genetic diversity and demographic history, and risks retaining one of the most problematic aspects of race—an essentialist link to biology—by allowing genetic ancestry categories to stand in its place.

THE CONTINUOUS, CATEGORY-FREE, NATURE OF GENETIC VARIATION

Colored dots (n = 4149) are reference panel individuals from 87 populations representing ancestry from seven continental or subcontinental regions projected onto the first two principal components (PC1 and PC2) of genetic similarity. Gray dots (n = 31,705) are participants from BioMe, a diverse biobank based in New York City. Clearly delineated continental ancestry categories (the islands of color) are shown to be a by-product of sampling strategy. They are not reflective of the diversity in this real-world dataset, which is made evident by the continuous sea of gray.



GRAPHIC: K. FRANKLIN/*SCIENCE* BASED ON (12)

Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals

A genome-wide association study in ~3 million individuals identifies 3,952 independent variants associated with educational attainment. A polygenic index explains 12–16% of variance for this trait and contributes to risk prediction for ten diseases.

Aysu Okbay, Yeda Wu, Alexander I. Young

Article | 31 March 2022 | *Open Access*

Nature Genetics, Volume 54 Issue 4, April 2022

Abstract

We conduct a genome-wide association study (GWAS) of educational attainment (EA) in a sample of ~3 million individuals and identify 3,952 approximately uncorrelated genome-wide-significant single-nucleotide polymorphisms (SNPs). A genome-wide polygenic predictor, or polygenic index (PGI), explains 12–16% of EA variance and contributes to risk prediction for ten diseases. Direct effects (i.e., controlling for parental PGIs) explain roughly half the PGI's magnitude of association with EA and other phenotypes. The correlation between mate-pair PGIs is far too large to be consistent with phenotypic assortment alone, implying additional assortment on PGI-associated factors. In an additional GWAS of dominance deviations from the additive model, we identify no genome-wide-significant SNPs, and a separate X-chromosome additive GWAS identifies 57.

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ACCESS, EQUITY, BENEFITS SHARING, PUBLIC TRUST

Expanding global access to genetic therapies

AWT Muigai, School of Biological Sciences, Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya

World View, Published: 07 January 2022

Nature Biotechnology, 40, pages 20–21 (2022)

Excerpt

…The era of genetic therapies — both gene-editing treatments and gene therapies, several of which are now on the market — has arrived for rare disease. But as more of these therapies come online, it is time to explore how current business models based on patents and restrictive licensing limit access to treatments. It is also time to explore whether there are other ways in which patents can still reward innovators and protect investments while ensuring that the widest number of patients who need these treatments can receive them…

Comparison of public discussions of gene editing on social media between the United States and China

J Ji, M Robbins, JD Featherstone, C Calabrese… -

PloS ONE, Published: May 2, 2022, https://doi.org/10.1371/journal.pone.0267406

Abstract

The world's first gene-edited babies event has stirred controversy on social media over the use of gene editing technology. Understanding public discussions about this controversy will provide important insights about opinions of science and facilitate informed policy decisions. This study compares public discussion topics about gene editing on Twitter and Weibo, as well as the evolution of these topics over four months.

Latent Dirichlet allocation (LDA) was used to generate topics for 11,244 Weibo posts and 57,525 tweets from September 25, 2018, to January 25, 2019. Results showed a difference between the topics on Twitter versus Weibo: there were more nuanced discussions on Twitter, and the discussed topics between platforms

focused on different areas. Temporal analysis showed that most discussions took place around gene-edited events. Based on our findings, suggestions were provided for policymakers and science communication practitioners to develop more effective communication strategies toward audiences in China and the U.S.

Balancing openness with Indigenous data sovereignty: An opportunity to leave no one behind in the journey to sequence all of life

AM Mc Cartney, J Anderson, L Liggins, et al.
Perspective, Evolution
PNAS, January 18, 2022, 119 (4) e2115860119
Abstract
The field of genomics has benefited greatly from its “openness” approach to data sharing. However, with the increasing volume of sequence information being created and stored and the growing number of international genomics efforts, the equity of openness is under question. The United Nations Convention of Biodiversity aims to develop and adopt a standard policy on access and benefit-sharing for sequence information across signatory parties. This standardization will have profound implications on genomics research, requiring a new definition of open data sharing. The redefinition of openness is not unwarranted, as its limitations have unintentionally introduced barriers of engagement to some, including Indigenous Peoples. This commentary provides an insight into the key challenges of openness faced by the researchers who aspire to protect and conserve global biodiversity, including Indigenous flora and fauna, and presents immediate, practical solutions that, if implemented, will equip the genomics community with both the diversity and inclusivity required to respectfully protect global biodiversity.

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CONSENT/PRIVACY

Moving from 'fully' to 'appropriately' informed consent in genomics: The PROMICE framework

Julian J Koplin, Christopher Gyngell, Julian Savulescu, Danya F Vears
Bioethics, 7 April 2022
Abstract
Genomic sequencing technologies (GS) pose novel challenges not seen in older genetic technologies, making traditional standards for fully informed consent difficult or impossible to meet. This is due to factors including the complexity of the test and the broad range of results it may identify. Meaningful informed consent is even more challenging to secure in contexts involving significant time constraints and emotional distress, such as when rapid genomic testing (RGS) is performed in neonatal intensive care units. In this article, we propose that informed consent matters not for its own sake, but because obtaining it furthers a range of morally important goals, such as promoting autonomy, well-being, and trust in medicine. These goals form the basis of a new framework [PROmoting Morally Important Consent Ends (PROMICE)] for assessing the ethical appropriateness of various informed consent models. We illustrate this framework with two examples: (a) a tiered and layered consent model for obtaining consent for GS, and (b) consent for RGS in critically ill newborns. We conclude that appropriately-rather than fully-informed consent provides the correct standard for genomic medicine and research.

Informed consent, genomic research and mental health: A integrative review

Nina Kilkku, Arja Halkoaho

Nursing ethics, 4 February 2022

Open Access

Abstract

Background

Research on genomics has increased while the biobank activities are becoming more common in different countries. In the mental health field, the questions concerning the potential participants' vulnerability as well as capacity to give the informed consent can cause reluctancy in recruiting persons with mental health problems, although the knowledge and understanding of mental health problems has remarkably changed, and practice is guided with inclusive approaches, such as recovery approach.

Aim

The aim of this study was to describe the current knowledge of informed consent practices in the context of genomic research on mental health from the nurses' viewpoint.

Methods

An integrative review was conducted with search from seven international databases. Data consist 14 publications which were analyzed with thematic analysis.

Ethical considerations

Ethical requirements were respected in every phase of the research process.

Findings

Most of the papers were published in USA and between 2000-2010. Eight reports were categorized as discussion papers, four qualitative studies and one quantitative study. The thematic analysis provided 7 information on five themes: complexity with the capacity to consent, mixed emotions towards participation, factors influencing the decision to participate, nurses' informed consent process competence and variations between consent procedures.

Discussion

In the informed consent practices, there are various aspects which may affect both the willingness to participate in the study and the informed consent process itself. Implications for practice, education, research, and policies are discussed.

Conclusion

There is a need for more updated international research on the topic in the context of different international and national guidelines, legislation, and directives. This study provided a viewpoint to the more collaborative research activities with people with lived experiences also in this field of research following the ideas of recovery approach.

Informed consent practices for exome sequencing: An interview study with clinical geneticists in the Netherlands

Original Article

Wendy Bos, Eline M. Bunnik

Molecular Genetics & Genomic Medicine, 14 January 2022

Open Access

Abstract

Background

Genomic sequencing is being used more frequently in the clinic, not only by clinical geneticists, but also by other specialists (“mainstreaming”). The use of genomic sequencing gives rise to challenges regarding informed consent, as it can yield more, and more complex results.

Methods

This study maps the informed consent process for exome sequencing in the Netherlands by means of semistructured interviews with 14 clinical geneticists. Interviewees were asked about their strategies for

informing patients about exome sequencing and supporting patients in their decision making, about what they think of as essential information elements, about the challenges they experience, and about their preferences for future policy and practice.
Results
Clinical geneticists typically discuss the following topics: the nature and aim of the test, the possible results (including unsolicited or incidental findings and Variants of Uncertain Significance) of the test and the consequences of those results for the patient and their family members. Some clinical geneticists use a

layered approach to informed consent, meaning that they give short and concise information at first, and provide more detailed information depending on the situation or the needs of the patient.
Conclusion
During pre-test counseling for genomic sequencing, clinical geneticists use various strategies to enhance patient understanding and personalization of the informed consent process. Going forward, layering information may be part of a solution to ethical challenges of informed consent, also in mainstream settings.

Functional genomics data: privacy risk assessment and technological mitigation

Gamze Gürsoy, Tianxiao Li, Mark B. Gerstein
Perspective | 10 November 2021
Nature Reviews Genetics
Abstract
The generation of functional genomics data by next-generation sequencing has increased greatly in the past decade. Broad sharing of these data is essential for research advancement but poses notable privacy challenges, some of which are analogous to those that occur when sharing genetic variant data. However, there are also unique privacy challenges that arise from cryptic information leakage during the processing and summarization of functional genomics data from raw reads to derived quantities, such as gene expression values. Here, we review these challenges and present potential solutions for mitigating privacy risks while allowing broad data dissemination and analysis.

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GENETIC/GENOMIC DATABASES, REPOSITORIES

Ethical, legal, and social issues in the Earth BioGenome Project

Jacob S. Sherkow, Katharine B. Barker, Robert Cook-Deegan, Richard Durbin et al.
Perspective, Evolution
PNAS, January 18, 2022 | 119 (4) e2115859119
Abstract
The Earth BioGenome Project (EBP) is an audacious endeavor to obtain whole-genome sequences of representatives from all eukaryotic species on Earth. In addition to the project's technical and organizational challenges, it also faces complicated ethical, legal, and social issues. This paper, from members of the EBP's Ethical, Legal, and Social Issues (ELSI) Committee, catalogs these ELSI concerns arising from EBP. These include legal issues, such as sample collection and permitting; the applicability of international treaties, such as the Convention on Biological Diversity and the Nagoya Protocol; intellectual property; sample accessioning; and biosecurity and ethical issues, such as sampling from the territories of Indigenous peoples and local communities, the protection of endangered species, and cross-border collections, among several others. We also comment on the intersection of digital sequence information and data rights. More broadly, this list of ethical, legal, and social issues for large-scale genomic sequencing projects may be useful in the consideration of ethical frameworks for future projects. While we do not—and cannot—provide simple,

overarching solutions for all the issues raised here, we conclude our perspective by beginning to chart a path forward for EBP's work.

The Human Pangenome Project: a global resource to map genomic diversity

Ting Wang, Lucinda Antonacci-Fulton, David Haussler
Perspective | 20 April 2022
Nature, Volume 604 Issue 7906, 21 April 2022
The Human Pangenome Reference Consortium aims to offer the highest quality and most complete human pangenome reference that provides diverse genomic representation across human populations.
Abstract
The human reference genome is the most widely used resource in human genetics and is due for a major update. Its current structure is a linear composite of merged haplotypes from more than 20 people, with a single individual comprising most of the sequence. It contains biases and errors within a framework that does not represent global human genomic variation. A high-quality reference with global representation of common variants, including single-nucleotide variants, structural variants and functional elements, is needed. The Human Pangenome Reference Consortium aims to create a more sophisticated and complete human reference genome with a graph-based, telomere-to-telomere representation of global genomic diversity. Here we leverage innovations in technology, study design and global partnerships with the goal of constructing the highest-possible quality human pangenome reference. Our goal is to improve data representation and streamline analyses to enable routine assembly of complete diploid genomes. With attention to ethical frameworks, the human pangenome reference will contain a more accurate and diverse representation of global genomic variation, improve gene–disease association studies across populations, expand the scope of genomics research to the most repetitive and polymorphic regions of the genome, and serve as the ultimate genetic resource for future biomedical research and precision medicine.

Uganda Genome Resource: A rich research database for genomic studies of communicable and non-communicable diseases in Africa

Segun Fatumo, Joseph Mugisha, Opeyemi Soremekun, Allan Kalungi, Richard Mayanja, Christopher Kintu, Ronald Makanga, Ayoub Kakande, Andrew Abaasa, Gershim Asiki, Robert Kalyesubula, Robert Newton, Moffat Nyirenda, Manjinder S Sandhu, Pontiano Kaleebu
medRxiv, 2022.05.05.22274740; doi: https://doi.org/10.1101/2022.05.05.22274740
Abstract
The Uganda Genome Resource (UGR) is a well characterised genomic database, with a range of phenotypic communicable and non-communicable diseases and risk factors generated from the Uganda General Population Cohort (GPC) - a population-based open cohort study established in 1989 by the Medical Research Council (MRC) UK in collaboration with the Uganda Virus Research Institute (UVRI).

In 2011, UGR was launched with genotype data on ~5000 and whole genome sequence data on ~2000 Ugandan individuals from 9 ethno-linguistic groups. Leveraging other available platforms at the MRC Uganda such as Biorepository centre for sample storage, Clinical Diagnostic Laboratory Service (CDLS) for sample diagnostic testing, sequencing platform for DNA extraction, Uganda Medical informatics Unit (UMIC) for large-scale data analysis, GPC for additional sample collection, UGR is strategically poised to expand and generate scientific discoveries.

Here, we describe UGR and highlight the important genetic findings thus far including how UGR is providing opportunities to: (1) discover novel disease susceptibility genetic loci; (2) refine association signals at new and existing loci; (3) develop and test Polygenic Risk Score (PRS) to determine individual's disease risk; 4) assess how some risk factors including infectious diseases are causally related to non-communicable diseases (NCDs) in Africa; (5) develop research capacity for genomics in Africa; and (6) enhance African participation in the global genomics research arena. Leveraging established research infrastructure, expertise, local genomic

leadership, global collaboration and strategic funding, we anticipate that UGR can develop further to a comparable level of European and Asian large-scale genomic initiatives.

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BIOBANKING - GENOMIC RESEARCH

Participant recall and understandings of information on biobanking and future genomic research: experiences from a multi-disease community-based health screening and biobank platform in rural South Africa

Authors: Manono Luthuli, Nothando Ngwenya, Dumsani Gumede, Resign Gunda, Dickman Gareta, Olivier Koole, Mark J. Siedner, Emily B. Wong and Janet Seeley
Research Open Access
BMC Medical Ethics, 2022 23:43 Published on: 18 April 2022
Abstract
Background
Limited research has been conducted on explanations and understandings of biobanking for future genomic research in African contexts with low literacy and limited healthcare access. We report on the findings of a sub-study on participant understanding embedded in a multi-disease community health screening and biobank platform study known as 'Vukuzazi' in rural KwaZulu-Natal, South Africa.
Methods
Semi-structured interviews were conducted with research participants who had been invited to take part in the Vukuzazi study, including both participants and non-participants, and research staff that worked on the study. The interviews were transcribed, and themes were identified from the interview transcripts, manually coded, and thematically analysed.
Results
Thirty-nine individuals were interviewed. We found that the research team explained biobanking and future genomic research by describing how hereditary characteristics create similarities among individuals. However, recollection and understanding of this explanation seven months after participation was variable. The large volume of information about the Vukuzazi study objectives and procedures presented a challenge to participant recall. By the time of interviews, some participants recalled rudimentary facts about the genetic aspects of the study, but many expressed little to no interest in genetics and biobanking.
Conclusion
Participant's understanding of information related to genetics and biobanking provided during the consent process is affected by the volume of information as well as participant's interest (or lack thereof) in the subject matter being discussed. We recommend that future studies undertaking biobanking and genomic research treat explanations of this kind of research to participants as an on-going process of communication between researchers, participants and the community and that explanatory imagery and video graphic storytelling should be incorporated into theses explanations as these have previously been found to facilitate understanding among those with low literacy levels. Studies should also avoid having broader research objectives as this can divert participant's interest and therefore understanding of why their samples are being collected.

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ANIMAL ENHANCEMENT/DISENHANCEMENT

Gene Editing, Animal Disenhancement and Ethical Debates: A Conundrum for Business Ethics?

N Thomas, A Langridge
Animals and Business Ethics
Book Chapter
Springer. 25 April 2022
The Palgrave Macmillan Animal Ethics Series. Palgrave Macmillan, Cham.
https://doi.org/10.1007/978-3-030-97142-7_10
Abstract
Despite the potential of genetic disenhancement to create livestock incapable of pain and thus reduce animal suffering in industrial farming, ethical theorists have rejected disenhancement as intuitively unethical or as part of a broader dismissal of industrial farming. Although criticisms of industrial farming may be valid, the suffering of animals involved still needs to be addressed, and business ethics is specially placed to do so. In

this chapter, a brief overview of the related ethical issues of industrial farming and disenhancement are outlined, and practical steps businesses should make to address animal suffering are provided. Explicit Corporate Social Responsibility policies that reflect the interest of animals, workers and consumers as stakeholders should be put in place, which would provide a mechanism to make businesses accountable for genetic modification and animal welfare more generally.

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GENE DRIVES

Governing Gene Drive Technologies: A Qualitative Interview Study

N. de Graeff, Karin R. Jongsma, Jeantine E. Lunshof & Annelien L. Bredenoord
Article
AJOB Empirical Bioethics, Volume 13, 2022 Issue 2
Abstract
Background
Gene drive technologies (GDTs) bias the inheritance of a genetic element within a population of non-human organisms, promoting its progressive spread across this population. If successful, GDTs may be used to counter intractable problems such as vector-borne diseases. A key issue in the debate on GDTs relates to what governance is appropriate for these technologies. While governance mechanisms for GDTs are to a significant extent proposed and shaped by professional experts, the perspectives of these experts have not been explored in depth.
Methods
A total of 33 GDT experts from different professional disciplines were interviewed to identify, better understand, and juxtapose their perspectives on GDT governance. The pseudonymized transcripts were analyzed thematically.
Results
Three main themes were identified: (1) engagement of communities, stakeholders, and publics; (2) power dynamics, and (3) decision-making. There was broad consensus amongst respondents that it is important to engage communities, stakeholders, and publics. Nonetheless, respondents had diverging views on the reasons for doing so and the timing and design of engagement. Respondents also outlined complexities and challenges related to engagement. Moreover, they brought up the power dynamics that are present in GDT research. Respondents stressed the importance of preventing the recurrence of historical injustices and reflected on dilemmas regarding whether and to what extent (foreign) researchers can legitimately make demands regarding local governance. Finally, respondents had diverging views on whether decisions about GDTs should be made in the same way as decisions about other environmental interventions, and on the decision-making model that should be used to decide about GDT deployment.
Conclusions

The insights obtained in this interview study give rise to recommendations for the design and evaluation of GDT governance. Moreover, these insights point to unresolved normative questions that need to be addressed to move from general commitments to concrete obligations.

Proceedings of an expert workshop on community agreement for gene drive research in Africa - Co-organised by KEMRI, PAMCA and Target Malaria

Gates Open Research
Open Letter metrics AWAITING PEER REVIEW
[version 1; peer review: awaiting peer review]
Delphine Thizy, Lea Pare Toe, Charles Mbogo, Damaris Matoke-Muhia, Vincent Pius Alibu, S. Kathleen Barnhill-Dilling, Tracey Chantler, Gershom Chongwe, Jason Delborne, Lydia Kapiriri, Esther Nassonko Kavuma, Sethlomo Koloi-Keaikitse, Ana Kormos, Katherine Littler, Dickson Lwetoijera, Roberta Vargas de Moraes, Noni Mumba, Lilian Mutengu, Sylvia Mwichuli, Silvia Elizabeth Nabukenya, Janet Nakigudde, Paul Ndebele, Carolyne Ngara, Eric Ochomo, Simon Odiwuor Ondiek, Stephany Rivera, Aaron J. Roberts, Rodrick Sambakunsi, Abha Saxena, Naima Sykes, Brian B. Tarimo, Nicki Tiffin, Karen H. Tountas
Peer Reviewers Invited
Funders: Bill and Melinda Gates Foundation, Silicon Valley Community Foundation, Open Philanthropy Project
PUBLISHED 29 Jan 2021
Abstract
Gene drive research is progressing towards future field evaluation of modified mosquitoes for malaria control in sub-Saharan Africa. While many literature sources and guidance point to the inadequacy of individual informed consent for any genetically modified mosquito release, including gene drive ones, (outside of epidemiological studies that might require blood samples) and at the need for a community-level decision, researchers often find themselves with no specific guidance on how that decision should be made, expressed and by whom. Target Malaria, the Kenya Medical Research Institute and the Pan African Mosquito Control Association co-organised a workshop with researchers and practitioners on this topic to question the model proposed by Target Malaria in its research so far that involved the release of genetically modified sterile male mosquitoes and how this could be adapted to future studies involving gene drive mosquito releases for them to offer reflections about potential best practices. This paper shares the outcomes of that workshop and highlights the remaining topics for discussion before a comprehensive model can be designed.

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PLANTS, CROPS, AGRICULTURE

Genome-edited crops for improved food security of smallholder farmers

Kevin V. Pixley, Jose B. Falck-Zepeda, Neal Gutterson
Comment | 07 April 2022
Nature Genetics, Volume 54 Issue 4, April 2022
[Excerpt]

Widespread enthusiasm about potential contributions of genome-edited crops to address climate change, food security, nutrition and health, environmental sustainability and diversification of agriculture is dampened by concerns about the associated risks. Analysis of the top seven risks of genome-edited crops finds that the scientific risks are comparable to those of accepted, past and current breeding methods, but failure to address regulatory, legal and trade framework, and the granting of social license, squanders the potential benefits…

Many countries are still uncertain about whether to grow and how to regulate genome-edited crop varieties[12]. Scientific, political and social considerations impact these decisions, which are complicated by the

rapidly evolving features of the science and inconsistent use of genome-editing terminology[13]. For example, genome editing may or may not involve the transitory introduction of foreign DNA sequences, may or may not result in transgenic products, and may or may not generate products that substantially differ from varieties bred through conventional breeding. Precise consistent use of accurate terminology (for instance, as proposed by the National Academies of Sciences Engineering and Medicine[14]) to transparently explain the process, products, benefits and potential risks and mitigation strategies is essential to build public trust and consistent regulatory oversight of technologies, including genome editing.

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DISEASE-SPECIFIC ISSUES

Global landscape of SARS-CoV-2 genomic surveillance and data sharing

Analyses on the global diversity of SARS-CoV-2 genomic surveillance across 118 countries and the extent of public availability of genomic data provide evidence to better inform SARS-CoV-2 surveillance policy.
Zhiyuan Chen, Andrew S. Azman, Hongjie Yu
Analysis | 28 March 2022 | Open Access
Nature Genetics, Volume 54 Issue 4, April 2022
Abstract
Genomic surveillance has shaped our understanding of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants. We performed a global landscape analysis on SARS-CoV-2 genomic surveillance and genomic data using a collection of country-specific data. Here, we characterize increasing circulation of the Alpha variant in early 2021, subsequently replaced by the Delta variant around May 2021. SARS-CoV-2 genomic surveillance and sequencing availability varied markedly across countries, with 45 countries performing a high level of routine genomic surveillance and 96 countries with a high availability of SARS-CoV-2 sequencing. We also observed a marked heterogeneity of sequencing percentage, sequencing technologies, turnaround time and completeness of released metadata across regions and income groups. A total of 37% of countries with explicit reporting on variants shared less than half of their sequences of variants of concern (VOCs) in public repositories. Our findings indicate an urgent need to increase timely and full sharing of sequences, the standardization of metadata files and support for countries with limited sequencing and bioinformatics capacity.

Ethical and practical considerations for cell and gene therapy toward an HIV cure: findings from a qualitative in-depth interview study in the United States

Authors: Karine Dubé, John Kanazawa, Hursch Patel, Michael Louella, Laurie Sylla, Jeff Sheehy, Lynda Dee, Jeff Taylor, Jen Adair, Kim Anthony-Gonda, Boro Dropulić, John A. Sauceda, Michael J. Peluso, Steven G. Deeks and Jane Simoni
Content type: Research
BMC Medical Ethics, 9 April 2022
Abstract
Background
HIV cure research involving cell and gene therapy has intensified in recent years. There is a growing need to identify ethical standards and safeguards to ensure cell and gene therapy (CGT) HIV cure research remains valued and acceptable to as many stakeholders as possible as it advances on a global scale.
Methods
To elicit preliminary ethical and practical considerations to guide CGT HIV cure research, we implemented a qualitative, in-depth interview study with three key stakeholder groups in the United States: (1) biomedical HIV cure researchers, (2) bioethicists, and (3) community stakeholders. Interviews permitted evaluation of informants' perspectives on how CGT HIV cure research should ethically occur, and were transcribed

verbatim. We applied conventional content analysis focused on inductive reasoning to analyze the rich qualitative data and derive key ethical and practical considerations related to CGT towards an HIV cure.
Results
We interviewed 13 biomedical researchers, 5 community members, and 1 bioethicist. Informants generated considerations related to: perceived benefits of CGT towards an HIV cure, perceived risks, considerations necessary to ensure an acceptable benefit/risk balance, CGT strategies considered unacceptable, additional ethical considerations, and considerations for first-in-human CGT HIV cure trials. Informants also proposed important safeguards to developing CGT approaches towards an HIV cure, such as the importance of mitigating off-target effects, mitigating risks associated with long-term duration of CGT interventions, and mitigating risks of immune overreactions.
Conclusion
Our study identified preliminary considerations for CGT-based HIV cure across three key stakeholder groups. Respondents identified an ideal cure strategy as one which would durably control HIV infection, protect the individual from re-acquisition, and eliminate transmission to others. Known and unknown risks should be anticipated and perceived as learning opportunities to preserve and honor the altruism of participants. Preclinical studies should support these considerations and be transparently reviewed by regulatory experts and peers prior to first-in-human studies. To protect the public trust in CGT HIV cure research, ethical and practical considerations should be periodically revisited and updated as the science continues to evolve. Additional ethics studies are required to expand stakeholder participation to include traditionally marginalized groups and clinical care providers.

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JOURNAL SPECIAL ISSUES

Assessing the Value of Treatments for Spinal Muscular Atrophy

Special Issue editors: Chris D. Skedgel, Nicole Gusset
PharmacoEconomics, Volume 40, supplement issue 1, April 2022
Editorial
Dramatic Innovations in the Treatment of Spinal Muscular Atrophy, But Many Unknowns Remain
Chris Skedgel
Published: 22 December 2021

Importance of Patient Involvement in the Value Assessment Process: On the Way Towards Personalised Treatments
Nicole Gusset
Content type: Editorial
Published: 16 December 2021

Systematic Literature Review to Assess the Cost and Resource Use Associated with Spinal Muscular Atrophy Management
Authors (first, second and last of 4): Noman Paracha, Pollyanna Hudson, C. Simone Sutherland
Content type: Systematic Review
Open Access
Published: 11 November 2021

Systematic Literature Review to Identify Utility Values in Patients with Spinal Muscular Atrophy (SMA) and Their Caregivers
Authors (first, second and last of 4): C. Simone Sutherland, Pollyanna Hudson, Noman Paracha
Content type: Systematic Review

Open Access
Published: 15 December 2021

Systematic Literature Review to Assess Economic Evaluations in Spinal Muscular Atrophy (SMA)
Authors (first, second and last of 4): Noman Paracha, Pollyanna Hudson, C. Simone Sutherland
Content type: Systematic Review
Open Access
Published: 18 October 2021

Preferences and Utilities for Treatment Attributes in Type 2 and Non-ambulatory Type 3 Spinal Muscular Atrophy in the United Kingdom
Authors (first, second and last of 6): Siu Hing Lo, Ksenija Gorni, Noman Paracha
Content type: Original Research Article
Open Access
Published: 18 October 2021

Patient and Caregiver Treatment Preferences in Type 2 and Non-ambulatory Type 3 Spinal Muscular Atrophy: A Discrete Choice Experiment Survey in Five European Countries
Authors (first, second and last of 5): Siu Hing Lo, Claire Lawrence, Andrew J. Lloyd
Content type: Original Research Article
Open Access
Published: 13 December 2021

Correction to: Dramatic Innovations in the Treatment of Spinal Muscular Atrophy, But Many Unknowns Remain
Authors: Chris Skedgel
Content type: Correction
Published: 25 February 2022

Correction to: Systematic Literature Review to Assess Economic Evaluations in Spinal Muscular Atrophy (SMA)
Authors (first, second and last of 4): Noman Paracha, Pollyanna Hudson, C. Simone Sutherland,
Content type: Correction
Open Access
Published: 26 Feb

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