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Inclusion of Racial and Ethnic Minorities in Genetic Research: Advance the Spirit by Changing the Rules?

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Introduction

As genetic and genomic research has progressed since the sequencing of the human genome, scientists have continued to struggle to understand the role of genetic and socio-cultural factors in racial and ethnic health disparities.¹ Recognition that race and ethnicity correlate imperfectly with differences in allele frequency, environmental exposures, and significant health outcomes has made framing the relationship between genetic variation, race, ethnicity, and disease one of the most heated debates of the genome era.² Because racial and ethnic identities reflect a complicated mix of social and genetic factors, critics have argued that use of racial and ethnic categories as analytical variables in biomedical research lacks rigor,³ leads to potentially dangerous stereotyping in medical practice, and sends harmful messages of innate racial difference to the broader public.⁴

Concerns over the current lack of diversity in human genetic and genomic studies have developed in parallel to discussions of the appropriate use racial and ethnic categories during the research process. Internationally, most genomic research occurs in populations of European ancestry, with racial and ethnic minority groups frequently absent from large-scale cohort studies, genome-wide association studies, and biobanks.⁵ This lack of diversity can be attributed to both scientific and logistical challenges, i.e., population structure and reduced linkage disequilibrium in certain populations, difficulty recruiting participants from minority and vulnerable populations, and unequal distribution of biomedical funding. Regardless of these barriers, inequities in the amount and quality of genetic and genomic data generated for various human populations has the potential to exacerbate existing health disparities as genetic discoveries are translated into clinical and public health interventions.⁶ Thus, inclusion of racial and ethnic minority groups in genetic research has become an important issue for the international scientific community.

In the United States (U.S.), the National Institutes of Health (NIH) Policy and Guidelines on the Inclusion of Women and Minorities as Subjects in Clinical Research (hereinafter *NIH Inclusion Policy and Guidelines*) sits at the intersection of conversations about diversity in genetic and genomic research and utilization of racial and ethnic categories in biomedical science. The policy, created in response to a mandate included in the NIH Revitalization Act of 1993, requires, "...that women and members of minority groups and their subpopulations must be included in all NIH-supported biomedical and behavioral research projects involving human subjects, unless a clear and compelling rationale and justification establishes to the satisfaction of the relevant Institute/Center Director that inclusion is inappropriate with respect to the health of the subjects or the purpose of the research."⁷ To

monitor adherence to the *Inclusion Policy and Guidelines*, NIH-funded intramural and extramural scientists are required to use the racial and ethnic categories specified in U.S. Office of Management and Budget (OMB) Directive No. 15 to collect data on research participation.⁸ The OMB Standards for the Classification of Federal Data on Race and Ethnicity (OMB categories) include the racial classifications, “American Indian or Alaska Native, Asian, Black or African American, Hawaiian or Pacific Islander, and White” and the separate ethnic designation, “Hispanic or Latino and Not Hispanic or Latino.”⁹ Principal investigators must address the *Inclusion Policy and Guidelines* in all extramural grant applications and intramural research protocols by providing information on their plan for including women and minorities in their project and outlining the proposed racial, ethnic, and gender composition of their study population, as defined by the OMB categories, using a targeted enrollment form.¹⁰ Once funded, scientists are required to classify the racial, ethnic, and gender distribution of recruited subjects as a part of the study progress report using the Inclusion Enrollment Report form.

Though the *Inclusion Policy and Guidelines* only mandate use of the OMB categories for internal reporting to the NIH, it has been suggested that these requirements are causing NIH-funded investigators to use these categories in conceptualizing study designs, developing research questions, performing data analysis, and communicating study results.¹² Thus, the policy has become a focal point in the debate about the use of race and ethnicity in genetic and genomic research in the United States. By linking two activities with different purposes, monitoring inclusion of racial and ethnic minorities in biomedical research and classification of participants, federal research regulations have been portrayed as an essential component of a pathway leading to misuse of racial and ethnic categories in genetic and genomic studies.¹³

A body of research exploring the NIH Policy and Guidelines on the Inclusion of Women and Minorities as Subjects in Clinical Research is emerging.¹⁴ However, empiric evidence of the *NIH Inclusion Policy and Guidelines*’ influence on the practice of genetic research in the United States is limited, as previous research has focused broadly on how genetic researchers conceptualize and employ race and ethnicity in their studies and not specifically on the role of the *NIH Inclusion Policy and Guidelines*.¹⁵ Additionally, there has been little recognition of the parallels between current calls for increased diversity in human genetic research and spirit of inclusion that sparked the original congressional mandate for increased participation of under-represented groups in government-funded research. This paper reports the findings of a qualitative study of genetic and genomic scientists working in the United States that specifically examined the influence of the *NIH Inclusion Policy and Guidelines*. In an effort to interrogate the tension between the policy’s underlying motivation to increase participant diversity and its potential to reifying race and ethnicity as biological constructs, we engaged genetic scientists in discussion around: (1) the influence of the *NIH Inclusion Policy and Guidelines* on use of the OMB categories in their research; (2) the utility of the OMB categories for genetic and genomic research; (3) their motivations for including minority groups in their work; (4) their opinions of the *NIH Inclusion Policy and Guidelines* and its influence on research practices; and (5) potential alternative methods of increasing diversity in government funded genetic and genomic research.

Methods

Study Recruitment

The data reported in this paper were collected as part of a larger study exploring scientists' use of population descriptors in genetic and genomic studies. Interviews were conducted with a purposive sample of scientists receiving extramural funding from the NIH or conducting research within its intramural research programs. Eligible scientists were the primary investigator (PI) or co-PI on a genetic or genomic study of a common disease that used population descriptors — such as race, ethnicity, nationality, and geographic location — to describe their study subjects. Additionally, scientists needed to have collected preliminary data that would allow them to complete an exploratory exercise re-conceptualizing the use of population descriptors in their study. The study was approved by the Institutional Review Board of the National Human Genome Research Institute (NHGRI) of the NIH.

In July 2008, a sample of extramural scientists were identified by a keyword search of the Computer Retrieval of Information on Scientific Projects (CRISP) database, which listed biomedical research projects funded by the NIH. As interviews were conducted in-person, the Mid-Atlantic region of the United States was targeted to facilitate the completion of the study. To maximize recruitment effectiveness, once an extramural investigator was enrolled in the study, their institutions' website was searched for additional scientists matching the recruitment criteria to invite to participate. Intramural investigators were identified through a keyword search of the NIH Intramural Database (NIDB). All identified investigators were invited to participate in the study with a goal of representing a range of research backgrounds, target study populations, and research aims, as well as, to represent roughly equal numbers of intramural and extramural scientists.

The research team sent all targeted scientists an e-mail explaining the study and inviting them to participate. A monetary incentive in the amount of \$245.00 (value of a membership in the American Society of Human Genetics for one scientist and one trainee) was provided to the extramural scientists. As federal employees, no monetary incentive could be offered to the intramural scientists. The research team followed the invitation e-mail with a telephone call after 5-7 business days. Four attempts were made to reach invited scientists by telephone or e-mail. Interested scientists were screened for eligibility over the telephone. Those scientists who met the recruitment criteria and expressed an interest in participating in the study were sent the study consent form before scheduling their interviews.

Data Collection

Interviews

Data was collected through two semi-structured, in-person interviews with each participating scientist. All interviews were conducted using a standard interview guide of open-ended questions and clarifying probes to allow for natural flow of conversation. The first semi-structured interview explored the scientist's research program and then focused on one specific study, covering the proposed research questions, selection of the study population, collection of demographic information, grouping of subjects in data analysis,

and description of the study population when reporting results. The second semi-structured interview generally occurred one to two weeks after the first interview and explored alternative options to describe their study populations and the *NIH Inclusion Policy and Guidelines*. A single interview, incorporating questions from both interview guides, was conducted with 4 scientists due to scheduling issues. All interviews were digitally recorded and transcribed by a professional transcription company for data analysis. A research team member reviewed all transcripts for accuracy by direct comparison with the audio files.

Additional Data

In addition to the interview data, each scientist was asked to provide a copy of their current curriculum vitae (CV), a copy of the protocol for the specific study discussed in the interviews, and complete a demographic questionnaire. At the time of their enrollment in the study the research team also created a list of each scientist's published papers by searching the SCOPUS database (www.scopus.com) by author name. When cross-referenced with the scientist's CVs, publication lists generated through SCOPUS accurately captured scientists' current publications. These supplementary data sources were collected to provide additional information about our study scientists' training, current research, and standing in their respective fields, as well as to serve as a source of triangulation with the interview data.

Data Analysis

Interviews

Interview transcripts were analyzed by qualitative content analysis.¹⁶ After a review of several transcripts, the research team developed a preliminary coding scheme. Based on the semi-structured interview guides, the initial codebook used the scientists' words to identify key topic areas that emerged during the interviews. The coding scheme was finalized through an iterative process in which two members of the research team critically reviewed the interview transcripts, adding and modifying codes until all major topic areas were represented. Changes to the codebook were cross-referenced and discussed by the research team. Codes were refined and given written definitions to create the final codebook. NVivo® 8 software was used to code all interview data. The lead interviewer performed all coding. To monitor coder reliability, a second member of the research team coded a set of randomly selected transcripts. All coding comparisons showed a high degree of agreement. The coded data was further analyzed by exploring specific codes of interest and grouping coded comments by central themes and key ideas.

Additional Data

To analyze the investigators' CVs, protocols, papers, and publications, the research team developed a standardized code form that covered two areas of interest: background (including scientists' demographics, training, and current field) and professional standing (including scientists' academic rank, high impact publications, and awards). After refining and modifying the coding form based on a preliminary analysis of two scientists' data, one member of the research team reviewed and coded all supporting documents. When possible, data was cross-referenced between sources. To aid in analysis of the supporting documents, descriptive statistics were calculated for all quantitative data.

Results

Sample

Thirty-five (35) scientists were invited to participate in the study. Eighteen (18) agreed, and the remaining scientists fell into three categories: those who directly declined (n=6), those who did not respond after four attempts to contact (n= 7), and those who agreed to participate, but were not interviewed due to scheduling conflicts (n=4), giving a response rate of 51% and a cooperation rate of 75%. A total of 31 interviews were conducted with these 18 scientists, whose descriptive characteristics are reported in Table 1. Ten (10) scientists were government employees, working within the intramural research programs of five NIH institutes and centers. The remaining eight (8) scientists were extramural scientists from four mid-Atlantic universities. Based upon their professional ranks, leadership positions, scientific contributions, and publication records, the scientists interviewed for this study were influential members of the scientific community (see Table 2). Most were full professors within their respective universities or senior scientists within the NIH and had been working in their field for an average of 23.3 years. A minority of the scientists were junior scientists with less than 10 years in the field (median years in the field: 22.5). Participants had published a median of 91.5 peer-reviewed articles, with a median of 11.5 in high impact journals (defined as an impact factor above 15 as listed on ISI Web of Knowledge, Journal Citation Reports in July, 2008). The scientists' median *h*-index score was 31.7. The majority of the scientists had teaching and mentoring responsibilities and served as an editor for at least two peer-reviewed scientific journals.

Study Limitations

As with any small qualitative study, the scientists in our sample do not necessarily represent the larger genetic research community. Additionally, as the scientists were informed during the recruitment process that the study was exploring issues related to race, ethnicity, health disparities, and research policy, the individuals who agreed to participate may be more comfortable with these topics than those who declined. During the interviews a number of the participants made it clear that though they perform genetic research, they do not consider themselves "geneticists." However, the professional stature of these 18 researchers suggests that their opinions and practices hold substantial weight and are highly influential in their respective research areas. Scientists conducting genetic research have diverse backgrounds and research experiences, which may impact the representativeness of their opinions and practices. Though these findings cannot be generalized beyond our sample, the themes relating to the *NIH Inclusion Policy and Guidelines* were robust and remarkably consistent between participants.

Key Themes: NIH Policy and Guidelines on the Inclusion of Women and Minorities in Clinical Research—The key themes related to the *NIH Inclusion Policy and Guidelines* identified during the interviews are presented in Table 3 along with representative quotations. All language that appears in quotations in the text appears as scientists used it during the interviews.

Theme 1: Use of OMB categories for internal reporting to NIH influences broader

research practices: It was clear from the scientists' discussions of their respective research projects during the interviews that the *NIH Inclusion Policy and Guidelines*, through use of the OMB Standards for the Classification of Federal Data on Race and Ethnicity, play a critical role in the utilization of racial and ethnic categories in genetic and genomic research in the United States. As described by one participant:

...we're sort of prisoners of correct practice and standards, which is that's how it's done, and that's how it is – you know, that's how HHS and the Executive Branch of government – actually and Congress – mandate that we do this stuff, right? We have to use these census categories, and we have to report our recruitment based on those categories, and it's long-established protocol that you report results in those categories.

The requirements outlined in the *NIH Inclusion Policy and Guidelines* shaped the use of racial and ethnic classifications throughout the research process, from the collection of information about racial and ethnic identity from study participants to the description of study population demographics in published papers. In the words of one participant, "There's a certain requirement from NIH that forces you to classify your groups and that's a requirement. Okay? But that, itself—you know, makes you to define your work in certain ways."

Some of the scientists explained that they made the decision to structure their studies around the OMB categories because they felt uncomfortable "retrofitting" other types of information, for example ancestral or geographic information, into the OMB categories when reporting back to the NIH (comment 1). Additionally, some of the researchers used the OMB categories because they believed that participants felt most comfortable identifying themselves using the OMB categories, as opposed to other potential methods of classification. Not all of the scientists, though, specifically stated that the NIH requirements were impacting their decisions about how to collect and report racial and ethnic information in their work. Instead the use of the OMB categories was portrayed simply as the way things were done, what one individual described as an unquestioned practice:

It's so inherent in the system here that, you know; every time you start an interview people know how to do the race/ethnicity question. I don't think we've—I mean, maybe we don't need to do it that way, but I don't think we've ever questioned it.

Themes 2-5: OMB categories are misleading for genetic and genomic research: Though the OMB Standards for the Classification of Federal Data on Race and Ethnicity were used in the majority of the genetic and genomic studies discussed during the interviews, all 18 scientists believed that the OMB categories do not represent genetically homogenous groups. Almost every scientist brought up the extreme genetic variability within these classifications, stating that they function as "catch-alls" and are not fully representative of the diversity of "stories"—historical, biological, and cultural— that can be present within each category (comments 2a, 2b).

Still, the majority of the scientists we interviewed felt that the OMB categories were frequently being used as a proxy for genetic homogeneity in NIH funded genetic and genomic research (comment 3). When asked about genetic scientists' use of the OMB categories as analytical variables during the research process, one researcher replied, "Of course it is happening. They could go from there [OMB classification] to do the genetic work, and describe a definition of populations." Recognizing the imprecise and complex, understanding of human genetic variation reflected in this practice, many of the scientists believed that there had to be "a way to do it better". Additionally, a few of our participants felt that addressing the OMB categories' flaws in the context of genetic and genomic science should be a top priority for the research community.

Specifically "Asian" and "Hispanic" were often mentioned as problematic for use in genetic research and President Barack Obama was often used to illustrate the OMB categories' flaws, as seen in this comment:

...especially it comes about in the Barack Obama example, where someone checks black or African-American and they may be even less than 50 percent African-American. And they may have one African-American grandparent, and yet that's what they check. And um, if it weren't such a politically charged issue, they would have checked Caucasian, because they're three-quarter Caucasian.

The idea that the OMB categories do not work for what scientists described as "mixed" individuals and populations was brought up frequently during the interviews. Several scientists mentioned that many individuals now identify with multiple racial and ethnic backgrounds and that research into human genetic variation is increasing recognition of the fact that "we are all mixed" (comment 4a). They also saw the OMB categories and the system of racial and ethnic classification that they represent as uniquely U.S. constructs that can be confusing or inappropriate when used in an international context (comment 4b).

Themes 6: Intention of Inclusion Policy and Guidelines critically important for genetic and genomic research: When the interview moved to discuss the *NIH Inclusion Policy and Guidelines* specifically, all eighteen scientists voiced strong beliefs that the social justice spirit reflected in the *Inclusion Policy and Guidelines* is essential for genetic and genomic science. They thought that increasing research participants' diversity was essential to understanding health differences between racial and ethnic groups and addressing health disparities both globally and within the United States, as seen in this scientist's discussion of prostate cancer:

... I think it's a great idea to include minorities, because for instance, just in prostate cancer, we know morbidity and mortality in prostate cancer is different for African-Americans than Caucasians, and we know it's not related – or we believe it's not related solely to health care access and health care choices. We believe that there really are, um, some different alleles floating around in those populations that – in that genetic background, you know, present, in different population frequency.

Scientists with public health training also mentioned the importance of generating representative and generalizable clinical and public health guidelines (comment 6). A prominent theme in the scientists' comments was that a comprehensive understanding of

human health and disease could only be achieved by studying all human populations. In the words of one individual, "... if we are to understand, I can make it as broad as biology. Studying only one or two – you know, groups is just not going to give us the picture."

Themes 7-8: NIH Inclusion Policy and Guidelines not motivating inclusion and not strongly enforced: While the scientists' awareness of the *Inclusion Policy and Guidelines* and support for its intent were universal, additional themes that emerged during the interviews suggest that the policy is not successfully motivating NIH-funded scientists to increase minority participation in their research. When asked if the policy had influenced the target study populations for the specific project discussed in the interviews, it was overwhelmingly clear that the choice of study populations is a scientifically, and sometimes socially, motivated decision for scientists. The *Inclusion Policy and Guidelines* is an afterthought, if considered at all. As one individual stated:

Well, that policy was in effect long before we did it [research study], but certainly the belief of the investigators that it was bad science and socially irresponsible to not study all ethnic groups and our almost anger when we realized how few African-American families were included in the international consortium. That did drive us. It was not the law; it was our agreement that that law was a just policy, and a just law, and we were just like what do you mean that's all the families there are?

Many scientists echoed that their primary motivation for conducting minority focused research was a belief that it was "bad science" not to study the full spectrum of human genetic diversity, as well as feelings of social responsibility to address health disparities. Other scientists were less idealistic and attributed their inclusion of minority populations simply to wanting to explore the potential genetic contribution to a documented health difference between groups (comment 7). Additionally, all of the participants who were asked if they would have changed their target study population if the *NIH Inclusion Policy and Guidelines* did not apply said they would not. It is possible that our participants are unique in their commitment for studying underrepresented populations and addressing health disparities by nature of our recruitment criteria. The increasing number of publications highlighting the need for diversity in genome-wide association studies specifically, and genomic research more broadly, supports the broader applicability of these findings.¹⁷

A number of the scientists stated directly that they thought that the *NIH Inclusion Policy and Guidelines* is not being strictly monitored (comment 8a) and only one out of the eighteen participants said that the policy had been thoroughly discussed in exchanges with their Institutional Review Board (IRB). Eight of the eighteen scientists (four intramural and four extramural) said that the extent of their engagement with the policy had been providing written justification that they had considered it in designing their research protocol. As explained by an extramural scientist:

Well, the question [about inclusion of women and minorities] is always there and usually I say it's not relevant. Because in most cases it's not relevant. And then I didn't have any problems. So, it's sort of not useful.

The cynical tone with which some of the scientists talked about requirements to address the policy in funding applications and during other review processes, illustrated in this individual's comment:

And I know we have written justifications explaining why we can't do it [recruit minority participants]. I mean, a lot of times we look and it's to say, "Oh, God. We've got to put this in."

Many scientists reported that compliance with the *NIH Inclusion Policy and Guidelines* is not scrutinized and seemed to have become indifferent to its requirements. During the interviews scientists referenced "boilerplate paragraphs" used to address the *Inclusion Policy and Guidelines* in grants and study protocols. They also described responding to comments from study sections that requested greater attention to inclusion by rewriting the justification of their choice of study populations and emphasizing previous difficulties recruiting minority individuals, as opposed to altering their study design. Scientists believed that as long as they initially made a "sincere effort" to think about how to recruit minorities and passed this hurdle in their review, they could move forward with their study without continued scrutiny of their project's population breakdown (comment 8b).

Themes 9-10: Current inclusion rules are inflexible and imperfect for genetic and genomic research; targeted studies are superior: The most prominent theme that emerged during discussion of the *NIH Inclusion Policy and Guidelines* was that the application of the current inclusion rules to biomedical, and specifically genetic, research is inherently flawed. Scientists saw the policy as bureaucratic and one-size-fits all and assumed that the administrators who crafted the policy did not understand the realities of conducting research in human populations. As one scientist commented:

...I'm sure the people who came up with this [*NIH Inclusion Policy and Guidelines*] – because I remember the politics – they didn't want to just create a whole lot of bureaucratic mess, and to some extent it has.

The scientists did not believe that the current policy was flexible enough to consider the scientifically appropriate study population for a specific research question. Additionally, many of the scientists spoke of the hardship encountered when trying to recruit study participants in geographic areas of the U.S. where smaller numbers of minorities reside in order to comply with the policy. In the words of one scientist,

...it may actually cause an undue burden on the researcher to try and meet these criteria, so I think that these are well intended – but as a blanket criteria for all studies, my opinion is that there needs to be a little more flexibility, and looking at what is it that – you know, what is the goal of the research?

The most frequent complaint about the *Inclusion Policy and Guidelines*, though, was that study sections, NIH staff, and other entities that monitor adherence have interpreted the policy as requiring recruitment of study participants with a racial and ethnic breakdown proportional to United States demographics. Thus, though a study's racial and ethnic composition may be equitable when compared to the U.S. population distribution, the genetic data generated for minority groups almost always lack the statistical power needed

to provide meaningful results (see comment 9). This theme illustrates scientists' concerns that the *NIH Inclusion Policy and Guidelines* are neither advancing genetic and genomic research, nor contributing to the scientific rigor of federally funded research. One scientist described his frustration:

The problem comes about when you don't have enough [minority participants], and you're statistically underpowered to do anything. And so, you end up giving away some of your slots, and to sort of satisfy a bureaucratic requirement – which is very well meaning, but basically you're going to throw that data away.

This finding is consistent with those of Smart and colleagues in the United Kingdom (UK), who identified the potential for conflicts between imperatives of “social inclusivity” and “analytical acuity” in a qualitative study exploring efforts to increase minority ethnic group participation in U.K. biobanks. Similarly to what we heard from these U.S. scientists, they reported that, “A common concern among...respondents centered on the potential limitations of ‘representative’ samples, given that they generate relative small sub-samples of participants in minority ethnic groups that might limit the ‘statistical power’ required for robust comparative subgroup analyses.”¹⁸

The eighteen scientists interviewed in this study felt that targeted studies of minority groups, where both the scientific question and the recruitment efforts are tailored directly to the population of interest, were a superior way to carryout the intentions of the *NIH Inclusion Policy and Guidelines*. One scientist described this alternative:

...this inclusion business is really not going to do it, because in certain places it just creates greater hardship. Investigators are not going to wait, you know, to do that. They will just find a way around it, so there needs to be a concerted effort to make sure that studies are funded in a way that we'll be able to have equal data, you know, for all of these, multiple ethnic groups, as many of them as we can get.

The scientists we interviewed overwhelmingly believed in the importance of studying diverse, globally representative populations, specifically for genomic research, and that emphasizing proportional recruitment of minority groups in NIH-funded studies was an insufficient method to achieve this goal. As one participant stated:

...I personally think the problem in genetic research of minority groups is that it's not – you know, it requires a very separate – ascertainment strategy. It really does. I just don't think it can be – you know, a simple, exhortation to recruit more minority samples. I think you need to have a real strategy to do that. You have to have a study to do that.

The most frequently proposed method for facilitating a shift from the reportedly “sloppy” methods of the current *NIH Inclusion Policy and Guidelines* to more targeted efforts to increase diversity was through the creation of what one individual described as “ethnic specific” research funding opportunities. These genetic scientists felt that the research community should, in the words of one participant, “do it right” by designing studies with specified research questions and recruitment strategies necessary to produce statistically significant findings for racial and ethnic minority groups in the United States (comments 10a, 10b).

Conclusions

This study's findings support previous assertions that the requirements of the *NIH Inclusion Policy and Guidelines* are influencing how scientists define and report race and ethnicity in their genetic and genomic studies.¹⁹ The themes that emerged during the interviews demonstrated a striking contradiction between scientists' recognition of the OMB categories' inadequacies for capturing information about genetic background and their continued use of these categories in genetic and genomic research studies. This observation is consistent with other qualitative studies exploring race and genetics and suggests that while genetic scientists acknowledge that racial and ethnic categories are imprecise proxies for individuals' genetic characteristics, they have yet to develop effective ways to translate patterns of genetic variation to socially and politically salient human populations.¹⁹ Uncoupling use of the OMB categories from internal monitoring of the *NIH Inclusion Policy and Guidelines* would allow government-funded scientists greater flexibility in how they collect and report information about racial and ethnic identity. It is possible that such a policy change could help generate momentum towards focusing U.S. studies of human genetic variation on ancestral groups, rather than politically and socially created categories.

The scientists who participated in this study made it overwhelmingly clear that increasing excitement about the potential for genetic and genomic research to help understand and eliminate health disparities has made the social justice spirit reflected in the *NIH Inclusion Policy and Guidelines* particularly salient to the genetic and genomic research community. Still, the interviews revealed a stark juxtaposition between scientists' support for increased representation of individuals from diverse backgrounds in genetic and genomic research and their indifferent attitude towards complying with the *NIH Inclusion Policy and Guidelines*. As our study participants were aware that the research team was situated within an NIH intramural research program, this finding is particularly salient. Our data suggests that this skeptical outlook is likely due to scientists' dissatisfaction with the policy's inherent limitations in the context of human genetic research. Scientists' concerns about genetic and genomic studies continually generating statistically underpowered results for racial and ethnic minority groups suggest that re-examination of the *NIH Inclusion Policy and Guidelines* as it applies to genetic and genomic science is warranted. Carefully tailoring efforts to increase diversity to groups with shared ancestral backgrounds, while recognizing the inherent variation that will exist within any human grouping, could preserve the original spirit of inclusion embodied by the National Institutes of Health Policy and Guidelines on the Inclusion of Women and Minorities as Subjects in Clinical Research.

BIOS

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Program Director/Principal Investigator (Last, First, Middle): _____

Inclusion Enrollment Report

This report format should NOT be used for data collection from study participants.

Study Title: _____

Total Enrollment: _____ Protocol Number: _____

Grant Number: _____

PART A. TOTAL ENROLLMENT REPORT: Number of Subjects Enrolled to Date (Cumulative) by Ethnicity and Race				
Ethnic Category	Females	Males	Sex/Gender Unknown or Not Reported	Total
Hispanic or Latino				**
Not Hispanic or Latino				
Unknown (individuals not reporting ethnicity)				
Ethnic Category: Total of All Subjects*				*
Racial Categories				
American Indian/Alaska Native				
Asian				
Native Hawaiian or Other Pacific Islander				
Black or African American				
White				
More Than One Race				
Unknown or Not Reported				
Racial Categories: Total of All Subjects*				*
PART B. HISPANIC ENROLLMENT REPORT: Number of Hispanics or Latinos Enrolled to Date (Cumulative)				
Racial Categories	Females	Males	Sex/Gender Unknown or Not Reported	Total
American Indian or Alaska Native				
Asian				
Native Hawaiian or Other Pacific Islander				
Black or African American				
White				
More Than One Race				
Unknown or Not Reported				
Racial Categories: Total of Hispanics or Latinos**				**

* These totals must agree.
** These totals must agree.

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Figure 1.

Table 1

Selected Descriptive Characteristics of Study Sample

Characteristic	N	%
<i>Gender</i>		
Male	11	61
Female	7	39
<i>Degree</i>		
M.D.	4	22
Ph.D.	7	39
M.D.,Ph.D.	1	6
M.P.H.,Ph.D.	4	22
D.D.S.,Ph.D	1	6
Pharm.D.	1	6
<i>Clinical Responsibilities</i>		
Yes	5	28
No	13	72
<i>Genetics Research Focus</i>		
Epidemiology	3	17
Genetic Epidemiology	3	17
Medical Genetics	3	17
Human Genetics	4	22
Molecular/Biochemical Genetics	2	11
Other ^a	3	17
<i>Current Institution</i>		
NIH Intramural	10	56
NIH Extramural	8	44

^a Other: Genetics, Genomics, and Pharmacogenomics

Table 2

Selected Professional Characteristics of Study Sample

Characteristic	N	%
<i>Academic Rank - Extramural</i>		
Professor	6	33
Associate Professor	1	6
Assistant Professor	1	6
<i>NIH Rank - Intramural</i>		
Senior Investigator	7	39
Investigator	3	17
<i>Years in the Field^a</i>		
<i>Range: 9-38, Median: 22.5</i>		
17 years	4	22
18-27 years	8	44
28 years	6	33
<i>Number of Peer-Reviewed Publications</i>		
<i>Range: 32-690, Median: 91.5</i>		
30-60	6	33
61-90	3	17
91-120	2	11
>120	7	39
<i>Number of High Impact Peer-Reviewed Publications</i>		
<i>Range: 1-104, Median: 11.5</i>		
15	11	61
16-30	3	17
>30	4	22
<i>H-Index Score^b</i>		
<i>Range: 13-99; Median 31</i>		
20	4	22
20-40	9	56
>40	4	22
<i>Number of Editorial Positions^b</i>		
<i>Range: 0-12, Median: 2</i>		
0-1	6	33
2-4	8	44
>4	3	17

^aYears since doctoral degree received^bData missing for 1 participant

Table 3

Identified Themes and Representative Quotations

1. Use of OMB categories for internal reporting to NIH influences broader research practices

And the newer studies have suggested the definitions based on whatever the census categories are, or you know, the six federal categories that we've used for quite some time. And the reason is very purposeful. The reason is, you know, when I sample anybody as a part of my study I've got to report back to the NIH if it fits into those boxes. So I might as well ask those questions if I've got to fit people in those boxes, because otherwise I have an interpretation problem.

2. OMB categories do not represent genetic groups; huge variation within categories

a) ... they're stupid categories. Biologically, that is just so far from reality that it's just pitiful.

b) I mean, there's just a huge difference between being a Japanese-American and a Han Chinese-American. There's a huge difference between those. Um, and you know, American Indian versus, um, American Eskimo, there's a huge difference, or Inuit – there's a huge difference. Black and African-American, how many countries are there in Africa? I mean, it just means so much. Native Hawaiian, or other Pacific Islander, ditto. I mean, and white it's just – Hispanic or Latino is just a joke.

3. OMB categories are being used as a proxy for genetic homogeneity

...I didn't even know Hispanic was a mix, or possibly a mix, or a range, until relatively recently in my life. It's like we just don't know about that. We don't acknowledge that it – in fact, even scientists, anthropologists use it as if it's a specific racial group. It's – well, I don't know. I'm being a little disrespectful, but I think it's nonsense.

4. OMB categories do not work for significantly ancestrally mixed populations or populations outside the United States

a) ...there are lots of mixed people, and there's no – you know, many forms, of course, do not account for any kind of mixed person, other than "other." Other is pretty useless.

b) So there's no actually major definitions [of race and ethnicity outside of the United States] like those studies here in the United States where we use the IRB definitions.

5. Scientists recognize need to better describe relationship between racial and ethnic identity and human genetic variation

...for all the huffing and puffing about wanting to do this, spend the time to do it right. And you'll never satisfy everyone. I mean, you're not going to give people a 15-page questionnaire. But you have to be able to do it better than this. You know? You just have to.

6. Intention of *Inclusion Policy* and *Guidelines* critically important for genetic and genomic research

I think people do understand that it's important – I mean, I think people really do understand that if we're going to make public health statements, and that guidance, we need to make sure that what we say for men is applicable to women-it isn't always. That what we say for whites is applicable to blacks. I mean, I think we get it. I mean, that from a public health point of view we better know that it's generalizable.

7. *Inclusion Policy* and *Guidelines* not motivating scientists to study minority groups

The reason why we study whites and blacks and Hispanics and Native Americans, and men and women, and adults and children is not to pander to any one or the other groups; it's because our understanding of the disease is absolutely incomplete if we only study it in one....so we have to study different groups to just get a mature understanding, but it won't come from legislating.

8. *Inclusion Policy* and *Guidelines* are easy to circumvent

a) I think it's a policy with a good intention, but it's not something that is working. Because it's very easy to, um – to get out of it.

b) Is it perfect? No, because I think – I still think there are – you know, maybe some studies slipping in under the radar – where, you know, they – you know, you write up a protocol proposal – And then when you start enrolling, and you encounter obstacles, and you say, well you know, I'm having trouble.

9. *Inclusion Policy* and *Guidelines* are imperfect for genetic and genomic research

...unless we focus on a population that we can acquire in sufficient size to get a meaningful result we end up with nothing. And we're going to just squander government resources.

10. Increasing diversity through targeted studies is a superior approach

a) I'm in favor of the policy, but I don't think the implications have been made clear to the policy makers who wrote this. And it's much better to do several good studies – some of which are ethnic specific, than to treat – than to bring ethnic – ethnic minorities – in kind of a sloppy way into a white study.

b) ... I would actually be better off with a series of six cohorts that are appropriate powered to do the studies with internal comparisons within those categories as they are defined, acknowledging all the weaknesses and problem with those categories.