

Ethical Issues in Genetics and Genomics

Summary: This set of projects examines a broad range of clinical- and research-related ethical and policy issues in genetics, including: 1) Research with collections of human biological samples and data; 2) Genetic and genomic research incorporating emerging technologies; 3) Return of genetic results to study participants and clinical patients; and 4) Characterizing and addressing individual and group risks associated with genetic and genomic information.

Section: Ethics and Genetics

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➤ **Background:**

Research with collections of human biological samples and data: Collections of human biological samples and associated data, including those collected in both clinical and research settings, are an important research resource. Efforts to create and maintain increasingly larger-scale collections of samples and data – as well as policies to promote broad data sharing – raise a number of ethical issues related to e.g., privacy and confidentiality protections; the scope and depth of informed consent; permissible ongoing uses; and potential obligations to disclose downstream research findings.

Genetic and genomic research incorporating emerging technologies: The availability of new technologies such as large-scale whole exome and genome (“next generation”) sequencing, and the ability to create human induced pluripotent stem cells (iPSCs), is expanding rapidly, bringing with it a need to reexamine the ethical issues associated with genetic and genomic research using these tools. The past several decades have been dominated by a targeted genetic research paradigm; the ethical issues associated with this earlier genetic research were focused primarily on concerns about informed consent, stigma (i.e., being judged or labeled as a result of genetic test results), privacy (both individual and group), and downstream worries about health insurance availability and discrimination based on genetic status. The past couple of years, however, have been marked by a transition into a new phase of research that focuses on the genome as a whole. The increasing availability of affordable next generation sequencing has made it easier for laboratories to engage in genomic research. The ethical concerns previously associated with targeted genetic research are amplified by the volume and types of information generated by large-scale genomic sequencing. Ethical concerns that had been rare now are becoming more prevalent and more complex, and institutional review boards are often called upon to review the ethics of research involving the use of these emergent, cutting edge technologies in research with human subjects prior to the development of consensus and ethical guidance about the use of these technologies.

Disclosure of genetic results to study participants and clinical patients: Genomic research with human subjects raises complicated questions about the management of incidental or secondary findings—including a determination of how, to whom, and under what circumstances to return results. Questions about the disclosure of results become more complicated as the number of results generated increases, which is precisely what is expected as whole exome and genome sequencing (WES/WGS) technologies begin to replace targeted genetic research techniques. As new genetic sequencing technologies move from a research context to the applied medical setting, it will also be important to reexamine the way that results are returned to patients in clinical settings.

Characterizing and addressing individual and group risks associated with genetic and genomic information: The research ethics literature is rich with discussion about the potential individual and group harms that can flow from inappropriate generation and dissemination of genetic information. This literature, however, is generally grounded in assumptions and speculation; there is little empirical study of the character, frequency, and magnitude of the direct individual and group harms that flow from genetic information. We are planning to perform a robust examination of these issues to inform the development of appropriate guidance and regulation.

➤ **Departmental Research Initiatives:**

Research with collections of human biological samples and data:

Genomic Databases: The ability of large-scale genomic databases (e.g., the Database of Genotypes and Phenotypes, or “dbGaP”) to pool and distribute large quantities of human genotypic and phenotypic data makes them an increasingly important research tool. The scientific community has begun using this tool to examine the role of genetic and environmental factors in a wide range of diseases. At the same time, because human genomic data are uniquely identifiable and are connected to potentially sensitive information about individual and familial health and future health-related risks, the use of human genomic databases prompts ethical questions about privacy and confidentiality, informed consent, and the potential risks and benefits of disclosing individual research results, among others. Our work looks at how these questions, which have been explored in the context of traditional genetic research for decades, are likely to be magnified and complicated by the ever-expanding quantities of data involved in genomic databases (Berkman and Hull, *in press*).

Public Attitudes about Genetic Research with Stored Samples: Understanding the reasons behind patients’ attitudes about the use of their stored samples for genetic research may foster more nuanced approaches to policy that balance the public’s interest in the advancement of research with concerns about control over handling biological samples for research. Hull, Wendler, and Lie have conducted several studies to better understand patients’ attitudes and preferences regarding the use of their previously collected samples in research and issues around informed consent. One study involved telephone interviews with 1,193 patients recruited from general medicine, thoracic surgery, or medical oncology clinics at five United States academic medical centers. Three different foci of the study included: (1) whether the regulatory distinction between non-identifiable and identifiable information — information used to determine informed consent practices for the use of clinically derived samples for genetic research — is meaningful to patients (Hull et al 2008); (2) attitudes about the need for consent for ongoing research use of pediatric samples when subjects reach the legal age of majority (Goldenberg *et al* 2009); and (3) views about the relevance of potential harms and benefits to groups and attitudes about research with one’s stored samples (Goldenberg *et al*, 2010).

In addition, the Department completed two multinational empirical projects examining attitudes about research with stored samples. One study evaluated participant understanding and participation rates of two different approaches to obtaining informed consent, using 2,192 research subjects in a genetic cohort study in Japan (Matsui et al. 2007). One group received the routine approach consisting of written materials and an oral explanation. The other group received a more intense approach consisting of educational lectures and group meetings. The study showed complex relationships between self perceived understanding and reading of the background material among the two groups, raising questions about the value of the informed consent forms.

In another project, 1857 subjects in an ongoing Japanese population-based genetic cohort were asked at entry about their preferences with regard to being recontacted by researchers in the future, and whether they wanted to receive reports on their individual genetic results if genetic problems relevant to their health are discovered for which efficacious interventions might be available (Matsui et al 2008). Most of the donors wished to be recontacted and receive reports, but some did not want any reports. Those who were younger, former/current drinkers, or had at least one parent who had had cancer were more likely to want the results, while those who had at least one sibling with a medical history of cancer were less likely to want the results.

Genetic and genomic research incorporating emerging technologies:

Oversight of Genomic Research Involving Emerging Technologies: As ethics consultants within the NIH CC Department of Bioethics and the NHGRI Bioethics Core, Hull and Berkman have received a number of requests for guidance on ethical issues pertaining to the complexities of next generation sequencing and the generation of iPSCs. Since late 2009, the NIH intramural research program has seen a significant increase in the number of research protocols proposing to utilize next generation sequencing technology. Similarly, there have been a small but growing number of protocols that are being amended to incorporate the creation of iPSC lines. Some of these protocols are prospective studies that will create broad informed consent requirements and collect new samples. Others are amendments of existing protocols, re-written to encompass plans for conducting novel research on previously collected samples. This has provided us with multiple opportunities to explore some of the pressing ethical issues raised by these emerging technologies, and to write about our experience with these issues in the context of the NIH intramural research program and beyond. (Berkman, Breugger, and Hull, submitted)

New Issues Raised by Next Generation Sequencing: Next generation sequencing, especially whole exome and genome sequencing, is likely to provide a new, transformative set of tools for gene discovery in research and medicine. An important difference between conventional gene discovery approaches that use genotyping arrays or targeted sequencing and those that incorporate next generation sequencing is the substantially greater information that the latter provides about variants in protein coding genes: virtually all functional, protein-coding variants in the genome for each individual participant. The routine availability of data on functional variants in virtually all protein-coding genes generates new manifestations of, and urgency around, existing ethical challenges in human genetics research. Our work endeavors to explain how these challenges differ from the standard ethical framework in which researchers operate and provide some guidance as to how to address if not resolve some of these challenges. Specifically, we have focused on three specific areas that require consideration: management of individual research results, data sharing, and the limitations of the current consent process. (Tabor *et al.*, submitted)

Re-Consent for Next Generation Sequencing Research: A challenge for next generation sequencing research is finding a consent process that balances researchers' desire for broad, open-ended consent with participants' interest in making well-informed choices about research participation. One question of particular importance is the extent to which prior informed consent for genetic research is sufficient to address the use of rapidly evolving technologies such as next generation sequencing with previously collected samples and when re-consent is required. Hull, Perkins, and Berkman, in collaboration with Porter, Bailey-Wilson, and Tierney, are conducting a study of parents of children with autism spectrum disorder (ASD) who previously participated in genetic research to examine the perceptions and attitudes regarding the need for re-contact and re-consent for next generation sequencing research. The goal of this quantitative-qualitative cross-sectional study is to measure the utility and necessity of the re-consent process from the perspective of parents whose children have donated samples for genetic research over the past 10 years, and the value that participants place on having specific information about research plans, risks, and benefits to allow them to make well-informed decisions. A total of 220 participants who signed consent forms for a whole exome sequencing study on ASD will be asked to complete a quantitative survey, and approximately 30 will be asked to participate in one-on-one qualitative interviews. The data gained from this study will provide a springboard for future studies that will investigate participant groups with a broader range of characteristics.

Creation of Human Induced Pluripotent Stem Cell (iPSC) Lines: Research that involves the generation and use of iPSC lines from human somatic cells also presents novel challenges to the informed consent process. Because the creation of iPSCs does not require the destruction of embryos, some argue that their creation raises no ethical concerns. However, additional ethically-relevant characteristics, particularly related to potential downstream uses for human transplantation and reproductive research, may require attention in the language of consent forms. Hull and Berkman, in collaboration with John O’Shea, are developing an appropriate approach to informed consent for the creation and future research uses of iPSC lines, using either prospectively- or previously-collected specimens.

Disclosure of genetic results to study participants and clinical patients:

Incidental Genetic Research Findings: The ethical obligation to return individual incidental genetic results remains unsettled, and there is no final consensus on this issue in the research ethics literature. Scholarly discourse on the threshold question of whether to return incidental results discusses the need for sound clinical practice, the balance between respecting participant autonomy and protecting participant health, and the importance of obtaining thorough and complete informed consent. While many ethicists favor the disclosure of genomic test results to participants in at least some circumstances, others argue that the nature of scientific research differs from the practice of clinical medicine and is inconsistent with an obligation to warn individual patients of disease risk by returning research test results.

Analysis of the relevant legal authorities does not provide further clarification about the specific conditions under which genetic research results should be returned. The Common Rule (and associated OHRP guidance) is largely silent on the question of what sort of disclosures of genetic and genomic research findings should be required.

In the absence of an ethical consensus, and without definitive regulatory guidance, Hull and Berkman are engaging in research to understand the normative foundations behind arguments for and against return of results. Our goal is to develop scholarship and practical tools useful for the development of policy and guidance on disclosure of incidental findings. As part of this initiative, we are conducting qualitative and quantitative studies of the views of investigators, subjects and IRB members.

One study involves conducting qualitative interviews with members of IRBs that review (or are likely to review) protocols using whole exome and/or genome sequencing. The goal of this project is to better understand IRB members’ views about the management and disclosure of incidental research findings in the context of genomic sequencing protocols. We will explore the extent to which IRB members believe that such results should be provided to subjects under various circumstances, and the reasoning behind these beliefs.

The collection of a wide range genetic test results, both related and incidental to the research questions, has become routine in clinical research. The ethics literature has focused largely on what is required to obtain consent for this research and the extent to which it places individuals at risk. For example, might identification of a gene that puts individuals at increased risk for Alzheimer disease undermine their ability to obtain insurance? In contrast, there are almost no data on the impact this practice has on research participants. To address this gap in the literature, Wendler and colleagues conducted a study to evaluate how individuals respond to the collection of genetic test results. The findings suggest that collection of genetic test results

increases many individuals' desire to know the results themselves. In contrast, a few respondents were less inclined to want to know their genetic test results once an investigator was aware of them. These results suggest that investigators and IRBs may need to do more to recognize and address these phenomena in the design and conduct of studies which collect genetic information. (Wendler and Pentz 2007)

Prenatal Whole Genome Sequencing: Whole genome sequencing is quickly becoming more affordable and accessible. Though some significant discussion has emerged regarding the use of this new technology in the research context, little has been written on its use in the clinical context, and most of this analysis has been largely hypothetical. This is problematic given the speed with which this technology is likely to be incorporated into clinical care. Hull and Berkman, working with a pre-doctoral fellow, are exploring this issue by analyzing one particular subset of this problem: the implications of an extemporaneous adoption of this technology in the prenatal context. Of special interest is the impact that this technology may have on the future autonomy of fetuses that are carried to term. We argue that the use of prenatal whole genome sequencing could remove the fetus' option in the future to not know their genetic information—a concern commonly raised for children but that has not yet been explicitly extended to fetuses. The guidelines for genetic testing in children have acknowledged the value of a child's future autonomy, whereas the guidelines for genetic testing in fetuses have largely not addressed this issue. As we know from case studies of the adoption of other new genetic technologies, cautious deliberation will be necessary to prevent whole genome sequencing from being adopted via market forces without due consideration of the morally ambiguous outcomes that could arise from its use. In the paper, we argue that careful discourse is needed to incorporate considerations of the future autonomy of fetuses into discussions of ethical and responsible utilization of prenatal whole genome sequencing. (Donley, Berkman, and Hull, submitted)

Characterizing and addressing individual and group risks associated with genetic and genomic information:

Identifiability: Concerns about privacy, confidentiality, and discrimination are grounded in the increasing potential to re-identify genomic information. Typically, genetic investigators protect subject information through the use of data coding and/or de-identification. However, these strategies are not completely effective. A person's genome is inherently unique; even if a database has been stripped of all traditional identifiers, such as name, address, physical characteristics or government identification numbers, there is no way to completely avoid the possibility of identifiability by deduction. As databases grow and statistical tools improve, it becomes increasingly possible to associate genetic data with individual characteristics. Researchers have recently demonstrated that bioinformatics techniques are capable of detecting an individual person's single nucleotide polymorphism (SNP) profile contained within a mixture of more than 1,000 distinct DNA samples. It is similarly possible to deduce whether a given research participant is part of a disease or control group. Researchers have also demonstrated that genetic information can be linked with publicly-available data or records that reveal familial relationships to connect de-identified data to identifiable individuals. While these techniques cannot yet confirm an individual's identity without additional external reference information, privacy concerns are nonetheless salient. As sequencing technologies evolve, data proliferates, and biostatistical methods become more powerful, it will become increasingly difficult to protect an individual's genetic information.

In addition to individual privacy risks, genetic information can also lead to group privacy concerns. Much genetic research has focused specifically on population-specific genotype-

phenotype connections. History has demonstrated that when identifiable racial, ethnic, or geographic groups are associated with a genetic predisposition, racism, discrimination, and stigmatization are possible. Extrapolating from these experiences, scholars have articulated concerns about the potential for unjustified denial of social services, coercive medical treatments, and an undermining of group identity and self-worth. These concerns raise important ethical questions about whether it is necessary to obtain group permission, and how to apply basic individual research protections (e.g. right to withdraw, confidentiality) in this larger context.

One ongoing research project has focused on whether the use of identifiability as a regulatory construct adequately protects research subjects from these potential harms. Under current regulatory guidance, the need for IRB review of studies that involve the analysis of human biological specimens depends largely on whether or not the samples and associated data are considered to be identifiable or de-identified. When a researcher wants to conduct secondary analyses on samples or data that are de-identified, and that were collected elsewhere, the regulations (and accompanying OHRP guidance) do not consider this to be human subject research. As such, IRB review is not required.

This means that as investigators incorporate increasingly powerful genetic sequencing technologies into their research, there might be little or no review of much proposed research. This could be problematic since next-generation sequencing technologies will produce significantly more data than has ever been produced before and will reflect a significantly higher proportion of the genome. It stands to reason that it will be more easily re-identified. Plus, there will be an increasing capacity to identify distinguishing characteristics (e.g., race/ethnicity) even in the absence of an external reference sample. Nevertheless, the frequency and severity of risks associated with re-identification remain unclear; we plan to conduct future empirical research to understand the scope of these identifiability risks and the accompanying risk of harm.

Our developing research agenda includes a focus on these issues. For example, Hull and Berkman are engaged in an analysis of existing OHRP guidance on identifiability to ascertain whether it would be appropriate to revisit the way that we define what is or is not human subject research in a genomic era. This is part of a larger effort to investigate how existing laws, regulations, and guidance are affecting the rapidly evolving universe of genetic and genomic research approaches. Does the general regulatory paradigm articulated by the Common Rule ensure appropriate review of novel genetic research methodologies? Does CLIA take the right approach to regulating genomic research technologies that can generate dozens of incidental findings for a single subject?

Genetic Information Non-discrimination Act: GINA has been heralded as the “first civil rights bill of the 21st Century.”¹ GINA creates important protections for individuals with genetic predispositions for or family histories of genetic conditions and illnesses. However, GINA differs from other civil rights bills in three main ways: 1) while the rest of the civil rights bills were enacted to address growing problems of discrimination, GINA was passed largely to address *fear* of discrimination and to prevent discrimination from occurring in the future; 2) GINA is more limited in scope than many of the civil rights bills because it only applies to employers and

¹ Annas GJ, Roche P, and Green RC (2008) “GINA, Genism, and Civil Rights,” *Bioethics*.; 22(7): ii–iv.

insurance companies; and 3), unlike other civil rights bills, GINA goes beyond simply preventing employers and insurance companies from discriminating against an individual due to their genetic information by disallowing employers and insurance companies from even obtaining genetic information in the first place.

The unique aspects of this statute led Berkman to examine questions about how the law is and should be implemented. One project is exploring the legal definition of “disease manifestation.” GINA only provides protections until one’s disease has manifested. The question of how to define, measure and demonstrate disease manifestation has important implications for the scope and application of the non-discrimination provisions. We have explored the range of ways that manifestation has been used in statutes and case law to see whether GINA’s definition of manifestation is optimal.

Rather than just punishing past discriminatory behavior, GINA also prophylactically prohibits employers and health insurers from even obtaining “genetic information.” This prohibition raises important questions about implementation. Who should bear the burden of separating genetic information (broadly defined to include family history) from non-genetic medical information? The regulations seem to impose a duty on health care providers to redact medical records before responding to requests from insurers or employers. What are the practical, legal and ethical implications of making health providers the responsible gatekeepers of genetic information? Our research will explore how this provision is being implemented and whether it is appropriate to place such a burden on a group that is not the law’s intended target.

➤ **Impact of Research:**

Research with collections of human biological samples and data:

The Department’s work on the ethics of research with collections of human specimens and data has had an impact on a number of related policy and teaching activities both in the United States and internationally. Sara Hull participates on the human subjects working group of the NIH Genomic Data Sharing Policy Group, whose goal is to expand the current GWAS data sharing policy to apply to a broader range of genomic data types. Hull has also participated in efforts to explore the feasibility of a rare disease registry through the NIH Office for Rare Disease Research (ORDR) and help to oversee a program that promotes data sharing of rare genetic disease test information through the ORDR Collaboration, Education, and Test Translation (CETT) Program. Hull presents a session on “Ethical Issues in Research with Stored Tissues” annually in the NIH-wide course on Ethical and Regulatory Aspects of Clinical Research and a similar annual session on ethical issues associated with genomic databases for the George Mason University bioinformatics program. Hull and Berkman have both shared their research results at the American Society of Bioethics and Humanities (ASBH) annual meeting, and Hull has been interviewed by a Science Magazine reporter about her work in this area.

Genetic research incorporating emerging technologies:

Our research and consultations on ethical issues pertaining to the next generation sequencing and the generation of iPSCs has led the effort to the develop intramural NIH-wide guidance, points to consider documents, and model consent form language for research that incorporates these novel technologies. In collaboration with the NIH Office of Human Subjects Research

Protections to develop policies for the review and oversight of such research at the NIH, and our recommendations were accepted by the NIH Human Subjects Research Advisory Committee. Hull and Berkman have developed a series of IRB training modules on the ethics of next generation sequencing presented to both intramural and extramural IRBs, as well as participating in panel discussions related to this topic at Society for Clinical Research Associates (SOCRA) and ASBH meetings.

Return of genetic results to study participants and clinical patients:

The Department's research on the return of genetic results to study participants and clinical patients has resulted in tangible impact across a range of academic and policy domains. Intramurally, Hull and Berkman have consulted with dozens of investigators who are struggling with whether and how to incorporate return of incidental genetic research findings into their protocols. Hull and Berkman have run training sessions for numerous intramural IRBs to educate members about these issues. Hull and Berkman have also been involved in efforts related to the development of NIH-wide policy about management of incidental findings.

Extramurally, we have participated in an ELSI working group meeting (funded by NHGRI) to explore the management of incidental findings and research results in genomic biobanks and archives. We have presented our work at a range of academic conferences, including the International Society of Nurses in Genetics (ISONG) Annual Meeting, American University Washington College of Law, American Society of Bioethics and Humanities, and Seattle Children's Hospital Pediatric Bioethics Conference.

Characterizing and addressing individual and group risks associated with genetic information:

Our efforts to characterize and address the individual and group risks associated with genetic information led to an opportunity for us to present our work on identifiability to the Secretary's Advisory Committee on Human Research Protections (SACHRP). We have also delivered lectures in academic settings, speaking about genetic information and discrimination at the Catholic University Columbus School of Law annual bioethics conference and discussing group harms and community-based participatory research at the American Public Health Association annual meeting. We also conduct an annual lecture on potential group harms associated with genetic research in the Clinical Center's Department of Bioethics first year fellowship seminar.

➤ **Future Initiatives:**

Research with collections of human biological samples and data: The Common Rule and associated guidance define a number of research-related activities that do not count as human subjects research, are exempt from IRB review, and are eligible for a waiver of informed consent requirements. Research involving collections of human biological samples and data often falls into one of these categories when it involves e.g., coded (“de-identified”) information, information collected from now-deceased subjects, or information from subjects it would now be difficult to recontact. These exceptions allow important research that involves minimal risk of harm to subjects to go forward expeditiously. However, these exceptions might also provide researchers with opportunities to circumvent requirements that are ethically (if not legally) indicated, such as disregarding prior limitations described in consent forms once the subjects who signed them are deceased. Furthermore, there are some circumstances in which some additional oversight and/or informed consent for new research activities seems to be warranted, even when IRB review is technically not required under the regulations. For example, results of genetic research on deceased subjects may have relevance to family members who either are or are not enrolled in the research. We are planning to examine the scope and applicability of prior consent once subjects are deceased and when their samples/data are de-identified, and identify requirements that are ethically important even when they are not legally required.

Genetic research incorporating emerging technologies: Consent language has not kept pace with the rapid development of new technologies such as next generation sequencing and iPSC generation. The nuances of these technologies, such as the magnitude and significance of the information that they are able to generate, are complicated concepts to convey to the lay public. How much do potential research subjects know – or need to know – about the details of genetic and genomic research in which they enroll? What level of detail is required in consent forms to ensure that potential subjects have an adequate level of understanding? A prior study conducted by this department demonstrated that NIH intramural consent forms in 2000 for genetic research were variable in their content, and a worrisome proportion lacked important information about the potential disclosure of genetic research results and associated risks.² We are planning a similar content analysis of consent forms approved in 2011 to examine the coverage of issues related to genetic and genomic research and how they have evolved nearly a decade after this original study.

Return of genetic results to study participants and clinical patients:

Overriding the right not to know genetic information: Investigators and guidance documents have explicitly begun discussing return of results procedures that could include a mechanism for returning (extraordinarily significant) results, even when subjects have expressed a desire not to have results relayed. We will examine the question of when, if ever, is it appropriate to override an individual’s right not to know, and when it is appropriate to give individuals an option not to know

Characterizing and addressing individual and group risks associated with genetic information:

² Hull SC, Gooding H, Klein AP, Warshauer-Baker E, Metosky S, and Wilfond BS (2004) “Genetic Research Involving Human Biological Materials: A Need to Tailor Consent Forms,” *IRB: Ethics & Human Research*, 126(3): 1-7.

Group Risks: Controversy exists about the extent to which IRBs should be responsible for evaluating group harms and reinforcing researchers' responsibilities to the groups they are studying. Some scholars have argued for a narrow definition of beneficence that assumes a researcher's fiduciary duty only extends to his or her subjects. Others have disputed this claim, arguing that researchers have a broad societal responsibility because of a social contract between researchers and society, where the research enterprise can operate autonomously in exchange for performing activities that promote the common good. From this broader perspective, it is not difficult to impose responsibilities on researchers that extend beyond individual research subjects. According to this account, researchers (and IRBs that monitor them) have a responsibility to consider the broad impact of their research on third-parties (e.g., groups and society as a whole). But if IRBs have a responsibility to consider the broad impact of research, many questions remain.

Do IRBs have the appropriate capability to consider broader policy questions and distributive justice concerns? One could argue that they are ill-suited to make decisions with expansive consequences given that they are designed to evaluate the importance and burden of an individual research proposal. To what extent are IRBs already engaged in this kind of analysis and to what effect? Are there structural changes or educational tools that could facilitate IRB consideration of group harms? Are there alternate mechanisms for review?

An appropriate system for evaluating group harms should include mechanisms for coordinating IRB decisions; equity demands that similar cases should receive comparable review. At present, IRBs have no easy way of speaking to each other to ensure consistency of review. What steps should be taken to ensure consistency of review?

If IRBs began considering group harms, this fact would necessarily lead to an expansion of their workload. This in a system where many feel that IRBs are already over-burdened and that long review times are a barrier to conducting research. Would an expanded IRB focus reduce the IRB's ability to effectively monitor individual human subject protections? What alternative structures and mechanisms could be proposed?

Publications:

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