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ARTICLE

Increasing access to individualized medicine: a matched-cohort study examining Latino participant experiences of genomic screening

Joel E. Pacyna[1], Gabriel Q. Shaibi[2], Alex Lee[3], Jamie O Byrne[3], Idali Cuellar[4], Erica J. Sutton[1], Valentina Hernandez[5], Noralane M. Lindor[4], Davinder Singh[5], Iftikhar J. Kullo[6] and Richard R. Sharp[1,7] ✉

PURPOSE: Multiple efforts are underway to increase the inclusion of racial minority participants in genomic research and new forms of individualized medicine. These efforts should include studies that characterize how individuals from minority communities experience genomic medicine in diverse health-care settings and how they integrate genetic knowledge into their understandings of health-care needs.

METHODS: As part of a large, multisite genomic sequencing study, we surveyed individuals to assess their decision to pursue genomic risk evaluation. Participants included Latino patients recruited at Mountain Park Health Center, a Federally Qualified Health Center in Phoenix, Arizona, and non-Latino patients recruited at a large academic medical center (Mayo Clinic in Rochester, MN). Both groups agreed to receive individualized genomic risk assessments.

RESULTS: Comparisons between cohorts showed that Latino respondents had lower levels of decisional conflict about pursuing genomic screening but generally scored lower on genetic knowledge. Latino respondents were also more likely to have concerns about the misuse of genomic information, despite both groups having similar views about the value of genomic risk evaluation.

CONCLUSION: Our results highlight the importance of evaluating sociocultural factors that influence minority patient engagement with genomic medicine in diverse health-care settings.

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INTRODUCTION

While genomic medicine has the potential to improve health-care outcomes for patients, it could also widen existing health disparities between different racial groups.[1,2] Already, racial disparities in access,[3–5] health service utilization,[6] and diagnosis[7,8] have been documented. Recognizing these very different possibilities, commentators have called for greater inclusion of racial minority populations in genomic research to enhance the utility of genomic findings and ensure the widest benefit for all.[2,9–16] In response, genomic implementation studies have expanded to include more racial minority participants and efforts have been made to prioritize the inclusion of diverse populations in genomic medicine. Additionally, federal investments in genomic medicine, such as the All of Us Research Program,[17] have made the inclusion of diverse populations a priority.

Despite these successes, however, we still have very limited familiarity with how individuals from minority racial or ethnic populations engage with translational genomic research or integrate genetic knowledge into their understandings of health-care needs. Of particular note is the limited body of published research describing the clinical support needs of racially diverse patients who receive genomic evaluation in health-care settings that are not academic medical centers or university hospitals.[18–22] This lack of data on patient receptivity to genomic medicine—specifically within more diverse clinical contexts where significant numbers of minority patients receive their health care—will complicate efforts to prevent the health disparities that commitments to greater inclusiveness are intended to address.

To begin to address this gap, we surveyed Latino patients who receive care at a Federally Qualified Health Center (FQHC) in Phoenix, Arizona. In parallel, the survey was conducted in a more affluent, predominantly non-Latino population of patients who receive care at a large academic medical center. Both groups received the same genomic risk evaluation as part of a multisite genomic research initiative, allowing us to compare their experiences directly. The aim of these parallel survey efforts was to characterize how the beliefs and experiences of patients from a less affluent, predominantly Spanish-speaking Latino community compare with the experiences of other populations that have been more fully characterized in prior studies examining the psychosocial impact of genomic medicine. Our results highlight several important challenges and patient-support needs that should be considered in promoting increased access to genomic medicine in diverse communities.

MATERIALS AND METHODS

Setting and participants

We surveyed individuals enrolled in the Return of Actionable Variants Empirical (RAVE) study, a genomic sequencing study at Mayo Clinic in Rochester, Minnesota and Mountain Park Health Center (MPHC) in Phoenix, Arizona. A full description of the RAVE study, including its aims and recruitment procedures, has been published previously.[23,24] Differences

[1]Biomedical Ethics Research Program, Mayo Clinic, Rochester, MN, USA. [2]Center for Health Promotion and Disease Prevention, Arizona State University, Phoenix, AZ, USA. [3]Division of Biostatistics and Informatics, Mayo Clinic, Rochester, MN, USA. [4]Center for Individualized Medicine, Mayo Clinic, Phoenix, AZ, USA. [5]Mountain Park Health Center, Phoenix, AZ, USA. [6]Department of Cardiovascular Medicine, Mayo Clinic, Rochester, MN, USA. [7]Center for Individualized Medicine, Mayo Clinic, Rochester, MN, USA. ✉email: sharp.richard@mayo.edu

between participant populations and the clinical care available at these sites provided a natural context in which to conduct a comparative analysis of participant experiences of genomic risk evaluation.

Inclusion criteria for the genomic sequencing study (at both sites) were ≥18 years of age and having either colon polyps and/or hyperlipidemia. Mayo Clinic participants were recruited from two biorepositories—the Mayo Clinic biobank[25] and the Mayo Clinic Vascular Disease Biorepository.[26] Since participants had previously donated biological materials as part of their enrollment in a biorepository, blood samples were available at the time participants were approached to participate in the study. Sequencing involved evaluation of 68 medically actionable genes, including 59 genes identified by the American College of Medical Genetics and Genomics[27] and 14 additional single-nucleotide variants. Participants who agreed to participate in the study were informed that they would be notified about their individual results when those results became available and that the results would be placed in their electronic health record.

Mayo Clinic participants were invited to participate by way of a mailed packet that contained an invitation letter, a study brochure, a "frequently asked questions" document, a consent form, and a self-addressed, stamped return envelope to facilitate completion and return of the informed consent form. MPHC participants were recruited from the Sangre Por Salud biobank,[28] and were sent a study invitation letter, followed by a phone call to set up an in-person educational session to discuss study participation. MPHC participants who attended the in-person educational session viewed an educational video describing genomic sequencing and reviewed the consent materials with a research staff member. Following the educational session, MPHC participants interested in participating in the study signed a written consent form.

Participants at both sites had the option to speak with a genetic specialist if they had additional questions about their participation in the study or about the genomic risk evaluation provided.[29] In Rochester, 3,037 individuals consented to participate in the RAVE study of 5,110 invited (59.4% participation rate);[24] in Phoenix, 500 individuals consented to participate of 1,626 invited (30.8% participation rate).[23]

Survey

We designed a 100-item survey examining participants' decision to pursue genomic risk evaluation. This survey included a 16-item Decisional Conflict Scale (DCS), an instrument designed to assess uncertainty and perceived effectiveness in making decisions about health or health care.[30] DCS scores range from 0 (no decisional conflict) to 100 (extreme decisional conflict). The DCS has been associated with decisional regret.[31] Lower DCS scores have also been associated with stability of choice, while higher scores have been associated with increased decisional instability.[32] In addition, our survey included a scale designed to measure respondents' knowledge about genomic sequencing.[33] Additional items included an assessment of participant perspectives about potential favorable and unfavorable outcomes resulting from the receipt of genomic screening results, including potential concerns about results, expectations of benefit, perceptions of value, and self-efficacy in coping with results. Demographic variables included sex, age, marital status, educational attainment, insurance coverage, employment status, and health literacy.[34] A full description of the survey can be found in Pacyna et al.[35]

A professional translation service created a Spanish-language version of the survey for use at MPHC. The translation process included forward and backward translation. To confirm appropriateness for use at MPHC, the Spanish-language version was reviewed by Spanish-speaking research and clinical staff, as well as a bilingual/bicultural research staff member who conducted cognitive testing of translated items with ten patients at MPHC.

Data collection

As noted above, participants in the Mayo Clinic cohort were invited to participate in the genome sequencing study by mail. A majority (69.5%) of invitees were mailed the survey with a stamped return envelope after the research team received their signed consent form. The remainder (30.5%) received the survey as part of the initial invitation to participate in the study and were asked to return the survey with their signed consent form. Additional information on survey data collection for the Mayo Clinic cohort can be found in Pacyna et al.[35]

As noted above, participants in the MPHC cohort provided consent during an in-person enrollment session. The survey was completed immediately following this discussion, in the participant's preferred language (Spanish or English). Education and consent discussions lasted an average of 81 minutes for Spanish-speaking participants and 67 minutes with English-speaking participants, including survey completion. A bilingual research coordinator (I.C.) was available to answer participant questions about the survey and assist lower literacy participants in completing the survey, as needed.

Completed surveys from both cohorts were double entered and verified by research staff from the Survey Research Center at Mayo Clinic. A research team member (J.E.P.) reviewed paper copies of all surveys containing anomalies in survey responses.

Data analysis

Descriptive statistics were produced for both cohorts, including frequency distributions for categorical variables and means and standard deviations for continuous variables. Decisional conflict scores[32] and proportions of correct responses to knowledge about genomic sequencing items were calculated. Summary statistics were calculated using JMP Pro 14 (2018 SAS Institute Inc.).

To compare perspectives on genomic screening in the MPHC cohort (which are not as well characterized) to the Mayo Clinic population (which has been studied more extensively), we created a simulated case–control cohort by matching MPHC participants 1-to-1 with participants in the Mayo Clinic cohort on as many variables as possible. Several candidate matching models were generated, which varied from each other with respect to (1) whether they employed imputation for missing data, and (2) the number of variables included in the matching model. Imputation enabled us to retain a few cases with data missing from the matching variables in each cohort. Our goal was to retain as many cases from the smaller MPHC cohort as possible, while minimizing standardized differences between cases and controls. To achieve this goal, the final model included an absolute match on sex and an approximate match on age (±5 years) and employed imputation for missing variables (average age and most-common sex). Matching was completed using version 9.4 of the SAS System for [Unix] (SAS Institute Inc., Cary, NC, USA).

We compared the demographic composition of the two cohorts using chi-square tests for categorical variables and two-sample *t*-tests for continuous variables. Comparisons of mean knowledge scores and decisional conflict scores were calculated using Wilcoxon rank sum tests. We conducted paired comparisons of the two cohorts on individual items from the decisional conflict scale, on anticipated favorable and unfavorable psychosocial outcomes, and on individual items from the knowledge about genome sequencing scale using McNemar's tests to estimate the odds of observing a differential response in the MPHC cohort when compared with the Mayo Clinic cohort. McNemar's tests were conducted using R version 3.6.2 and the exact2x2 library.[36]

RESULTS

We received completed surveys from 438 of the 500 individuals who enrolled in the RAVE study at MPHC (87.6% completion rate) and completed surveys from 2,895 of the 3,037 individuals enrolled at Mayo Clinic (95.3% completion rate). The matching model we selected yielded 401 matched pairs. Missing age values were imputed for 7 (1.7%) of the Mayo Clinic cases and 19 (4.7%) of the MPHC cases. Missing sex values were imputed for 7 (1.7%) of the Mayo Clinic cases and 6 (1.5%) of the MPHC cases. The cohorts differed on other demographic variables as displayed in Table 1. A greater proportion of Mayo Clinic participants were married or partnered (85.7% vs. 70.6%, $p < 0.01$), employed full time (67.3% vs. 23.4%, $p < 0.01$), had adequate health literacy (95.5% vs. 75.3%, $p < 0.01$), were more educated ($p < 0.01$), and were planning to share their results with a family member (82.5% vs. 73.1%, $p < 0.01$). A greater proportion of participants from MPHC reported having a physical exam within the last two years (84.3% vs. 75.1%, $p < 0.01$), and a substantially higher percentage of MPHC respondents reported that they planned to share their genomic test results with a physician (84.8% vs. 44.6%, $p < 0.01$).

The decisional conflict scale was calculated, with scores ranging from 0 to 100 (see Supplemental Fig. 1). The MPHC cohort had a lower mean decisional conflict score (10.6, SD = 12.0, median = 6.3) compared with the Mayo Clinic cohort (15.1, SD = 13.4, median = 14.1, $p < 0.0001$). Table 2 compares responses to

Table 1. Demographic characteristics of two cohorts of participants who received genomic risk evaluation; $n = 802$.

	Mayo Clinic *N* (%)	Mountain Park Health Center *N* (%)	*p* value
Sex			0.95[b]
Male	104 (26.5)	104 (26.3)	
Female	288 (73.5)	291 (73.7)	
Ethnicity			<0.01[b]
Latino	2 (0.5)	383 (99.2)	
Not Latino	390 (99.5)	3 (0.8)	
Survey language			<0.01[b]
English	401 (100)	73 (18.2)	
Spanish	0 (0)	328 (81.8)	
Marital status			<0.01[b]
Married/partnered	336 (85.7)	276 (70.6)	
Not married/ partnered[a]	56 (14.3)	115 (29.4)	
Age (years)			0.57[c]
Mean (SD)	48.6 (10.2)	48.2 (10.5)	
Range	26–71	23–73	
Insurance coverage			
Employer-based	343 (85.5)	35 (8.7)	<0.01[b]
Privately purchased	13 (3.2)	7 (1.7)	0.17[b]
Government program	51 (12.7)	138 (34.4)	<0.01[b]
No insurance	4 (1.0)	203 (50.6)	<0.01[b]
Employment			<0.01[b]
Full time	270 (67.3)	94 (23.4)	
Part time	52 (13.0)	58 (14.5)	
Not currently employed	79 (19.7)	249 (62.1)	
Health literacy			<0.01[b]
Adequate	380 (95.5)	281 (75.3)	
Inadequate	18 (4.5)	92 (24.7)	
Education			<0.01[b]
Less than high school graduate	1 (0.3)	245 (63.1)	
Grade 12 or GED	32 (8.0)	78 (20.1)	
College 1–3 years	144 (36.1)	44 (11.3)	
College 4 years or more	134 (33.6)	15 (3.9)	
Graduate school	88 (22.1)	6 (1.5)	
Physical exam within last two years	301 (75.1)	338 (84.3)	<0.01[b]
Plan to share results with a physician	178 (44.6)	330 (84.8)	<0.01[b]
Plan to share results with a family member	329 (82.5)	282 (73.1)	<0.01[b]

[a]Includes divorced, separated, widowed, or single.
[b]Chi-square.
[c]Two-sample *t*-test.

individual items in the decisional conflict scale across cohorts. On all but four items, the MPHC cohort was at statistically higher odds of indicating agreement. For example, MPHC participants were more likely to indicate agreement with the statement "I am clear about which benefits of participating in the study matter most to me" than their Mayo Clinic counterparts (odds ratio [OR]: 16.00, 95% confidence interval [CI]: 5.16–80.31, $p < 0.0001$). Similarly, MPHC participants were more likely to agree that they "knew the benefits of participating" (OR: 15.00, 95% CI: 3.81–129.54, $p < 0.0001$) and "knew the risks of participating" (OR: 13.67, 95% CI: 4.36–68.99, $p < 0.0001$). All 16 items from the decisional conflict scale are presented in Table 2 in descending order of comparative odds of agreement by MPHC survey respondents.

Paired comparisons of cohort responses to anticipated psychosocial outcomes are included in Table 3. For each item examining a favorable outcome of participating in the study, MPHC participants were more likely than Mayo Clinic participants to indicate endorsement. For example, MPHC participants were much more likely to endorse the notion that "favorable results will bring me peace of mind" when compared with the Mayo Clinic cohort (OR: 4.2, 95% CI: 2.53–7.36, $p < 0.0001$). MPHC participants also were more likely to believe that their results would give them more control over their health (OR: 3.70, 95% CI: 2.50–5.61, $p < 0.0001$). Finally, MPHC participants were more likely to value a genomic result of any kind, including learning about a genetic predisposition to disease not associated with the study's phenotypic inclusion criteria (hyperlipidemia or colon polyps) (OR: 2.29, 95% CI: 1.27–4.32, $p < 0.05$).

Paired comparisons of cohort responses to items examining psychosocial outcomes related to unfavorable outcomes of receiving genomic screening results are also included in Table 3. MPHC participants were more likely to express concern about the effect of the results on their family relationships (OR: 9.93, 95% CI: 5.83–18.19, $p < 0.0001$) and more likely to believe that a positive genomic screen result would cause them to worry about their health (OR: 7.92, 95% CI: 5.16–12.66, $p < 0.0001$). MPHC participants also were more likely to be concerned about discrimination (OR: 6.44, 95% CI: 4.21–10.25, $p < 0.0001$) and confidentiality than their Mayo Clinic counterparts (OR: 2.46, 95% CI: 1.80–3.39, $p < 0.0001$). Additionally, MPHC participants were more likely to expect a pathogenic genomic result and more likely to express insecurity about their ability to cope with learning they were at increased genetic risk of disease.

Knowledge of genomic sequencing scores were calculated as a proportion of correct responses (0 to 1). The mean knowledge score for the Mayo Clinic cohort was 0.76 (SD = 0.20, median = 0.82). Knowledge scores for the MPHC cohort were lower, with a mean of 0.55 (SD = 0.24, median = 0.55, $p < 0.0001$; see Supplemental Fig. 2). Table 4 compares the cohorts on individual items in the knowledge of genomic sequencing measure. While the MPHC cohort was more likely to provide an incorrect answer to any individual item in the knowledge measure, when compared with the Mayo Clinic cohort, four items stood out with the highest comparative likelihood of an incorrect response from the MPHC cohort. The first item stated, "once a variant in a gene that affects a person's risk of a disease is found, that disease can always be prevented or cured." MPHC participants were at 12.3 times higher odds of providing an incorrect or uncertain response (i.e., True or Don't Know; 95% CI: 7.62–21.20, $p < 0.0001$). Similarly, MPHC participants were more likely to respond incorrectly (i.e., False or Don't Know) to the following statement: "Even if a person has a variant in a gene that affects their risk of a disease, they may not develop that disease" (OR: 9.00, 95% CI: 5.06–17.41, $p < 0.0001$). MPHC participants also were more likely to answer incorrectly (i.e., True or Don't Know) to the item, "Scientists know how all variants of genes will affect a person's chances of developing diseases"

Table 2. Comparison of beliefs about the potential benefits and risks of genomic risk evaluation.

	Mayo Clinic *N* (%)	MPHC[b] *N* (%)	Comparative odds of MPHC[b] indicating agreement	95% confidence interval (CI)
Beliefs about the decision to pursue genomic screening[a]				
I am clear about which benefits of participating in the study matter most to me	348 (87)	371 (99)	16.00[d]	5.16–80.31
I know the benefits of participating in the study	368 (92)	375 (99)	15.00[d]	3.81–129.54
I know the risks of participating in the study	353 (88)	364 (98)	13.67[d]	4.36–68.99
I am clear about which risks matter most to me	340 (85)	368 (98)	11.00[d]	4.44–35.21
I am clear that participating in the study was the best choice for me	347 (87)	377 (99)	10.20[d]	4.10–32.75
My decision reflects what is important to me	370 (93)	383 (98)	5.80[d]	2.22–19.19
I am clear about which is more important to me (the benefits or the risks)	351 (88)	358 (97)	4.50[d]	2.24–10.01
I feel sure about my choice	376 (94)	378 (98)	4.00[c]	1.59–11.96
I feel I have made an informed choice	383 (96)	378 (99)	3.40[c]	1.20–11.79
I had enough support from others when I made my choice	232 (58)	292 (82)	3.11[d]	2.13–4.63
The decision was easy for me to make	354 (89)	369 (96)	3.07[c]	1.65–6.08
I am satisfied with my decision	389 (97)	378 (99)	2.20	0.70–8.08
I had enough advice when I made my choice	292 (73)	289 (83)	1.82[c]	1.22–2.76
I chose without pressure from others	390 (98)	378 (98)	1.13	0.39–3.35
I know I had the option to participate or not participate in the study	396 (99)	373 (99)	1.00	0.13–7.47
I expect to stick with my decision	393 (98)	349 (94)	0.29[c]	0.11–0.70

[a]Items are from the decisional conflict scale, *N* (%) of respondents indicating Agree or Strongly Agree.
[b]Mountain Park Health Center.
[c]$p < 0.05$.
[d]$p < 0.0001$.

(OR: 8.83, 95% CI: 5.78–14.09, $p < 0.0001$). Fourthly, MPHC participants were more likely to answer incorrectly (i.e., True or Don't Know) the item, "A health-care provider can tell a person their exact chance of developing a disease based on the results from genome sequencing" (OR: 7.64, 95% CI: 5.02–11.51, $p < 0.0001$). Odds ratios were smaller for the remaining knowledge measure items (see Table 4).

DISCUSSION

Our study examined psychosocial outcomes associated with participation in a genomic sequencing study in the context of a FQHC. In this context, we also conducted a comparative psychosocial analysis of a minority population with a "matched control" cohort of participants receiving the same test in the context of an academic medical center.

Very few studies, to date, have focused on minority community perspectives on genomic medicine in care settings that are not academic medical centers. Kaphingst and colleagues conducted a hypothetical vignette-based survey in urban community health centers and assessed minority perspectives about genomic research.[19] As in our study, Kaphingst and colleagues focused on the perspectives of racial minority populations not connected to an academic medical center. Sanderson and colleagues interviewed 205 individuals at an outpatient clinic in an inner-city hospital (29% of whom were Latino) to assess willingness to participate in a hypothetical genomic research study.[22] Additionally, Hoskins and colleagues conducted a study examining the feasibility of increasing recommended referrals for genetic counseling for breast cancer within a FQHC,[18] and Komenaka and colleagues assessed the participation of low-income women (70% of whom where Latino) in *BRCA1/2* testing within the context of a safety net institution.[20] Finally, Rana and colleagues examined the comparative outcomes of cancer genetics consultations in an academic medical center and an FQHC and found lower uptake of genetic testing among patients from the FQHC.[21] These studies represent rigorous efforts to reach outside the environment of the academic medical center and characterize minority perspectives on genomic research.

To date, however, few (if any) studies have examined the experiences and decision making processes of Latino patients who elect to received genomic evaluation of disease risks (i.e., assessment of multiple genetic risks across multiple diseases) in lower resource settings such as a FQHC. While our data have limitations, which are discussed below, at least three observations can be made that may inform future efforts to increase the inclusiveness of genomic medicine and research.

First, our results suggest that the decisional support provided to MPHC participants when they enrolled enhanced their feelings of being well prepared when compared with the Mayo Clinic cohort.

Table 3. Comparison of anticipated psychosocial outcomes resulting from genomic risk evaluation.

	Mayo Clinic *N* (%)	MPHC[a] *N* (%)	Comparative odds of MPHC[a] indicating agreement	95% confidence interval (CI)
Favorable psychosocial outcomes				
Results indicating no genetic disease risk will bring me peace of mind[b]	313 (78)	363 (94)	4.21[h]	2.53–7.36
Results will give me more control over my health[b]	256 (64)	329 (87)	3.70[h]	2.50–5.61
Results indicating no increased genetic risk for disease are valuable to me[c]	298 (75)	331 (90)	3.33[h]	2.09–5.50
Results indicating elevated risk for heart disease or colorectal cancer are valuable to me[c]	356 (89)	344 (93)	1.86[g]	1.07–3.32
Results indicating I have some other disease risk are valuable to me[c]	354 (89)	346 (95)	2.29[g]	1.27–4.32
Unfavorable psychosocial outcomes				
I am concerned about detrimental effects of results on family relationships[d]	23 (6)	158 (41)	9.93[h]	5.83–18.19
Results indicating increase risk of disease will cause me to worry[b]	154 (39)	313 (82)	7.92[h]	5.16–12.66
I am concerned that I will feel labeled or singled out if I tell others that I have elevated genetic risk for disease[d]	57 (14)	191 (49)	6.44[h]	4.21–10.25
I am concerned that my results may not stay confidential[d]	137 (34)	213 (56)	2.46[h]	1.80–3.39
I am not completely confident about coping with a positive test result[e]	250 (63)	283 (73)	1.57[g]	1.15–2.15
I am expecting a genomic result indicating increase risk of disease[f]	259 (65)	279 (74)	1.53[g]	1.11–2.12

[a]Mountain Park Health Center.
[b]*N* (%) indicating Agree or Strongly Agree vs. Neither Agree nor Disagree, Disagree, or Strongly Disagree.
[c]*N* (%) indicating Extremely Valuable or Quite Valuable vs. Slightly Valuable or Not At All Valuable.
[d]*N* (%) indicating Very Concerned or Somewhat Concerned vs. Slightly Concerned or Not At All Concerned.
[e]*N* (%) indicating they were less than "extremely confident" in their ability to cope with any result.
[f]*N* (%) indicating Likely or Very Likely vs. Neither Likely nor Unlikely, Unlikely, or Very Unlikely.
[g]$p < 0.05$.
[h]$p < 0.0001$.

This conclusion assumes that the decision to participate in a genomic sequencing study would have otherwise been a difficult one for some participants in the MPHC cohort due to a historic underrepresentation in research and known literacy and health literacy challenges in Latino populations.[37] We were reassured by the low levels of decisional conflict measured in the MPHC cohort, and we attributed the decisional clarity we observed to the in-person, culturally competent engagement that participants received at the time of study enrollment. Future research could explore in greater depth the sources and meaning of decisional conflict in Latino communities, including the potential influence of knowledge, health literacy and English-language proficiency on decisional conflict. Future research could also explore potential implications of elevated decisional conflict for the pursuit of genomic risk evaluation.

Second, our data suggest that Latino participants from a FQHC in the Phoenix area may have stronger opinions about the potential impact of genomic screening compared with non-Latino participants who receive care at an academic medical center in the Upper Midwest. For example, MPHC participants were more likely than Mayo Clinic participants to endorse the potential for favorable psychosocial outcomes from participating in a genomic screening study, such as greater peace of mind as a result of receiving a negative result, and greater control over their health. More participants at MPHC exhibited appreciation for genetic information of any kind, and more intended to share their screening results with a physician. Conversely, MPHC participants also were more likely to have significant reservations about genomic screening and its potential to produce negative outcomes. For example, MPHC participants were significantly more likely to express concerns about confidentiality, discrimination, and the potential for negative effects on family members. MPHC participants also were more likely to anticipate unfavorable test results and were more likely to express personal insecurities about their ability to cope with learning they have a greater risk of disease due to their genetics. These more extreme views of both the potential positive and negative outcomes of genomic screening may be the result of limited familiarity with new forms of genomic medicine. Our findings suggest that some of the traditional ethical considerations in genomic medicine and research may require additional evaluation as access to genomic medicine is expanded to include historically underrepresented populations in genetic research.

Third, our results highlight several potential priority areas for future educational interventions. The MPHC cohort scored lower than the Mayo Clinic cohort on several items related to knowledge about genomic sequencing. The top four questions most likely to be answered incorrectly by the MPHC cohort had to do with beliefs about penetrance ("Even if a person has a variant in a gene that affects their risk of a disease, they may not develop that disease"), beliefs about the capability of the health system to effect prevention or cure ("Once a variant in a gene that affects a person's risk of a disease is found, that disease can always be prevented or cured"), and beliefs about the role of health professionals (physicians and scientists) in utilizing genomic information ("Scientists know how all variants of genes will affect a person's chances of developing diseases" and "A health-care provider can tell a person their exact chance of developing a

Table 4. Comparative performance on knowledge about genomic sequencing items.

	Mayo Clinic *N* (%)	MPHC *N* (%)	Comparative odds of MPHC giving incorrect answer	95% confidence interval (CI)
Once a variant in a gene that affects a person's risk of a disease is found, that disease can always be prevented or cured	331 (84)	115 (30)	12.33[c]	7.62–21.20
Even if a person has a variant in a gene that affects their risk of a disease, they may not develop that disease	359 (92)	245 (65)	9.00[c]	5.06–17.41
Scientists know how all variants of genes will affect a person's chances of developing diseases	316 (81)	111 (29)	8.83[c]	5.78–14.09
A health-care provider can tell a person their exact chance of developing a disease based on the results from genome sequencing	315 (80)	119 (31)	7.64[c]	5.02–11.51
Genome sequencing may find variants in a person's genes that they can pass on to their children	369 (94)	330 (86)	2.58[b]	1.49–4.64
Genome sequencing may give a person information about their chances of developing several different diseases	368 (94)	316 (84)	2.50[b]	1.50–4.31
A person's health habits, like diet and exercise, can affect whether or not their genes cause diseases	234 (60)	158 (42)	2.06[c]	1.53–2.80
Genome sequencing may find variants in a person's genes that may determine how they respond to certain medicines	242 (62)	176 (47)	1.74[b]	1.29–2.37
Genome sequencing may find variants in a person's genes that will increase their chance of developing a disease in their lifetime	337 (86)	294 (79)	1.67[b]	1.12–2.50
Genome sequencing is a routine test that most people can have through their physician's office	234 (60)	184 (49)	1.52[b]	1.12–2.07
Genome sequencing may find variants in a person's genes that will decrease their chance of developing a disease in their lifetime	194 (49)	173 (48)	1.06	0.80–1.42

[a]Items are from the knowledge about genomic sequencing scale, *N* (%) correct responses.
[b]$p < 0.05$.
[c]$p < 0.0001$.

disease based on the results from genome sequencing"). Cultural constructs related to fatalism (i.e., *fatalismo*)[38] and deference to medical expertise and authority (i.e., *respeto*)[39] that have been described in Latino populations may contribute to observed differences in cohort responses to these items. Specifically, responses to these items may be reflective of more foundational differences in cultural views related to health, health care, and health-care specialists.

Finally, our findings highlight the need for further research examining underlying factors that mediate participants' knowledge and beliefs about genomic screening. Although we were unable to formally assess the impact of the in-person educational support provided to the MPHC cohort, it is possible that differences in education level or literacy between the two cohorts may have been associated with observed differences in knowledge and comprehension of genomic screening. Innovative and tailored approaches to patient education (and studies of their effectiveness) may be necessary to support individuals with lower literacy or educational attainment while also addressing some of the cultural conceptions of health and health care that inform understandings of genomic medicine.[40]

Limitations

Our data should be interpreted in light of several limitations. First, the two cohorts we compared are limited in their representativeness. All participants in both study cohorts were recruited from biobank registries and it is possible that biobank donors have more favorable attitudes about the value of genetic research. The Mayo Clinic cohort was mostly non-Latino, well-educated, insured, and received care at an academic medical center. As such, the Mayo Clinic participants in our study are not fully representative of the diversity of patients who receive care at academic medical centers in the United States. As described elsewhere, participants in the MPHC cohort were difficult to recruit, in part, due to factors such as restrictive work schedules, transportation limitations, changing mailing addresses, and low literacy.[28] A majority of our MPHC cohort was female, had adequate health literacy, and reported having had a physical exam within the last two years. These considerations suggest that the MPHC cohort may be limited in its representativeness of the regional Latino community in Phoenix, as well as other Latino communities nationwide. Future research into the experiences of Latino participants receiving genomic evaluation at Federally Qualified Health Centers should seek to further characterize the heterogeneity in both regional and national Latino populations who receive care in those settings.

Secondly, because our survey was fielded in English and Spanish, the comparison of survey item responses across cohorts may be limited by cultural and linguistic factors. We attempted to address this using a rigorous translation and back-translation process, with subsequent cognitive testing in native Spanish speakers from the population we surveyed. We did not do psychometric validation, however, to confirm the fidelity of our items across languages.

Finally, there are limitations in our method of cohort comparison. We were unable to match the cohorts on variables beyond sex and age. The cohorts differed significantly on several other levels (see Table 1). Furthermore, as described above, recruitment procedures for participants in the RAVE study differed between the two cohorts, with in-person decision support and education provided to MPHC participants as part of the

enrollment process. The additional support provided to the MPHC cohort may confound our analysis of perceived psychosocial outcomes, particularly results pertaining to decisional conflict, in which the MPHC cohort reported less decisional ambivalence overall than the Mayo Clinic cohort. Additionally, we were unable to examine the intersectional impact of ethnicity and race on psychosocial outcomes in our comparison.

Despite these limitations, our findings illuminate broad differences in the psychosocial impact of genomic screening on differentially advantaged populations. Comparative studies examining the psychosocial impacts of genomic medicine are uncommon but much needed as genomic medicine is extended to more diverse clinical contexts. While the specific differences we observed may not be confirmed in future studies, it is unlikely that the observed variation in psychosocial impact we observed would disappear altogether in other studies examining the impact of genomic medicine on racial and ethnic minorities that historically have not been adequately represented in genomic research.

Conclusion

As genomic medicine expands, continued engagement with racial and ethnic minority populations is critical to ensure that the needs of diverse communities are met in culturally sensitive ways. Our data suggest that bioethical concerns that have been studied extensively in more affluent majority populations will need to be re-evaluated in lower resource settings where racial and ethnic minorities often receive care. Our findings also suggest that differences in attitudes and beliefs about genomic medicine may be influenced by broader cultural norms that are themselves reflective of shared social, economic, political, and other experiences that shape Latino perspectives on health and health care.[41] As a result, interventions that have been created in support of majority populations may not be appropriate or effective in other clinical settings. If we fail to develop culturally appropriate forms of genomic medicine, we risk alienating patients who would benefit from these medical advances, thereby widening health disparities and limiting the potential benefits of individualized medicine.

Supplemental data

Supplemental data include two boxplot figures showing the distributions, medians, and interquartile ranges of the total Decisional Conflict Scale scores and the Knowledge About Genome Sequencing scale scores for both cohorts.

DATA AVAILABILITY

Survey data may be made available on a case by case basis by contacting the principal investigator of the study.

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AUTHOR CONTRIBUTIONS

Conceptualization: J.E.P., G.Q.S., E.J.S., R.R.S. Formal analysis: J.E.P., A.L., J.O., R.R.S. Funding acquisition: I.J.K., R.R.S. Methodology: J.E.P., G.Q.S., A.L., J.O., E.J.S., R.R.S. Project administration: J.E.P. Supervision: G.Q.S., V.H., N.M.L., D.S., I.J.K., R.R.S. Visualization: J.E.P. Writing—original draft: J.E.P. Writing—review & editing: G.Q.S., A.L., J.O., I.C., E.J.S., V.H., N.M.L., D.S., I.J.K., R.R.S.

COMPETING INTERESTS

The authors declare no competing interests.

ETHICS DECLARATION

This survey study was embedded in two parent genomic sequencing studies, each of which was reviewed and approved by the Mayo Clinic Institutional Review Board (#15–005013 and #16-004342). Written informed consent was obtained for all participants.

ADDITIONAL INFORMATION

The online version of this article (https://doi.org/10.1038/s41436-020-01079-5) contains supplementary material, which is available to authorized users.

Correspondence and requests for materials should be addressed to R.R.S.