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Multi-Ethnic Minority Nurses' Knowledge and Practice of Genetics and Genomics

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Abstract

Purpose—Exploratory studies establishing how well nurses have integrated genomics into practice have demonstrated there remains opportunity for education. However, little is known about educational gaps in multi-ethnic minority nurse populations. The purpose of this study was to determine minority nurses' beliefs, practices, and competency in integrating genetics-genomics information into practice using an online survey tool.

Design—A cross-sectional survey with registered nurses (RNs) from the participating National Coalition of Ethnic Minority Organizations (NCEMNA). Two phases were used: Phase one had a sample of 27 nurses who determined the feasibility of an online approach to survey completion

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and need for tool revision. Phase two was a main survey with 389 participants who completed the revised survey. The survey ascertained the genomic knowledge, beliefs, and practice of a sample of multi-ethnic minority nurses who were members of associations comprising the NCEMNA.

Methods—The survey was administered online. Descriptive survey responses were analyzed using frequencies and percentages. Categorical responses in which comparisons were analyzed used chi square tests.

Findings—About 40% of the respondents held a master's degree (39%) and 42% worked in direct patient care. The majority of respondents (79%) reported that education in genomics was important. Ninety-five percent agreed or strongly agreed that family health history could identify at-risk families, 85% reported knowing how to complete a second- and third-generation family history, and 63% felt family history was important to nursing. Conversely, 50% of the respondents felt that their understanding of the genetics of common disease was fair or poor, supported by 54% incorrectly reporting they thought heart disease and diabetes are caused by a single gene variant. Only 30% reported taking a genetics course since licensure, and 94% reported interest in learning more about genomics. Eighty-four percent believed that their ethnic minority nurses' organizations should have a visible role in genetics and genomics in their communities.

Conclusions—Most respondents felt genomics is important to integrate into practice but demonstrated knowledge deficits. There was strong interest in the need for continuing education and the role of the ethnic minority organizations in facilitating the continuing education efforts. This study provides evidence of the need for targeted genomic education to prepare ethnic minority nurses to better translate genetics and genomics into practice.

Clinical Relevance—Genomics is critical to the practice of all nurses, most especially family health history assessment and the genomics of common complex diseases. There is a great opportunity and interest to address the genetic-genomic knowledge deficits in the nursing workforce as a strategy to impact patient outcomes.

Keywords

Minority nurses; nursing; genetics; survey; nursing practice

As the proliferation of knowledge and understanding of genomics accelerates, it becomes clearer that understanding heritability and its intersection with environment has now become foundational to nursing science, theory, and practice. Genetic and genomic literacy now distinguishes all nursing professionals as state-of-the-art academicians, researchers, and clinicians who will provide the best care possible. We are emerging into an era whereupon nursing assessments, interventions, and the promotion of wellness will only attain scientific merit with the translation of genomic knowledge to practice. Health care increasingly demands that the registered nurse (RN) use genomic information and technology when designing and providing care to those concerned about health or disease. These expectations have direct implications for RN preparatory curricula, as well as for the 2.9 million practicing nurses (U.S. Department of Health and Human Services, Health Resources and Services Administration, 2010).

Complex diseases such as cardiovascular and heart disease, diabetes, and cancer have disproportionally affected racial and ethnic minority populations (National Center for Health Statistics, 2012). While genetics research explores single gene disorders, the scientific discoveries now inclusive of genomics are beginning to illuminate all genetic variation in the human genome and the environmental influences on health outcomes for persons with complex chronic diseases. A transformative change in the genomic knowledge of disease pathophysiology has produced a knowledge gap for nurses. A previous study assessed nurses' knowledge of genomics integration into practice (Calzone et al., 2012; Calzone, Jenkins, Culp, Bonham, & Badzek, 2013); however, the study was not representative of ethnic minority nurses. In fact, very little is known about genomic knowledge gaps of minority nurses (Spruill, Coleman, & Collins-McNeil, 2009). These findings support the need for further investigation of multi-ethnic minority nurses' knowledge and practice of genetics and genomics.

Background

The National Coalition of Ethnic Minority Nurse Associations (NCEMNA) was incorporated in 1998 as a unified voice in nursing for the elimination of health disparities for ethnic minority populations. This national nursing collaboration represents 350,000 nurses and is composed of five ethnic minority nursing organizations. Its member organizations are:

- Asian American/Pacific Islander Nurses Association, Inc. (AAPINA)
- National Alaska Native American Indian Nurses Association, Inc. (NANAINA)
- National Association of Hispanic Nurses, Inc. (NAHN)
- National Black Nurses Association, Inc. (NBNA)
- Philippine Nurses Association of America, Inc. (PNAA)

The goals of the NCEMNA focus on development of a cadre of ethnic nurses reflecting the nation's diversity, advocating for cultural competence, and accessible and affordable health care. This coalition of ethnic minority nurse organizations collectively supports the development of professional and educational advancement of ethnic nurses, and the education of consumers, health-care professionals, and policy makers on health issues of ethnic minority populations. The NCEMNA's primary objective is to develop ethnic minority nurse leaders in areas of health policy, practice, education, and research. Through this approach, the endorsement of best nursing practice models inclusive of genetics-genomics, education, and research to improve the health of minority populations is paramount (NCEMNA, 2013). One of the first initiatives that the NCEMNA undertook was implementing strategies to increase minority nurse participation and success in research careers at the doctoral level. An area determined as a collective interest to the NCEMNA member organizations was the need to improve the health of the representative ethnic minority patient populations through research. Given the anticipated emerging majority of these minority populations, the NCEMNA member organizations identified the need to increase minority faculty and doctorally prepared nurses conducting research through mentorship. Nurses from the NCEMNA member organizations received competitive grants to participate in the mentorship program that culminated in a yearly conference where

genetic-genomic information was presented as a foundational contributor to common diseases found in ethnic patient populations represented by the NCEMNA member organizations.

Representatives from the National Human Genome Research Institute (NHGRI) and the National Cancer Institute (NCI) along with the primary investigator of this current work have presented on genetics and genomics at the National NCEMNA conferences. The response and interest in genomic topics led to the interest in gathering baseline information from these representative nursing groups regarding how ethnic minority nurses utilized genetic-genomic core competencies and information in their practice. Fundamental to this undertaking was the establishment and endorsement of the Essential Nursing Competencies and Curricula Guidelines for Genetics and Genomics in October 2006 and expanded in 2008, and an established strategic implementation plan that focused on practicing nurses, regulatory oversight of nursing practice, and academic preparation of nurses (Consensus Panel on Genetic/Genomic Nursing Competencies, 2006, 2009).

Theoretical Framework

The theoretical framework guiding this study was Rogers' Diffusion of Innovations (DOI; Rogers, 2003). This theory consists of four components: (a) the innovation, which in this study is genomics; (b) dissemination communication channels; (c) time; and (d) the social system, which in this study is the minority nursing community. Factors that influence diffusion of the innovation are antecedents and consist of adopter characteristics as well as their attitudes. Adopters in this study are the minority nurses, and their characteristics include their genomic competency. Attitudes are the underlying beliefs the adopters hold about the innovation (i.e., genomics).

Study Aims

The ultimate goal of this collaborative project was to assure that in this genomic era of health care, ethnic minority nurses are prepared to assure quality care in a diverse population that has concerns/experiences with health disparities. Study aims were approached in two phases to allow for testing of the study instrument followed by administration of the instrument in the target population.

Phase One Pilot Test Aims

1.1 Establish the feasibility of an online survey method of data collection.

1.2 Evaluate the degree of respondent burden and survey response rates to establish whether this method of data collection would be adequate for future target population implementation.

Phase Two Aims

2.1 Determine minority nurses' beliefs, practices, and competency of integrating into practice genomic information related to common multifactorial diseases.

2.2 Assess knowledge of human genetic variation and the use of patient characteristics, including ethnicity, gender, genes, and race in diagnostics, treatment, and referral decisions.

Analysis of aim 2.2 will be reported in a subsequent article.

The NCEMNA Board approved moving forward with a plan to utilize the diverse expertise of the NCEMNA communities to create a genetics-genomics initiative. The NANAINA chose to abstain from participation in this research. Representatives from NCEMNA were identified to organize this initiative with representatives of the NHGRI and NIH. This study was approved by the Cedars Sinai Institutional Review Board as well as the NIH Office of Human Subjects Research.

Materials and Methods

Instrument

The survey instrument used in this study was collaboratively developed by all investigators. Multiple telephone meetings were held to identify the process and required survey content to benchmark the genetic-genomic knowledge of nurses via a membership survey. The final draft survey is a compilation of the following five instruments, which have been combined, reviewed, and pretested by the research team.

1. The knowledge, attitude, and interest of African American nurses toward genetics (Spruill et al., 2009).
2. Bonham and Sellers' Genetic Variation Knowledge Assessment Index (GKAI; Bonham, Sellers, & Woolford, submitted for publication).
3. Bonham and Sellers' Health Professionals Beliefs about Race (HPBR) scale.
4. Bonham and Sellers' Racial Attributes in Clinical Evaluation (RACE) scale.
5. The Genetics and Genomics in Nursing Practice (GGNPS; Calzone et al., 2012).

The first survey instrument, the knowledge, beliefs, and practices of African American nurses of genetics, was designed to assess the interest, knowledge, and practice of genetics and genomics among African American Nurses. At tool construction, both face validity and construct validity were obtained using a panel of experts to evaluate the items of the tool to ensure the construct was captured (Spruill et al., 2009). The Cronbach α standardized is 0.652 for this 21-item survey instrument.

The survey instrument used in this study also included questions modified from a study with physicians to evaluate nurses' knowledge of genetic variation using the Genetic Variation Knowledge Assessment Index (GKAI). The GKAI scores range from 0 to 6, mean 3.28 (SD = 1.17) and was found to be symmetric and unimodal. To evaluate nurses' utilization of race in clinical practice, questions from the exploratory Health Professionals Beliefs about Race (HPBR; HPBR-BD, α = 0.69, four items, and HPBR-CD α = 0.61, three items) and Racial Attributes in Clinical Evaluation (RACE) scales (α = 0.86, seven items; Bonham et al., submitted for publication).

In addition to the instruments described in the preceding paragraph, the survey utilized for this study included questions from the GGNPS instrument (Calzone et al., 2012; Jenkins, Woolford, Stevens, Kahn, & McBride, 2010). This survey tool is constructed to evaluate Rogers DOI theoretical domains, including attitudes, receptivity, confidence, competency, knowledge, decision, and adoption. Instrument validation was performed using structural equation modeling, which confirmed that the instrument items aligned with the domains of the DOI (Jenkins et al., 2010).

The final compiled study instrument included seven sections assessing beliefs, knowledge, practice, use of race or ethnicity, education, and demographics. There were a total of 61 questions, including multiple choice, dichotomous (yes or no), and Likert scale questions. The questions were consistent with the Essentials of Genetic and Genomic Nursing Competencies and assessed family history utilization as well as the genomics of common disease, which represent knowledge and practice expected of all RNs irrespective of their role, level of academic training, or specialty in which they practice (Consensus Panel on Genetic/Genomic Nursing Competencies, 2009). The selection of family history as evidence of practice integration was intentional because family history collection falls within the scope of practice of all RNs and is not cost or technology dependent.

Data Collection

Phase One

The target population consisted of nurses attending the March 2009 NCEMNA conference. Nurses of all levels of academic preparation, role, and clinical specialty were invited to participate in the online survey methodology assessing genetic and genomic knowledge, belief, and skills. The only member organization exclusion was NANAINA per their request. Conference leaders provided notice to the 125 participants about the pilot testing study, inviting them to test the instrument online. No individual nurses were approached. Rather, interested conference attendees self-selected to participate.

During Phase One pilot testing, computers were made available at the NCEMNA annual meeting. A researcher was stationed by the computer with an access code to assist with survey access. A target of 30 participants was desired for the study pilot phase. Prior to participation, each participant was informed of the study aims and provided his/her verbal consent. In addition, upon launching the survey online, the participant also had a written consent as part of the instructions prior to encountering any survey questions.

Phase Two

The following NCEMNA Associations chose to participate: AAPINA, NAHN, NBNA, and PNAA. Recruitment of study participants was done through each participating NCEMNA member association. A link to the survey was posted on the NCEMNA website as well as each participating NCEMNA member association website. Recruitment consisted of email announcements to association constituencies as well as notifications through association newsletters. The survey offered no incentives. The survey was open for a total of 10 months, with slightly varying start dates for each association.

Instructions for the survey included the phone numbers and email addresses of study investigators to contact with any questions. Participants also received instructions that the survey was voluntary, no identifying information would be collected or stored, and they could skip any question.

Eligibility was limited only to licensed RNs who accessed the online survey. Membership in an NCEMNA participating association was not required. Inclusion and exclusion criteria were the same for both Phase One and Phase Two studies.

Survey data were collected using the online survey tool SurveyMonkey (SurveyMonkey, Inc., Palo Alto, CA, USA). The survey took approximately 20 min for completion and collected no personal identifying information. All data were stored in a password-protected file that was available only to study investigators.

Statistical Analysis

Data were analyzed using SAS 9.3 (SAS Institute Inc., Cary, NC, USA). The answers to all survey questions were summarized using descriptive statistical techniques. Chi-squared tests were used to assess the relationships between survey items with categorical responses. The level of significance was $\alpha = 0.05$, and all tests of statistical significance were two tailed.

Results

Phase One

A total of 27 participants completed the online survey. Participants found the length of the survey to be just right. On average, participants spent 23 min completing the survey. There were some technical problems with obtaining online access that were remedied during Phase One of the study. The majority agreed or strongly agreed that the directions for survey completion were adequate 70% ($n = 16/23$), the survey was organized 86% ($n = 20/23$), the survey was easy to navigate 69% ($n = 16/23$), question sequence was clear and predictable 70% ($n = 16/23$), terminology was consistent and appropriate 82% ($n = 19/23$), and the survey was technically easy to complete 78% ($n = 18/23$). Most (82%, $n = 18/22$) indicated that there were no questions worded in a way that were not sensitive to their ethnic group. Survey tool modifications were made based on recommendations from the participants to enhance respondent response by decreasing the number of survey items. The final instrument for use in Phase Two consisted of seven sections and a total of 61 questions.

Phase Two

Demographic and work characteristics of participants—A total of 392 respondents completed an online survey located on their nursing organization's website in Phase Two of the study. Excluding three ineligible participants reporting a highest nursing degree of a licensed practical nurse, a total of 389 were included in the data analysis. Table 1 summarizes the characteristics of the eligible nurses. Participants' ages ranged from 23 to 82 years, with a mean of 52 years, the majority were female (93%, $n = 304/326$). The majority of participants were Asian (43%, $n = 138/322$) and African American (33%, $n = 107/322$). Eighteen percent ($n = 60/329$) stated that they considered themselves to be Hispanic/Latino,

and 8% (*n* = 27/322) reported that they were White. The majority (39%, n = 130/331) reported their highest level of education was a master's degree, 35% (*n* = 115/331) had a baccalaureate degree, 16% (*n* = 53/331) held a doctoral degree, 8% (*n* = 28/331) had an associate degree, and 2% (*n* = 5/331) were diploma prepared. The primary work setting reported was a hospital (68%, *n* = 163/241). The average number of years they had worked in nursing was 20 years, and more than half (51%, *n* = 166/326) had worked at their current work setting for over 10 years. Forty-two percent (**n** = 139/330) indicated their primary role was patient care, 22% (*n* = 71/330) were in education, and 19% (*n* = 63/330) were in administration.

Beliefs—The majority of respondents felt it was very important (79%, *n* = 301/383) or somewhat important (19%, *n* = 71/383) for nurses to become more educated about the genomics of common disease. The most frequent advantages of integrating genomics into practice identified included better decisions about recommendations for preventive services (87%, *n* = 332/383), better treatment decisions (73%, *n* = 280/383), improved services to patients (68%, *n* = 259/383), better adherence to clinical recommendations by patients (56%, *n* = 216/383), and genetic risk triaging (46%, *n* = 177/383). The highest reported potential disadvantages to integrating genomics into practice included that it would increase insurance discrimination (61%, *n* = 224/366), genetics could increase patient anxiety about risk (52%, *n* = 191/366), and it would be not reimbursable or too costly (49%, *n* = 181/366).

Knowledge—Self-reported genetic knowledge assessments are provided in Table 2. Half of the participants (50%, *n* = 182/364) felt their understanding of the genetics of common diseases was poor or fair. The majority (95%, *n* = 371/389) agreed or strongly agreed that family history could help to identify at-risk families and 85% (*n* = 323/381) knew how to complete it. The majority had completed a family history for themselves (74%, *n* = 279/378) and 51% (*n* = 195/381) had collected one for a family member.

Responses varied by disease as to the degree to which nurses felt genetics had clinical relevance to a wide range of common health conditions. For example, only 54% (*n* = 191/353) reported that hemochromatosis, an inherited condition, had a great deal to do with genetics. The majority correctly identified that genetic risk (e.g., as indicated by family history) has clinical relevance for breast, colon, and ovarian cancers; coronary heart disease; and diabetes. However, 54% of respondents (*n* = 105/193) thought diabetes and heart disease are caused by a single gene variant, which is incorrect.

Practice—When presented with the option to identify what was important to consider when delivering nursing care, genes (29%, *n* = 53/185) and insurance (10%, *n* = 37/362) were the two lowest items identified as essential. Other items scored as more essential to consider included race (52%, *n* = 196/376), gender (53%, *n* = 196/371), age (63%, *n* = 231/369), and family history (63%, *n* = 238/375).

Seventy-two percent (*n* = 274/380) also reported collecting family histories for patients in their practice setting. When a patient indicated a disorder in the family, nurses always collected the age of diagnosis (64%, *n* = 231/361), the relationship to the patient (91%, *n* =

330/363), race or ethnic background (77%, n = 242/315), age at death from the condition (65%, n = 237/362), as well as maternal and paternal lineages (77%, n = 278/359).

With regard to family history specific knowledge elements, nurses with higher levels of education tended to accurately report that a family history should include age at diagnosis of condition (p = .0146). More years of practice influenced the collection by nurses of standard family history information that also included race or ethnic backgrounds (p = .0197), age at death from conditions (p = .0268), and age at diagnosis of condition (p = .0009). Most nurses (98%, n = 380/386) agreed or strongly agreed that family health histories could be used to teach patients and family members about the importance of genetics-genomics and disease prevention. However, there was no relationship between the proportion of work time spent seeing patients and the perceived value of family history, use of family history, or variable collected (i.e., age, relationship, race, or lineages).

Genetics and genomics education—Only 35% (n = 123/356) indicated that they had taken a course that included genetics as a major component since they obtained their nursing license. While the majority of nurses (94%, n = 335/357) indicated that they intended to learn more about genetics, only 30% (n = 107/352) knew whether there were any courses on genetics available to them. More than half (55%, n = 196/358) identified workshops that included a mixture of presentations and group activities as the preferred format for learning about genetics. Overall, most (90%, n = 318/354) would encourage NCEMNA or their organization to support a genetics and genomics awareness initiative and 81% (n = 289/357) responded that they would attend training if offered at their annual conference. Similarly, 84% (n = 297/354) believed that their national organization should have a visible role in genetics-genomics in their community.

Discussion

This study assessed the knowledge, beliefs, and practice of a sample of multi-ethnic minority nurses recruited through NCEMNA for Phase One and through the NCEMNA Member associations for Phase Two. Phase One of the study showed the feasibility of an online survey method of data collection, indicating minimal difficulty and taking an average of 23 min to complete. Instrument modifications were made based on respondent recommendations to assure accurate and complete responses from the broader membership, and the investigators chose to enhance response by decreasing the number of survey items.

In Phase Two, it was determined that most respondents in this study felt genetics-genomics are important to integrate into practice, but they demonstrated knowledge deficits. The majority of respondents felt it was very important (79%) for nurses to become more educated about the genomics of common disease. Half of the participants felt their understanding of the genetics of common diseases was poor or fair. They indicated a strong interest in learning more, with 94% reporting that they intended to learn more about genetics. Study participants were also supportive (90%) of encouraging a genetics and genomics awareness initiative.

These results were very similar to those reported recently from a study of nurses responding to an American Nurses Association (ANA) study (Calzone et al., 2013). Both studies included similar populations (NCEMNA, 93% female, *n* = 304/326; ANA, 96% female, *n* = 461/481; NCEMNA, average age 52 years; ANA, average age 51 years). However, this study population had different ethnicity/race characteristics, enhancing the understanding of differences in knowledge, beliefs, and practices of genetics and genomics for all nurses. This study included more nurses who were Asian (NCEMNA, 43%, *n* = 138/322; ANA, 2%, *n* = 8/476); Black/African American (NCEMNA, 33%, *n* = 107/322; ANA, 3%, *n* = 14/476); Hispanic (NCEMNA, 18%, *n* = 60/329; ANA, 2%, *n* = 8/478); and fewer who were White (NCEMNA, 8%, *n* = 27/322; ANA, 89%, *n* = 424/476). There were also more nurses with advanced degrees in nursing who participated in this study (NCEMNA: master's degrees 39%, *n* = 130/331, doctoral degrees 16%, *n* = 53/331; ANA: master's degrees 31%, *n* = 148/483, doctoral degrees 2%, *n* = 39/483). The two populations also differed in their primary role, indicating variation in the number of nurses involved in research (NCEMNA, 6%, *n* = 20/330; ANA, 4%, *n* = 16/427) and administration (NCEMNA, 19%, *n* = 63/330; ANA, 9%, *n* = 38/427). Most nurses indicated that their primary role was patient care (NCEMNA, 42%, *n* = 139/330; ANA, 54%, *n* = 231/427).

A correlation was found between higher academic education and years in nursing, which increased family history collection in practice. Seventy-two percent (*n* = 274/380) reported collecting family histories for patients in their practice setting. This result is higher than that reported in other nursing populations. The National Nursing Workforce Study conducted through the ANA found that nurses who indicated they actively saw patients (60%, *n* = 216/359) had rarely or never assessed a family history in the preceding 3 months (Calzone et al., 2013). Additional study is needed to ascertain the basis for these differences, which could be associated differences in the question asked between these two surveys, with the ANA asking about family history utilization in the past 3 months, whereas the NCEMNA survey asked about use of family history at any time in practice. The perceived value of family history may also contribute to this difference, or the difference may be the direct result of family history education initiatives undertaken by some NCEMNA member associations, but data on these specific details were not assessed in this study.

Three hundred and five study participants stated that they belonged to one (299/305) or more than one (6/305) NCEMNA member organization. Two identified themselves as American Indian/Alaska Native, even though NANAINA members did not participate in this study. So either those participants were a member of another organization or answered independently. There were also 39 who reported their race or ethnicity as other and their write-in answers indicated mixed race responses. Those who specified their race or ethnicity as White may have been of mixed race or felt this choice best reflected their race or ethnicity.

Health disparities in chronic diseases such as cancer (Wallace, Martin, & Ambs, 2011), cardiovascular disease (Cambien & Tiret, 2007; Kathiresan & Srivastava, 2012), and diabetes are mediated by complex gene interactions (Tekola-Ayele, Adeyemo, & Rotimi, 2013; Zorka et al., 2013), which are changing the management of chronic disease in vulnerable populations. In the 10 years since the Human Genome Project was completed, rapid changes in genetic technology have resulted in substantial changes in the care of

patients with these and other chronic diseases, which disproportionally affected racial and ethnic minority groups (Goldenberg et al., 2013; Wallace et al., 2011). This rapid infusion of genetic-genomic knowledge and changes in clinical practice present both a burden and opportunity for multi-ethnic minority nurses.

Nurses remain trusted healthcare providers (Gallop Poll, 2012). The nurse–patient professional relationship is foundationally supported by perceived professional competencies and caring attributes that underpin this trust (Dinc & Gastmans, 2012). Health disparities have prevailed in minority populations despite policy initiatives and new knowledge in genetics and genomics (Agency for Healthcare Research and Quality, 2012). Establishing a culturally competent nursing workforce is suggested as a key component to improving communication and the patient-centered trust relationship with minority populations (Viseanath & Ackerson, 2011). Within these populations, culture, race, and perceived discrimination can negatively affect the interpretation of communication delivered by healthcare providers (Subban, Terwoord, & Schuster, 2008). An important component to establishing a trust relationship is the healthcare provider using culturally competent communications with minority populations that support patient engagement of the value of genetic and genomic information in their health care. Radwin, Cabral, and Woodworth (2013) conducted a study using path analysis in a multi-ethnic sample of in-patient cancer patients. The investigators sought to determine what contributed to the development of trust in the population of African Americans, Caucasian Americans, Hispanics, Native Hawaiians or Pacific Islanders, and American Indians or Alaska Natives. Data were collapsed into two ethnic groups—Caucasians and all other ethnic groups combined. For the multiminority groups only, responsiveness and proficiency were positively related to greater trust in nurses.

The multi-ethnic minority nurse sample in this study reported gaps in genetic and genomic knowledge. These gaps are similar to findings from a study conducted using a sample collected through the ANA, and both studies demonstrate that education is required in basic genetic and genomic core concepts (Calzone et al., 2013). The majority of the current sample (65%) had not received continuing education with a focus on genetics and genomics. Respondents in this study were interested, open, and motivated to engage in education that would support proficiency in genetics and genomics. These findings support the need for further genetics-genomics education in this multi-ethnic study population, consistent with similar findings in an African American nurse sample (Powell-Young & Spruill, 2013) that clearly demonstrated the need for a focused education in both the formal and continuing education areas. Patients expect that care providers approach them knowledgeable about their conditions, sensitive about their culture, and aware of their sometimes intergenerational experiences of unequal and sometimes discriminatory care that may predicate perceptions of mistrust (Benkert, Peters, Pate, & Dinardo, 2007). This is the first study investigating multi-ethnic minority nurses' knowledge of genetics and genomics. Designing education for this population of nurses who are requisite in the knowledge and culture of caring for minority populations is a first and crucial step to preparing nurses that may well influence health disparity outcomes.

Limitations

Ascertainment bias is recognized as a limitation of this study. Nurses were recruited through the minority nursing organizations that are members of NCEMNA. Therefore, nurses self-identifying as minority nurses that are members or follow activities of these organizations would have been notified of the study. Furthermore, participants may have had some motivation to complete the survey, which could include concern about genomics or other influencing factors. As such, the findings cannot be generalized to the overall minority nurse community. However, this is the first study of its kind despite this limitation, so the insights gleaned from the data can still be useful in planning targeted education for this diverse constituency.

Notably, the study population consisted of a highly educated group of nurses, with 39% holding a master's degree and 16% a doctoral degree. These education levels differ drastically from the national nursing workforce. Overall, 13% of nurses of any race hold a master's or doctoral degree. By race and ethnic categories, 13% of Caucasian/Non-Hispanics, 15% of Black/African American/Non-Hispanics, 11% of Hispanic/Latino/any race, and 8% of Asian/Non-Hispanics hold a master's or doctoral degree (U.S. Department of Health and Human Services, Health Resources and Services Administration, 2010). Additional study is clearly needed in a more representative minority nurse population. Overall, the data indicate that study participants had a strong interest in gaining knowledge and or refining knowledge about genetics and genomics. This information more broadly informs the NCEMNA Board and member organizations on the need, scope, and optimal design of a collaborative NCEMNA member organizations education initiative in genetics-genomics.

Lastly, participants were informed that they could skip any survey item. As such, the per-question response rate varied. To assess this further, the dataset was queried to ascertain whether there was a pattern to the per-question response rate. Overall, the lowest response rates were associated with Sections 6 and 7 located at the end of the survey. Section 6 correlates with the knowledge, use, and beliefs about race and genetic variation items (Bonham and Sellers' GKAI, Bonham and Sellers' HPBR scale, and Bonham and Sellers' RACE scale). Of these three instruments in Section 6, the GKAI had the lowest response rates. Section 7 consisted of the demographic questions. Overall, this analysis revealed that participants seemed to respond less as the survey progressed, with over 13% of responders answering no question, as opposed to earlier sections, where this rate was 6% to 7%. Additional psychometrics on the instrument are needed to inform refinement of the tool, including reduction in the number of items.

Conclusions

This study was designed to determine minority nurses' beliefs, practices, and competency of integrating into practice genomics information related to common multi-factorial diseases. This goal was supported by the leadership of NCEMNA and provided the opportunity to assess minority nurses' knowledge of human genetic variation and the use of patient characteristics, including ethnicity, gender, genes, and race in diagnostics, treatment, and

referral. This study population had different ethnicity or race characteristics, more nurses with advanced degrees, and higher proportions reporting primary functional areas such as research or administrative than previous studies. However, genomic knowledge deficits in the nursing workforce revealed in this study were similar to that found in other nurses previously reported. Therefore, the recommendation is that genomics education is needed by all nurses. Only then can we assure in this genomic era of health care that nurses as integral members of the workforce are prepared to deliver responsible, effective, and accountable care that includes genomics.

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Clinical Resources

- Essentials of Genetic and Genomic Nursing: Competencies, Curricula Guidelines, and Outcome Indicators (2nd ed.): http://www.genome.gov/pages/careers/healthprofessionaleducation/geneticscompetency.pdf
- Genetics and Genomics Competency Center for Education: http://www.g-2-c-2.org/
- Greco, K., Tinley, S., & Seibert, D. (2012). Essential Genetic and Genomic Competencies for Nurses with Graduate Degrees. American Nurses Association and International Society of Nurses in Genetics: http://www.genome.gov/Pages/Health/Health-CareProvidersInfo/GradGenComp.pdf
- U.S. Surgeon General's My Family Health Portrait: https://familyhistory.hhs.gov/fhh-web/home.action

Table 1

Demographic Characteristics of Study Participants

Demographics (*N* = 389)	***n* (%)**
Sex (*n* = 326)	
Male	22 (7%)
Female	304 (93%)
Age (*n* = 261)	
Mean (range)	52 (23–82)
Race (*n* = 322)	
White	27 (8%)
Asian	138 (43%)
Black/African American	107 (33%)
American Indian/Alaska Native	2 (1%)
Native Hawaiian/Pacific Islander	9 (3%)
Other	39 (12%)
Hispanic/Latino (*n* = 329)	60 (18%)
Highest level of nursing education (*n* = 331)	
Diploma	5 (2%)
Associate degree	28 (8%)
Baccalaureate degree	115 (35%)
Master's degree	130 (39%)
Doctoral degree	53 (16%)
Primary role (*n* = 330)	
Administration	63 (19%)
Education	71 (22%)
Research	20 (6%)
Patient care	139 (42%)
Other	37 (11%)
Percent of time spent seeing patients (*n* = 311)	
Mean	51%
Range	0–100%
NCEMNA organization affiliation (*n* = 305)	
Asian American/Pacific Islander Nurses Association	37 (12%)
National Association of Hispanic Nurses	53 (17%)
National Black Nurses Association	109 (36%)
Philippine Nurses Association of America	112 (37%)

Table 2

Knowledge Measures

Measure	*n* (%)
Understanding of genetics of common diseases (*n* = 364)	
Excellent	6 (2%)
Very good	47 (13%)
Good	129 (35%)
Fair	149 (41%)
Poor	33 (9%)
Do you think that genetic risk (e.g., as indicated by family health history) has clinical relevance for breast cancer? (*n* = 378)	
Correct	378 (100%)
Incorrect	0 (0%)
Do you think that genetic risk (e.g., as indicated by family health history) has clinical relevance for colon cancer? (*n* = 375)	
Correct	366 (98%)
Incorrect	9 (2%)
Do you think that genetic risk (e.g., as indicated by family health history) has clinical relevance for coronary heart disease? (*n* = 372)	
Correct	333 (98%)
Incorrect	9 (2%)
Do you think that genetic risk (e.g., as indicated by family health history) has clinical relevance for diabetes? (*n* = 376)	
Correct	372 (99%)
Incorrect	4 (1%)
Do you think that genetic risk (e.g., as indicated by family health history) has clinical relevance for ovarian cancer? (*n* = 369)	
Correct	354 (96%)
Incorrect	15 (4%)
The DNA sequences of two randomly selected healthy individuals of the same sex are 90%–95% identical. (*n* = 208)	
Correct	82 (39%)
Incorrect	126 (61%)
Most common diseases such as diabetes and heart disease are caused by a single gene variant. (*n* = 193)	
Correct	88 (46%)
Incorrect	105 (54%)
Genetics course since licensure (*n* = 356)	
Yes	123 (35%)
No	233 (65%)