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Evaluation of family health history collection methods impact on data and risk assessment outcomes

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ABSTRACT

Information technology applications for patient-collection of family health history (FHH) increase identification of elevated-risk individuals compared to usual care. It is unknown if the method of collection impacts data collected or if simply going directly to the patient is what makes the difference. The objective of this study was to examine differences in data detail and risk identification rates between FHH collection directly from individuals using paper-based forms and an interactive web-based platform. This is a non-randomized epidemiologic study in Singaporean population from 2016 to 2018. Intervention was paper-based versus web-based interactive platform for FHH collection. Participant demographics, FHH detail, and risk assessment results were analyzed. 882 participants enrolled in the study, 481 in the paper-based group and 401 in the web-based group with mean (SD) age of 45.4 (12.98) years and 47.5% male. Web-based FHH collection participants had an increased number of conditions per relative (p-value < 0.001), greater frequency of reporting age of onset (p-value < 0.001), and greater odds of receiving ≥ 1 risk recommendation both overall (OR: 3.99 (2.41, 6.59)) and within subcategories of genetic counselling for hereditary cancer syndromes (p-value $= 0.041$) and screening and prevention for breast (p-value $= 0.002$) and colon cancer (p-value $= 0.005$). This has significant implications for clinical care and research efforts where FHH is being assessed. Using interactive information technology platforms to collect FHH can improve the completeness of the data collected and result in increased rates of risk identification. Methods of data collection to maximize benefit should be taken into account in future studies and clinical care.

1. Introduction

Family health history (FHH) is a key component of risk assessment for many conditions across multiple guidelines (Watts et al., 2014; Evans et al., 2013; NCCN Guidelines, 2017). FHH is frequently a significant component or the sole indicator for additional screening or testing. This is especially true with identifying individuals in need of genomic services (Cohn et al., 2010; Welch et al., 2018; Orlando et al., 2014). Recognition of the value of FHH collection and use is apparent from the widespread public messaging campaigns from governments, advocacy groups, and professional societies (Welch et al., 2015; Committee Opinion No., 2011; Australia Familial Risk, 2018; Department of Health and Human Services, 2019).

The recent growth of information technology (IT) applications in healthcare has resulted in the creation of multiple web-based FHH applications (Welch et al., 2018). These tools are typically patient-facing and collect FHH in an assortment of ways with varying levels of interactivity. Such platforms have been shown to increase identification

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of elevated-risk individuals as compared to routine clinical care methods and also to impact patient and provider behavior (Cohn et al., 2010; Orlando et al., 2014; Orlando et al., 2016; Hulse et al., 2011; Rubinstein et al., 2011).

The detail of FHH collected with such applications has been shown to be better than what is collected in routine practice (Cohn et al., 2010; Hulse et al., 2011; Rubinstein et al., 2011; Wu et al., 2014; Qureshi et al., 2012). Routine practice typically involves a very basic check box worksheet that patients complete in their provider's waiting room and/or a brief conversation between the provider and the patient about what their FHH risks might be. What has not been explored is if greater FHH detail with IT applications is due simply to having a patient-facing collection method, which could be achieved with either comprehensive pen and paper forms or electronically, or does the way data is captured through IT interfaces, where answers to one question guides the platform in what information to query next, affect FHH detail differently than pen and paper forms? Do IT applications simply offer the same FHH data but in electronic format or do their designs allow for more robust data capture?

The Singapore Health Services (SingHealth) and its academic affiliate Duke-National University of Singapore (Duke-NUS) Medical School established the SingHealth Duke-NUS Institute of Precision Medicine (PRISM) in 2016 (SingHealth Duke-NUS Institute, 2018). The first major project of PRISM was to analyze data derived from SPECTRA, a biorepository of multi-dimensional data from healthy Singaporeans incorporating genomic, clinical, lifestyle, and imaging data (Bylstra et al., 2019). In its initial phase, FHH was collected using a detailed paper and pen worksheet (i.e. "paper-based") (Fig. S1). The worksheet included spaces for the participant to provide FHH information on at least three generations of relatives and in more detail than is traditionally collected in routine care. The project subsequently transitioned to using MeTree, a web-based patient-facing FHH risk assessment platform with guideline-driven clinical decision support (CDS) (i.e. web-based) (Orlando et al., 2013). MeTree provides recommendations on genetic counselling and screening/surveillance based on most commonly used U.S. guidelines in primary care. In addition to building education, the web-based platform was interactive in nature, prompting participants to enter additional detail about a reported condition and reminding them if they left a critical field blank (ex: age of onset for a condition). The objective of this paper is to examine differences between paper-based and web-based FHH capture in 1) level of detail of FHH data and 2) rate of elevated-risk identification.

2. Methods

SPECTRA is a longitudinal epidemiologic study designed to establish a South East Asian healthy cohort biorepository (Bylstra et al., 2019). Participants were enrolled on a rolling basis starting in 2016 with over 2000 participants enrolled through June 2018 when data collection was stopped for purpose of this analysis. The study was approved by IRB of Duke University and SingHealth.

2.1. Study population

Participants were recruited from the general population of Singapore through an advertisement placed in the national newspaper, The Straits Times. Inclusion criteria were: aged 16–90 years old (16 years old is age of adulthood in Singapore), no significant medical conditions, on no medications other than ≤ 1 anti-hypertensive, asthma control, oral contraceptive, or over-the-counter medication, have no FHH of hypertrophic cardiomyopathy or dilated cardiomyopathy (an exclusion based on primary outcomes of the parent study), and have no family members already enrolled in the study. Thus each pedigree presented in the analysis should be considered independent as it represents a unique family and the number of participants is equal to the number of pedigrees.

2.2. Study design

Individuals called the clinical research coordinator (CRC) who explained the study and scheduled an initial study visit, if they met inclusion criteria. They were informed that FHH would be collected at that study visit and they were encouraged to gather the necessary information beforehand. At the study visit, after informed consent, participants filled out a series of lifestyle and FHH questionnaires. Participants enrolling from September 2016 to July 2017 reported FHH using the paper-based FHH questionnaire (i.e. paper-based group). Participants enrolling from July 2017 to June 2018, when data for this analysis was closed, used MeTree, a patient-facing web-based FHH risk assessment platform with integrated patient education and clinical decision support (i.e. web-based group) (Orlando et al., 2013). Analysis was done in 2018. A CRC was present throughout the study visit to answer any questions participants had and to help them with the MeTree software as needed. Participants were given as much time as needed to complete the FHH questionnaire or software program. It was anticipated to take about 30 min to complete based on prior studies (Wu et al., 2013). For the paper-based group, FHH data was later entered into MeTree by a CRC to facilitate data analysis. The CRC used only information provided by the participant on the paper-based questionnaire. They did not have contact with the participant at the time of electronic data entry. There was no difference in recruitment strategies or inclusion/exclusion criteria between the paper-based and web-based groups.

2.3. Measures

Measures reported in this paper were collected from questionnaires and MeTree. Participant demographic categories evaluated included age, sex, and race (Chinese, Malay, Indian, Asian other, Other). Data collected from MeTree included personal and FHH on 128 medical conditions for at least 3 generations of relatives (Fig. S1).

2.4. Outcomes

The first outcome of interest was variations in amount of FHH detail provided between the groups, as defined by: 1) number of relatives per pedigree entered overall, and by 1st degree (i.e. parents, siblings, and children) and 2nd degree or higher (i.e. all relatives other than parents, siblings and children), 2) frequency of conditions entered, 3) number of medical conditions entered per relative overall and by 1st degree, and 2nd or higher degree relatives, 4) percent of relatives with cancer per pedigree, and 5) percent of relatives' conditions where age of onset was reported. The second outcome of interest was variations in likelihood of receiving an elevated-risk recommendation by the MeTree software based on FHH entered using paper-based entry versus web-based entry.

2.5. Statistical analysis

We summarized categorical and continuous data as frequency (percentage) and mean (95% CI) respectively, based on web-based and paper-based groups. We compare the differences between these two groups using Fisher's exact test and two sample Student's *t*-test for categorical and continuous data respectively. To compare proportion of relatives with condition's age of onset reported per pedigree, two sample independent *t*-test was used. Proportion of relatives with reported age of onset was first calculated for each participant and then mean proportion of relatives with 95%CI was calculated. Later mean for both groups was compared using two sample independent *t*-test. We fit univariate logistic regression models to find associated predictors of different recommendations when using the web-based approach. We also fit univariate and multivariable models to find associated predictors for receiving at least one recommendation. We expressed associated risks from the logistic regression model as odds ratios with

Table 1
Demographics of paper-based and web-based groups in Singapore (2016–2018).

Characteristics	Paper-based (N = 481)	Web-based (N = 394)	P – value
Age (years), Mean (95% CI)	45.5 (44.3–46.7)	45.2 (43.9–46.4)	0.7209
Male gender, n (%)	220 (45.7)	195 (49.5)	0.2769
Race, n(%)			0.0842
Asian Chinese	437 (90.9)	346 (87.8)	
Asian Indian	14 (2.9)	24 (6.1)	
Asian Malay	17 (3.5)	9 (2.3)	
Asian Others	11 (2.3)	14 (3.6)	
Others	2 (0.4)	1 (0.3)	

Note: p – values are based on Fisher's exact and two sample *t*-test for categorical and continuous data respectively.

corresponding 95% CI. All the variables with p-value < 0.2 were included in the multivariable model. Then we used stepwise variable selection method to find the multivariable model with entry and exit threshold of p-value as 0.2 and 0.05. We have also reported area under the curve (AUC) of receiver operating curve (ROC) based on the final multivariable model. Statistical significance was set at p – value < 0.05. All the statistical tests used in this study were two sided. All the analyses were performed using SAS Institute Inc 2013. SAS/ACCESS® 9.4. Cary, NC: SAS Institute Inc.

3. Results

3.1. Demographics

Eight hundred eighty-two participants enrolled in the study. Seven participants were excluded from the study (2 failed inclusion criteria, 1 was adopted, and 4 declined to provide FHH). The paper-based group has 481 participants and the web-based group had 394. There was no significant difference in sex, age and race between the two groups (Table 1).

3.2. Family health history detail

There was no significant difference between the groups in how many relatives were recorded per pedigree or how many were recorded when broken down by 1st degree and 2nd or higher degree (Table 2). Significantly higher number of conditions per relative were entered in the web-based group compared to the paper-based group. The same trend was also observed in 1st degree relatives, and 2nd or higher degree relatives. The web-based group also reported a greater mean number of relatives with cancer than the paper-based group. There was a higher mean number of relatives with age of onset for their conditions reported in the web-based group than the paper-based group with a mean of 88% of relatives with a reported condition having age of onset reported as compared to a mean of 50% for the paper-based group.

3.3. Risk recommendations

Frequency of risk recommendations were significantly different between the two groups (Table 3). The web-based group had almost 4 times higher odds of receiving at least one recommendation. Web-based group was also more likely to have at least two recommendations. However, this comparison was not significant (p-value = 0.0987). The web-based group had significantly higher odds of receiving recommendations specifically for: a) cancer genetic counselling (p-value = 0.0409), b) breast MRI and/or chemoprophylaxis due to breast cancer risk (p-value = 0.0020), and c) earlier and/or more frequent colonoscopies (p-value = 0.0045). The multivariable logistic regression model suggested receiving at least one risk recommendation was significantly more likely for: older participants (adjusted (adj) OR (95%CI): 1.05 (1.03, 1.08, p-value < 0.0001)), the web-based group (adjOR (95%CI): 2.93 (1.63, 5.28), p-value = 0.0003), those with a higher percentage of cancer per pedigree (adjOR (95%CI): 1.08 (1.05, 1.12), p-value < 0.0001) and percentage of age of onset provided per pedigree (adj OR (95%CI): 1.14 (1.04, 1.25), p-value = 0.0043). AUC of this model was 0.801. No adverse events occurred in the study.

4. Discussion

We have shown here that using an interactive patient-facing web-based IT platform to collect FHH leads to more complete and detailed FHH information and significantly greater odds of receiving an increased risk recommendation than having individuals report FHH using static paper-based forms. There are several mechanisms within web-based risk assessment tools which may contribute to greater data detail and thus more risk identification. Links to educational resources are possible with web-based applications that would be more difficult with a static paper-based formation, thus allowing participants to confirm that they are selecting the correct diagnosis for their relative (ex: cirrhosis versus psoriasis). Having an interactive tool can prompt participants to enter data by leading them through a series of questions based on prior responses. For example, if they enter a FHH of breast cancer, the application can then prompt questions regarding unilateral or bilateral, applicable genetic markers, and age of onset. Such interactivity is not possible with a paper-based form thus limiting the level of detail that can be collected. An interactive web application can also draw participants' attention to data they forgot to enter and not allow them to proceed without reporting something in the field (e.g., age of

Table 2
Family health history data characteristics in Singapore (2016–2018).

FHH characteristics	Paper-based (N = 481)	Web-based (N = 394)	P – values*
Relatives per pedigree, Mean (95% CI)			
All relatives	015.1 (14.6–15.7)	15.9 (15.2–16.6)	0.1004
1st degree relatives	005.9 (5.6–6.1)	5.8 (5.6–6.1)	0.8155
2nd and higher degree relatives	009.3 (8.8–9.8)	10.1 (9.4–10.7)	0.0538
	Paper-based[a] (N = 1571)	Web-based[a] (N = 1735)	P – values*
Conditions per relative, Mean (95% CI)			
All relatives	1.26 (1.23–1.29)	1.87 (1.82–1.92)	< 0.0001
1st degree relatives[†]	1.32 (1.28–1.36)[a]	1.99 (1.91–2.07)[a]	< 0.0001
2nd and higher degree relatives[†]	1.18 (1.14–1.22)[a]	1.76 (1.68–1.83)[a]	< 0.0001
Relatives with cancer per pedigree, Mean (95% CI)	0.81 (0.71–0.92)	1.07 (0.93–1.21)	0.0037
Mean number of relatives with condition's age of onset reported per pedigree, Mean (95% CI)	0.50 (0.47–0.54)	0.88 (0.85–0.90)	< 0.0001

Note: p –values were based on two sample student's t – test. [a]Total number of paper-based and web-based relatives were 1571 and 1735 respectively.
[†] Total number of paper-based and web-based 1st degree relatives was 889 and 863 respectively; total number paper-based and web-based 2nd and higher degree relatives was 682 and 872 respectively.

Table 3
Risk Recommendations in paper-based and web-based groups in Singapore (2016–2018).

Risk Recommendations	Paper-Based N = 481 (%)	Web-Based N = 394 (%)	Odds Ratio* (95% CI)	p – Value
≥1 Recommendations	22 (4.57)	64 (16.24)	3.99 (2.41–6.59)	< 0.0001
≥2 Recommendations	3 (0.62)	8 (2.03)	3.01 (0.81–11.12)	0.0987
Genetic counselling				
Cancer	3 (0.62)	10 (2.54)	3.73 (1.06–13.19)	0.0409
Cardiovascular	0 (0.0)	2 (0.51)	6.15 (0.15–254.75)	0.3392
Surveillance				
Breast MRI/Chemoprophylaxis	7 (1.46)	22 (5.58)	3.82 (1.63–8.95)	0.0020
CRC Screening Early Or More Frequent	16 (3.33)	31 (7.87)	2.45 (1.32–4.53)	0.0045

Note: Variables were summarized as frequency (percentage). Univariate logistic regression is fit to find association between risk recommendations (yes/no) and group type (web based/paper based participants)."

onset). Age of onset is a particularly critical data element in FHH as many risk-based recommendations are dependent on the age of disease onset in the affected relative. These built-in features of web applications allow for greater detail in data capture and result in more complete risk predictions.

These results have significance both for clinical care and research studies where FHH is of interest. Prior work in the United States has shown that such platforms are reported by patients to be easy to use and helpful in understanding their risks and by providers to improve the quality of care they are able to provide without disruption to workflow (Cohn et al., 2010; Wu et al., 2013; Wu et al., 2018). Findings from prior studies demonstrate that the potential value of such platforms is not limited to an Asian context but has shown benefit across a diversity of populations. There is some indication that these tools may be more difficult for elderly and those with less education to complete and these are areas that need to continue to be evaluated and improved on (Wu et al., 2019).

4.1. Limitations

There are limitations to this study. Participants were not randomized to the two arms but were enrolled sequentially (i.e. paper-based group first and then web-based group). While randomization would have been ideal, analysis of FHH collection methods was not a predefined outcome of the parent study. There is no reason to expect that the two groups would be inherently different. They were recruited in the same way and all other aspects of their recruitment, enrollment, and completion of the study were the same. Analysis shows that demographics did not vary between the groups except for slight discrepancy in racial group breakdown (90.9% Asian Chinese in paper-based versus 87.5% in web-based group). An additional limitation is that participants were not provided any education on FHH in advance so that they would know what information they needed to provide. Education on FHH and the key data elements has been shown to improve the level of detail of FHH collected and has an impact on risk identification (Beadles et al., 2014). But the lack of FHH education was consistent across both groups and should not limit the ability to compare the groups to each other. While we have demonstrated that using a web-based platform, increasing the amount of detail provided in FHH collection, we cannot make any conclusions regarding whether the information provided is more accurate than that collected in a paper-based format.

5. Conclusion

From a clinical perspective, as more medical records systems are becoming electronic, this should translate into how we collect information from patients as well. Interactive platforms hold the potential to improve the quality of the data we collect by leading patients through a series of questions in a way that is responsive and reactive to what information the patient has already provided. Electronic FHH capture could potentially help minimize redundancy in medical questionnaires, provide shareable electronic formats between patients, their family members, and multiple providers, and as shown here potentially produce more comprehensive data with potentially greater accuracy in risk identification.

In the research arena, in addition to the benefits outlined above of improved quality, using such IT platforms to capture FHH will allow data to be stored as discrete data elements and more easily deposited in data repositories. The linking of FHH data and genomic data is critically important for the greater understanding of how both contribute to population health risks (Antoniou et al., 2014; Begg, 2002).

Further work should be done to understand how populations of varying racial make-up, socio-demographics, and literacy and numeracy abilities interact with and understand FHH and the use of patient-facing platforms to capture this data. There are additional ways that these platforms can be improved upon to further maximize quality of the data and utility for clinical care, population health, and scientific discovery.

Name (date) of IRB approval: Duke University IRB (3/21/2017); SingHealth IRB (11/15/2016)

6. Trial registration

This study is registered at www.clinicaltrials.gov (NCT00672828).

CRediT authorship contribution statement

R. Ryanne Wu: Conceptualization, Methodology, Software, Writing - original draft, Funding acquisition. **Rehena Sultana:** Formal analysis, Data curation, Writing - review & editing. **Yasmin Bylstra:** Methodology, Investigation, Writing - review & editing. **Saumya Jamuar:** Writing - review & editing, Supervision. **Sonia Davila:** Resources, Writing - review & editing, Supervision, Project administration, Funding acquisition. **Weng Khong Lim:** Validation, Data curation, Writing - review & editing, Project administration. **Geoffrey S. Ginsburg:** Resources, Writing - review & editing, Supervision, Funding acquisition. **Lori A. Orlando:** Conceptualization, Methodology, Software, Writing - review & editing, Visualization, Supervision, Funding acquisition. **Khung Keong Yeo:** Writing - review & editing, Supervision, Project administration. **Stuart A. Cook:** Writing - review & editing, Supervision, Project administration, Funding acquisition. **Patrick Tan:** Conceptualization, Resources, Writing - review & editing, Supervision, Funding acquisition.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.pmedr.2020.101072.

References

Antoniou, A.C., Casadei, S., Heikkinen, T., et al., 2014. Breast-cancer risk in families with mutations in PALB2. N. Engl. J. Med. 371 (6), 497–506.

Australia Familial Risk Assessment – Breast and Ovarian Cancer. https://canceraustralia.gov.au/clinical-best-practice/gynaecological-cancers/fra-boc/evaluate, 2018.

Beadles, C.A., Ryanne, Wu.R., Himmel, T., et al., 2014. Providing patient education: impact on quantity and quality of family health history collection. Fam. Cancer 13 (2), 325–332.

Begg, C.B., 2002. On the use of familial aggregation in population-based case probands for calculating penetrance. J. Natl. Cancer Inst. 94 (16), 1221–1226.

Bylstra, Y., Davila, S., Lim, W.K., et al., 2019. Implementation of genomics in medical practice to deliver precision medicine for an Asian population. NPJ Genomic Med. 4 (1), 12.

Cohn, W.F., Ropka, M.E., Pelletier, S.L., et al., 2010. Health Heritage(c) a web-based tool for the collection and assessment of family health history: initial user experience and analytic validity. Public Health Genomics 13 (7–8), 477–491.

Committee Opinion No. 478: family history as a risk assessment tool. Obstet. Gynecol. 2011 117(3),747–750.

Department of Health and Human Services (US) Surgeon General's Family Health History Initiative. http://www.hhs.gov/familyhistory (accessed October 24, 2019).

Evans, D.G., Graham, J., O'Connell, S., Arnold, S., Fitzsimmons, D., 2013. Familial breast cancer: summary of updated NICE guidance. Br. Med. J. 346.

Hulse, N.C., Ranade-Kharkar, P., Post, H., Wood, G.M., Williams, M.S., Haug, P.J., 2011. Development and early usage patterns of a consumer-facing family health history tool. In: AMIA Annual Symposium proceedings AMIA Symposium, pp. 578–587.

NCCN Guidelines: Genetic/Familial High-Risk Assessment: Colorectal. 2017; Version 3. 2017: https://www.nccn.org/professionals/physician_gls/pdf/genetics_colon.pdf (accessed 11 July 2018), 2018.

Orlando, L.A., Buchanan, A.H., Hahn, S.E., et al., 2013. Development and validation of a primary care-based family health history and decision support program (MeTree). N. C. Med. J. 74 (4), 287–296.

Orlando, L.A., Wu, R.R., Beadles, C., et al., 2014. Implementing family health history risk stratification in primary care: impact of guideline criteria on populations and resource demand. Am. J. Med. Genet. C: Semin. Med. Genet. 166C (1), 24–33.

Orlando, L.A., Wu, R.R., Myers, R.A., et al., 2016. Clinical utility of a Web-enabled risk-assessment and clinical decision support program. Genet. Med. 18 (10), 1020–1028.

Qureshi, N., Armstrong, S., Dhiman, P., et al., 2012. Effect of adding systematic family history enquiry to cardiovascular disease risk assessment in primary care: a matched-pair, cluster randomized trial. Ann. Intern. Med. 156 (4), 253–262.

Rubinstein, W.S., Acheson, L.S., O'Neill, S.M., et al., 2011. Clinical utility of family history for cancer screening and referral in primary care: a report from the Family Healthware Impact Trial. Genet. Med. 13 (11), 956–965.

SingHealth Duke-NUS Institute of Precision Medicine. https://research.singhealth.com.sg/Pages/PRISM-Overview.aspx (accessed October 29, 2018).

Watts, G.F., Gidding, S., Wierzbicki, A.S., et al., 2014. Integrated guidance on the care of familial hypercholesterolaemia from the International FH Foundation. Int. J. Cardiol. 171 (3), 309–325.

Welch, B.M., O'Connell, N., Schiffman, J.D., 2015. 10 years later: assessing the impact of public health efforts on the collection of family health history. Am. J. Med. Genet. Part A 167 (9), 2026–2033.

Welch, B.M., Wiley, K., Pflieger, L., et al., 2018. Review and comparison of electronic patient-facing family health history tools. J. Genet. Counsel.

Wu, R.R., Orlando, L.A., Himmel, T.L., et al., 2013. Patient and primary care provider experience using a family health history collection, risk stratification, and clinical decision support tool: a type 2 hybrid controlled implementation-effectiveness trial. BMC Fam. Pract. 14, 111.

Wu, R.R., Himmel, T.L., Buchanan, A.H., et al., 2014. Quality of family history collection with use of a patient facing family history assessment tool. BMC Fam. Pract. 15, 31.

Wu, R.R., Myers, R.A., Sperber, N., et al., 2018. Implementation, adoption, and utility of family health history risk assessment in diverse care settings: evaluating implementation processes and impact with an implementation framework. Genet. Med.

Wu, R.R., Myers, R.A., Buchanan, A.H., et al., 2019. Effect of sociodemographic factors on uptake of a patient-facing information technology family health history risk assessment platform. Appl. Clin. Inform. 10 (2), 180–188.