2022

Validation of the Knowledge of Genome Sequencing (KOGS) scale in cancer patients

P Butow

C Napier

R Campbell

N Bartley

Megan Best

See next page for additional authors

This article was originally published as:
Butow, P., Napier, C., Campbell, R., Bartley, N., Best, M., & Ballinger, M. L. (2022). Validation of the Knowledge of Genome Sequencing (KOGS) scale in cancer patients. *Patient Education and Counseling, Early View (Online First)*.

Original article available here:
10.1016/j.pec.2022.06.009

Authors
P Butow, C Napier, R Campbell, N Bartley, Megan Best, and M L. Ballinger

This is the accepted manuscript version of an article published as:

Butow, P., Napier, C., Campbell, R., Bartley, N., Best, M., & Ballinger, M.L. (2022). Validation of the Knowledge of Genome Sequencing (KOGS) scale in cancer patients. *Patient Education and Counseling*, *Early View (Online First)*, https://doi.org/10.1016/j.pec.2022.06.009

This article has been published in its final form at:

https://doi.org/10.1016/j.pec.2022.06.009

Patient Education and Counseling xxx (xxxx) xxx

Contents lists available at ScienceDirect

Patient Education and Counseling

journal homepage: www.journals.elsevier.com/patient-education-and-counseling

Validation of the Knowledge of Genome Sequencing (KOGS) scale in cancer patients

P. Butow [a,*], C. Napier [b], R. Campbell [c], N. Bartley [a], M. Best [a,d], ML Ballinger [b,e]

[a] The University of Sydney, School of Psychology, Psycho-Oncology Co-operative Research Group (PoCoG), Sydney, Australia
[b] Cancer Theme, Garvan Institute of Medical Research, Darlinghurst, Australia
[c] The University of Sydney, School of Psychology, Centre for Medical Psychology and Evidence-based Medicine (CeMPED), Australia
[d] The University of Notre Dame Australia, Institute for Ethics and Society, Sydney, Australia
[e] University of NSW, St Vincent's Clinical School, Sydney, Australia

ARTICLE INFO

Keywords:
Patient reported outcome
Genome sequencing
Psychometric evaluation
Cancer, patients

ABSTRACT

Introduction: The Knowledge of Genome Sequencing (KOGS) questionnaire was recently developed to measure knowledge of genomic sequencing (GS), with preliminary psychometric data supporting its reliability and validity. The aim of this study was to test the reliability and validity of the KOGS in a larger sample, and to confirm its utility in a cancer setting.

Methods: The Genetic Cancer Risk in the Young (RisC) study recruits participants with a personal history of cancer, to investigate heritable cancer causes and future cancer risk using germline GS. Participants (n = 261) in a psychosocial substudy of RisC completed a questionnaire after consent to RisC but before GS, including the KOGS, the Intolerance of Uncertainty Scale, the Chew health literacy scale and items assessing demographic and disease variables. Confirmatory factor analysis (CFA), Cronbach alpha and correlational analyses were undertaken.

Results: The CFA testing a single-factor model yielded a good model fit, $\chi 2/df = 2.43$, comparative fit index (CFI) = 0.97, root mean square error of approximation (RMSEA) = 0.07 and weighted mean root square (WRMR) = 1.03. Factor loadings of all items were above 0.60 and ranged between.66 and.93. The single factor score demonstrated excellent internal consistency ($\alpha = 0.82$). KOGS scores were significantly associated with health literacy ($r = 0.23$, $p < .001$), having a university education [$t(258) = -4.53$, $p < .001$] and having a medical or science background [$t(259) = -3.52$, $p < .001$] but not with speaking a language other than English at home, time since diagnosis, previous genetic counselling/testing or intolerance of uncertainty.

Discussion: This study confirmed a single-factor structure for the KOGS, and its reliability and validity in a cancer population. Associations with measures of health literacy and education were significant and positive as expected, supporting the KOG's construct validity. Previous genetic counselling may not be sufficient to provide specific knowledge of GS.

1. Introduction

Germline genome sequencing (GS), **which identifies in the germline (individual genomic code inherited from the parental egg and sperm cells that sexually reproducing organisms use to pass on their genomes from one generation to the next) any disease-related variants that can be passed from parents to child,** is increasingly being used to identify risk of disease, with the goal of improving prevention [1].

However, unless people understand GS and its ramifications, and can process the findings, they may experience confusion and uncertainty in response to findings [2], and may not change their behaviours or take up preventive options if actionable findings are detected [3]. Furthermore, misunderstanding raises ethical and psychological concerns around the quality of consent, and potential harmful psychological consequences if overly optimistic expectations are dashed [4].

GS knowledge will likely vary according to patient characteristics, such as health literacy, education level and previous exposure to genetic counselling, all of which may make it easier to understand and process GS information, as has been shown in previous studies [5,6]. According

* Corresponding author.
E-mail address: phyllis.butow@sydney.edu.au (P. Butow).

https://doi.org/10.1016/j.pec.2022.06.009
Received 2 April 2022; Received in revised form 9 June 2022; Accepted 13 June 2022
Available online 16 June 2022

to uncertainty management theory [7,8], patients with a higher intolerance of uncertainty are more likely to seek information (such as the probability of a positive and actionable result from GS) in order to reduce uncertainty, while those who tolerate uncertainty (and may even welcome it as a way of maintaining optimism and hope for a positive outcome) may avoid this information. Knowledge has also been shown to increase after genetic counselling, which provides personalised genetic information to patients [9]. Patients who have lived longer with a cancer diagnosis, may also have had more exposure to genomic information over time.

To determine the quality of knowledge in those undertaking GS, and to evaluate the impact of interventions designed to improve knowledge, an accurate and valid measure of GS knowledge is required. Several measures have been developed for this context [10–12], but one [10] has been criticised for having an unstable factor structure and low-scale reliability when administered to different populations [13], while **another** [11] assess**es** knowledge of general genetics or genomics in general rather than GS specifically.

Recently, a novel measure, the Knowledge of Genome Sequencing (KOGS) questionnaire, has been developed which appears promising [12]. The measure was intended to be appropriate for diverse patients, health professionals and the general population. An initial item pool of 17 items was developed based on a review of professional guidelines and recommendations, patient information materials and existing measures, input from an expert panel of health professionals, and interviews with consumers with rare diseases **to identify items about the genome and GS which should be understood to ensure adequate informed consent to GS** [12]. Following administration to 243 students, healthcare providers, university staff and patients, exploratory factor analysis, Mokken analysis and item-response theory analyses were undertaken. Ultimately, nine items conforming to a single unidimensional factor achieved excellent fit to the observed data with acceptable reliability (Cronbach's alpha of 0.79). The items, assessed on a response scale of "true", "false", or "don't know" address uncertainties associated with GS (e.g. The effects of all DNA variants identified through germline genome sequencing on disease are known) and the nature of GS (e.g. Whole genome sequencing is different to other genetic tests because it looks at almost all of a person's DNA, rather than only a small bit of it).

One context for which the KOGS may be very useful is cancer, where GS is just starting to be introduced into routine care. However, the **patient subsample in the** original validation study for the KOGS [12] was small (n = 54), **comprising** people with varied rare diseases; the number of participants with cancer was not specified. Furthermore, validity testing was limited to sensitivity testing before and after attendance at a lecture on genomics. Therefore, a validation study with a larger sample of patients specifically diagnosed with cancer is required.

The aim of this study, therefore, was to confirm the single-factor structure and examine the psychometric properties of the KOGS in a large sample of people diagnosed with cancer (primarily rare), including construct validity testing via comparisons with scores on other measures likely to be related to GS knowledge. We expected that higher KOGS scores (higher knowledge) would be associated with higher health literacy and education and a scientific or medical background, previous exposure to genetic counselling/testing, a longer time since diagnosis, and uncertainty intolerance.

2. Methods

2.1. Participants and study design

The Genetic Cancer Risk in the Young (RisC) study is a cohort study of participants with a personal history of cancer, investigating heritable cancer causes and future cancer risk using germline GS. Participants in the RisC study (adults with a likely genetic predisposition to cancer: a cancer diagnosis between 16 and 40 years of age, or two cancer diagnoses at <50 years of age, or three separate cancer diagnoses at any age) are recruited by clinical cancer geneticists, genetic counselors and oncologists, or through self-referral. While gaining consent, a researcher provides participants with written information about germline GS and the study, offers participants the opportunity to ask questions, and gives contact information for study personnel if questions arise **(see Supplementary File for information sheet).** Participants provide a blood sample from which DNA is extracted and germline GS performed. If pathogenic variant(s) in the current clinically actionable American College of Medical Genetics reportable gene list are found, participants are referred to a familial cancer clinic (FCC) or other appropriate clinical service and offered tailored risk management plans. Participants receive GS results approximately 18 months after consent.

When consenting to the RisC study, a cohort of participants also consented to a psychosocial sub-study - Psychosocial Issues in Genomic Oncology 2 (PiGeOn 2) – that explored psychosocial and behavioural issues regarding GS. PiGeOn 2 participants completed a questionnaire administered at baseline (after consent and before any GS testing). Participants were reminded by phone and/or email if their questionnaire was not received within three weeks of sending.

All participants in the RisC and PiGeOn 2 studies provided written, informed consent. Human ethics approval was obtained from Human Research Ethics Committees at St Vincent's Hospital, Sydney, Australia (HREC/16/SVH/24).

3. Measures

3.1. Demographic variables

Participant demographics included: gender, age, education, occupation, language spoken at home used as a proxy of a culturally and linguistically diverse background, postcode (for SES and remoteness [Accessibility and Remoteness Index of Australia]), and marital and parental status. An occupation was designated a medical/science occupation if the education toward or the occupation itself involved scientific learning or evidence-based medical practice (e.g. research scientists, registered medical practitioners, allied health professionals). Classifications were made by one member of the research team and cross-checked by another.

3.2. Cancer variables

Personal and family history of cancer, previous attendance at a family cancer centre (FCC), previous genetic testing and time since (first) cancer diagnosis were collected.

3.3. Knowledge of genomics

Patients completed the 9-item KOGS questionnaire [12]. Response options were "true", "false" or "don't know". Incorrect and "don't know" responses were scored as incorrect. Correct scores were summed yielding a score from 0 to 9 and converted to a percentage, with higher scores indicating greater knowledge.

3.4. Health literacy

While different definitions of health literacy have been proposed, a commonly accepted definition proposed by the Institute of Medicine is: the degree to which individuals can obtain, process, and understand the basic health information and services needed to make appropriate health decisions [14]. The 3-item Chew Health Literacy questionnaire was used to assess health literacy [15]. Items address degree of difficulty reading and understanding hospital-based information, and completing medical forms. A Likert response scale (all of the time to none of the time) is utilized, with high scores indicating **greater** health literacy.

3.5. Tolerance of uncertainty

The 12-item Intolerance of Uncertainty Scale (short version) [16] was used to assess attitude to uncertainty. Responses are on a Likert scale from 1 to 5 from "not at all characteristic of me" to "entirely characteristic of me". Higher scores indicate greater intolerance of uncertainty.

4. Analyses

Confirmatory factor analysis (CFA) was performed to evaluate the fit of a single-factor model in this sample. CFA model fit was assessed by the χ^2 test, the comparative fit index (CFI), root mean square error of approximation (RMSEA) and weighted root mean square residual (WRMR). An acceptable fit was indicated by χ^2 /degrees of freedom of $\leq$ 2, CFI values of $\geq$ 0.90, RMSEA of $\leq$ 0.08 and WRMR $\leq$ 1.0 [17,18]. Internal consistency was assessed by computing the Cronbach's Alpha ($\alpha < 0.7$).

Construct validity was assessed via independent sample t-tests which examined differences in the total KOGS score across key variables (i.e. previous genetic counselling and education). Spearman correlations were computed to examine associations between the total KOGS score and health literacy, time since diagnosis and intolerance of uncertainty. Analyses were performed using SPSS (v24) and Mplus (v8).

5. Results

Of the 279 participants enrolled in the study from January 2020 to August 2021, 261 (94 %) completed the baseline questionnaire (Table 1). Participants' mean age was 41.4 years (SD 14.2; range 18–84) and the majority were female (60 %), married or lived with their partner (66 %) and had biological children (60 %). Time since first cancer diagnosis was 90 months on average (SD 125.4) and half had not previously undergone genetic testing. The mean total KOGS score in this sample was 47.9 % (SD = 30.1 %, n = 261).

5.1. Confirmatory factory analysis

CFA was performed to evaluate the fit of a single-factor model. The CFA used weighted least squares mean and variance adjusted estimation to account for dichotomous data. The CFA yielded a good model fit, $\chi 2/df = 2.43$, CFI = 0.97, RMSEA = 0.07 and WRMR = 1.03. The factor loadings of all items were above 0.60 and ranged between.66 and.93 (Fig. 1). The single factor score demonstrated excellent internal consistency ($\alpha = 0.82$). **Inter-item correlations are displayed in** Table 2**.**

5.2. Construct validity

Higher KOGS scores were positively associated with higher health literacy scores ($r = 0.23$, $p < .001$). Those with university level education scored significantly higher on the KOGS (M=55.9, SD=28.3) compared to those with secondary level education or vocational training (M=39.7, SD=29.7) [$t(258) = -4.53$, $p < .001$]. Participants with a medical or science occupation (M=68.6, SD=28.4) also had significantly higher KOGS scores [$t(259) = -3.52$, $p < .001$] than those who did not (M=45.9, SD=29.5). KOGS scores did not differ significantly [$t(259) = 0.55$, $p = .290$] between those who spoke English (M=48.4, SD= 30.0) or another language (M=45.6, SD=30.4) at home.

Although there was a trend for KOGS scores to be higher among respondents who had previously received genetic counselling (M=51.5, SD=29.3) compared to those who had not (M=45.6, SD=30.5), this difference was not statistically significant [$t(259) = 1.56$, $p = .061$]. Similarly, there was a trend for KOGS scores to be higher among those who had previously undergone genetic testing (M=51.2, SD=30.1) versus those who had not or did not know whether they had (M = 45.3, SD=29.9), but this difference was not statistically significant [$t(259) = 1.57$, $p = .058$]. KOGs scores were unrelated to both time since diagnosis ($r = -0.03$, ns) and intolerance of uncertainty ($r = 0.04$, ns).

Table 1
Participant characteristics.

	Total sample (n = 261) N (%)
Sex	
Female	157 (60.2)
Male	104 (39.8)
Marital status	
Married/De facto or living with partner	172 (65.9)
Single/Separated/Widowed	89 (34.1)
Education level	
Secondary school/vocational training	126 (48.5)
University	134 (51.5)
Medical/science occupation	
Yes	23 (8.8)
Place of residence	
Urban	244 (93.5)
Remote	17 (6.5)
Parental status	
Yes, has biological children	157 (60.1)
Speaks a language other than English at home	
Yes	40 (15.3)
Cancer incidence	
Common (>12 incidences/100,000 population)	76 (29.1)
Less common (6–12 incidences/100,000 population)	10 (3.8)
Rare (<6 incidences/100,000 population)	175 (67)
Multiple primary cancers	
Yes	87 (33.3)
First degree relatives with cancer	
Yes	106 (40.6)
Previously attended family cancer clinic	
Yes	36 (11.6)
Previous genetic testing	
Yes	119 (45.6)
No	130 (49.8)
Don't know	12 (4.6)
Age at consent	
Mean (SD)	41.4 (14.2)
Median	38.0
Range	18–84
Time since first cancer diagnosis (months)	
Mean (SD)	90.8 (125.4)
Median	38.0
Range	0–695
KOGS total score	
Mean (SD)	47.9 (30.1)
Median	55.6
Range	0–100
Health literacy score	
Mean (SD)	9.7 (2.5)
Median	11.0
Range	0–12
Intolerance of uncertainty	
Mean (SD)	28.4 (9.1)
Median	28.0
Range	12–60

6. Discussion

In this study of 261 patients diagnosed with cancer (primarily rare) offered GS, we were able to confirm the robust single-factor structure of the KOGS found in the original validation study [12]. The KOGS demonstrated strong internal consistency in this sample ($\alpha = 0.82$), indicating that the items address a core set of issues in GS, of which patients have either an overall good or poor understanding. This study therefore confirms that the KOGS has overcome several of the deficiencies reported for previous measures of genetic knowledge, including an unstable factor structure and low-scale reliability in different populations [10], and items addressing genomic tests other than GS [11].

As expected, the KOGS was significantly correlated with indices of

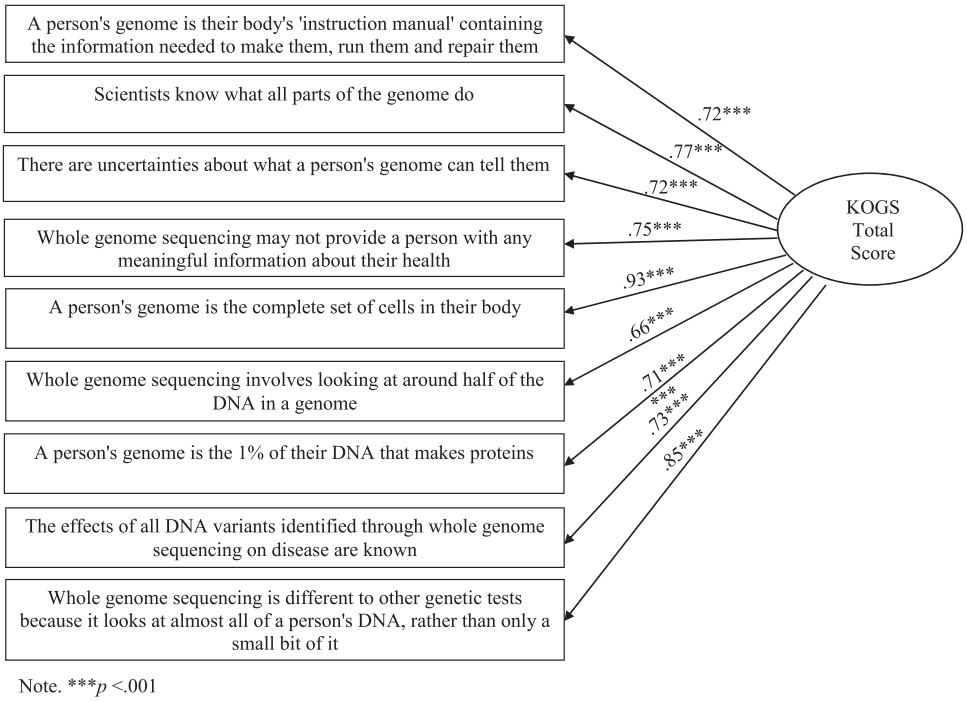

Fig. 1. Results from the CFA model displaying standardized factor loadings for each item, Note. *** $p < .001$.

health literacy, education and a scientific or medical background, suggesting that it is a valid measure of understanding, and is able to differentiate those who may be expected to have more difficulty understanding genetic concepts from those with greater resources to do so. We had also expected that previous exposure to genetic counseling or testing would be associated with higher KOGS scores. However, while previous attendees did score higher on the KOGS than those who had not previously attended genetic counseling or had testing, this difference was not significant. It may be that other genetic tests were under discussion during previous genetic counseling consultations, and knowledge accrued then did not generalize to the GS context. This reinforces the need for a GS-specific measure of knowledge. **Alternatively, participants may simply have forgotten information received during genetic counselling or were left with a "gist" understanding rather than the specifics.**

Speaking a language other than English at home was not correlated with KOGS scores, as predicted. Only 15 % of our sample did not speak English at home, thus power may have been an issue here. Furthermore, additional variables exploring the quality of spoken and written English were not included in the study, thus it is not clear whether and to what degree these participants experienced language barriers. Future research should explore this issue further to determine if non-English speakers need additional, culturally appropriate resources in their own language and interpreters to allow them to gain greater knowledge of GS.

We had expected that with a longer time since diagnosis, patients would accrue more knowledge, but this variable was not associated with KOGS scores. It is possible that, as GS is only beginning to be introduced into clinical oncology, GS had not previous come up for these patients, thus time since diagnosis did not afford greater exposure to GS information. In analyses of qualitative data from a previous set of participants from the RisC study [19], we documented high patient trust in medical and scientific expertise and a low need to understand the detail behind GS. Thus, it is possible that even with time, patients did not seek a greater understanding of GS **or had converted what they were told into a "gist" understanding.** Given that consent to GS is a relatively short process with limited feasibility to provide extensive GS information, offering patients access to online or written resources over time, if they desire, may allow them to slowly accrue knowledge at their own pace.

We had hypothesized that patients with *low* tolerance of uncertainty would seek information to reduce uncertainty, as has been reported in the previous literature [20,21], and would therefore achieve higher KOGS scores; however we found no such association. Brashers et al. [8] suggested that people with a *high* tolerance of uncertainty may also seek information to identify contrary or disconfirming evidence when they want to escalate uncertainty. This may be a partial explanation for our negative finding. Our participants had only just agreed to have GS and may therefore not have yet had a chance to seek out further information. Alternatively, we may have had insufficient variability in tolerance for uncertainty in our sample to identify an association with KOGS scores. Our participants, all of whom had volunteered to be in a research project involving GS, had greater intolerance of uncertainty than that reported in previous studies of patients hypothetically considering genetic testing for colon and breast cancer risk [22]. Braithwaite et al. [22] found intention to pursue testing was associated with a more negative attitude towards uncertainty, supporting this possibility. Further research is required to explore the relationships between tolerance of uncertainty, information seeking and knowledge in cancer populations undergoing GS.

This study had some limitations. The sample were participating in a research project, rather than receiving GS within a purely clinical context. However, they were informed they would be offered tailored risk management if they received an actionable result, and our qualitative study with a previous set of participants from the RisC study indicated they were highly motivated to find out information that could benefit their family, suggesting they were obtaining clinical benefit from their participation [18]. **Because they were participating in a research project, participants received carefully curated information (covering most of the KOGS items) via the information sheet (see Supplementary File 1) and from recruiters. Therefore, their KOGS scores may have been higher than would be found in the general population of cancer patients, whose oncologists may provide less detailed information. However, we do not believe this would have impacted the psychometric testing conducted for the study, as there was still a good spread of scores on the KOGS.**

Table 2
Knowledge of Genome Sequencing (KOGS) inter-item correlations.

	1	2	3	4	5	6	7	8	9
1. A person's genome is their body's 'instruction manual' containing the information needed to make them, run them and repair them	–								
2. Scientists know what all parts of the genome do	.35	–							
3. There are uncertainties about what a person's genome can tell them	.31	.44	–						
4. Whole genome sequencing may not provide a person with any meaningful information about their health	.37	.34	.35	–					
5. A person's genome is the complete set of cells in their body	.38	.58	.43	.35	–				
6. Whole genome sequencing involves looking at around half of the DNA in a genome	.26	.20	.23	.22	.32	–			
7. A person's genome is the 1 % of their DNA that makes proteins	.26	.21	.21	.49	.31	.23	–		
8. The effects of all DNA variants identified through whole genome sequencing on disease are known	.24	.23	.28	.29	.32	.35	.40	–	
9. Whole genome sequencing is different to other genetic tests because it looks at almost all of a person's DNA, rather than only a small bit of it	.37	.43	.45	.38	.58	.33	.35	.31	–

While we examined correlations between education, heath literacy and knowledge, we did not conduct differential item response by education or health literacy. Thus, it is possible there was conflation of health literacy skills with specialized knowledge, which is an issue which should be explored further in future research.

The KOGS was developed with feedback from patients with rare diseases. While our sample was comprised primarily of patients with rare cancers, some issues specific to the cancer setting may have been omitted, impacting validity for this context. Further fundamental qualitative work with cancer patients to elicit their perspectives on appropriate items may resolve this issue. Finally, as we did not conduct a "think aloud" study while participants were completing KOGS items, we cannot be sure they understood all terms used in included items. However, KOGS items are worded very simply, with a conscious avoidance of jargon, to minimise this issue.

We would like to propose some future research directions for this area. Firstly, the development of the KOGS' was not guided by an information framework, such as that proposed by Rogers [23]. Rogers suggested there are three types of information: awareness, "how to" and principles information. The KOGS covers the first and last of these areas: awareness (e.g. Whole genome sequencing is different to other genetic tests because it looks at almost all of a person's DNA, rather than only a small bit of it); and principles (e.g. A person's genome is their body's 'instruction manual' containing the information needed to make them, run them and repair them.) However, "how to" information, which covers practical information concerning how to use GS results, is absent. Given that a proportion of people undergoing GS will be provided with actionable results, on the basis of which they will be expected to make decisions about their health, this represents a gap in the current scale. Future research could explore the utility of "how to" information from consumers' perspectives, and suggest additional items for the KOGS if this is shown to be valued. Future research could also explore the predictive validity of the KOGS, such as its ability to predict patients' attitudes to GS and their decision-making regarding undergoing GS and receiving results, as would be predicted by Rogers' framework [23].

In conclusion, this study supported the single-factor structure of the KOGS, provides further evidence of its reliability and validity, and affirms that the KOGS can be used to assess understanding of GS in a variety of populations including cancer patients.

Ethical

Participants gave consent to PiGeOn when consenting to MoST, and informed consent was obtained from all individual participants. Human ethics approval was obtained from the Human Research Ethics Committees at St Vincent's Hospital, Sydney, Australia (HREC/16/SVH/23).

Funding

This study was funded by a National Health and Medical Research Council (NHMRC) of Australia Project Grant (ID1124749). Investigators received the following support: PNB: NHMRC Senior Principal Research Fellowship (APP1121630); MCB: Post-Doctoral Research Fellowship from the Cancer Institute of NSW, Australia (MB00352). All authors declare they have no conflicts of interest.

CRediT authorship contribution statement

Phyllis Butow contributed to the conceptualisation of the study, guided the formal analysis, wrote the initial draft of the paper and prepared the final paper, **Christine Napier** contributed to the conceptualisation of the study, curated the data and reviewed and commented on successive paper drafts, **Rachel Campbell** conducted the formal analysis and reviewed and commented on successive paper drafts, **Nicole Bartley** contributed to the conceptualization of the study, and reviewed and commented on successive paper drafts, **Megan Best** contributed to the conceptualisation of the study, and reviewed and commented on successive paper drafts, **Mandy Ballinger** contributed to the conceptualisation of the study, and reviewed and commented on successive paper drafts.

Author contributions

All authors made substantial contributions to conception and design, or acquisition of data, or analysis and interpretation of data; drafting the manuscript; and revising it critically for important intellectual content. All authors have given final approval of the version to be published and agreed to be accountable for all aspects of the work.

Declaration of Interests

None.

Data Availability

The data is available upon request

Acknowledgements

The authors would like to thank the MoST Program PiGeOn participants for their time and willingness to share their experiences. We also acknowledge Members of the PiGeOn Project not listed as authors: David Goldstein, Chris Jacobs, Ilona Juraskova, Judy Kirk, Bettina Meiser, Ainsley Newson, Jacqueline Savard, Timothy Schlub, David Thomas, Katherine Tucker, Sabina Vatter, Kate Vines, Richard Vines, Mary-Anne Young.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.pec.2022.06.009.

References

[1] Jackson SE, Chester JD. Personalised cancer medicine. Int J Cancer 2015;137:262–6. https://doi.org/10.1002/ijc.28940.
[2] Bartley N, Napier CE, Butt Z, Schlub T, Best MC, Beisecker BB, et al. Cancer patient experience of uncertainty while waiting for genome sequencing results. Frontiers in Psychology. Front Psychol 2021;12:647602. https://doi.org/10.3389/fpsyg.2021.647502. section Psycho-Oncol.
[3] Lumish HS, Steinfeld H, Koval C, Russo D, Levinson E, Wynn J, et al. Impact of panel gene testing for hereditary breast and ovarian cancer on patients. J Genet Couns 2017;26:1116–29.
[4] Martinez-Martin N, Magnus D. Privacy and ethical challenges in next-generation sequencing. Expert Rev Precis Med Drug Dev 2019;4(2):95–104. https://doi.org/10.1080/23808993.2019.1599685.
[5] Napier CE, Davies G., Butow PN, Schlub TE, Best MC, Bartley N. et al. Cancer patient knowledge about and behavioral intentions after germline genome sequencing. Patient Education and Counseling; 2021:S07383991(21)004390.
[6] Kaphingst KA, Blanchard M, Milam L, Pokharel M, Elrick A, Goodman MS. Relationships between health literacy and genomics-related knowledge, self-efficacy, perceived importance, and communication in a medically underserved population. J Health Commun 2016;21(Suppl 1):58–68. Suppl 1.
[7] Brashers DE. A theory of communication and uncertainty management. In: Whaley B, Samter W, editors. Explaining communication theory. Mahwah, NJ: Erlbaum; 2007. p. 201–18.
[8] Brashers DE, Neidig JL, Haas SM, Dobbs LK, Cardillo LW, Russell JA. Communication in the management of uncertainty: the case of persons living with HIV or AIDS. Commun Monogr 2000;67:63–84.
[9] Madlensky L, Trepanier AM, Cragun D, Lerner B, Shannon KM, Zierhut H. A rapid systematic review of outcomes studies in genetic counseling. J Genet Couns 2017;26(3):361–78.
[10] Kaphingst KA, Facio FM, Cheng MR, Brooks S, Eidem H, Linn A, et al. Effects of informed consent for individual genome sequencing on relevant knowledge. Clin Genet 2012;82:408–15. https://doi.org/10.1111/j.1399-0004.2012.01909.x.
[11] Langer MM, Roche MI, Brewer NT, Berg JS, Khan CM, Leos C, et al. Development and validation of a genomic knowledge scale to advance informed decision-making research in genomic sequencing. MDM Policy Pract 2017;2. https://doi.org/10.1177/2381468317692582 2381468317692582.
[12] Sanderson SC, Loe BS, Freeman M, Gabriel C, Stevenson DC, Gibbons C, et al. Development of the knowledge of genome sequencing (KOGS) questionnaire. Patient Educ Couns 2018;101(11):1966–72. https://doi.org/10.1016/j.pec.2018.07.011.
[13] Sanderson SC, Suckiel SA, Zweig M, Bottinger EP. Development and preliminary evaluation of an online educational video about whole-genome sequencing for research participants, patients and the general public. Genet Med 2015;18:501–52.
[14] Ratzan SC, Parker RM. 2000. Introduction. In: National Library of Medicine Current Bibliographies in Medicine: Health Literacy. Selden CR, editor;, Zorn M., editor;, Ratzan SC, editor;, Parker RM, editor., Editors. NLM Pub. No. CBM 2000–1. Bethesda, MD: National Institutes of Health, U.S. Department of Health and Human Services.
[15] Chew LD, Griffin JM, Partin MR, Noorbaloochi S, Grill JP, Snyder A, et al. Validation of screening questions for limited health literacy in a large va outpatient population. J Gen Intern Med 2008:561–6.
[16] Carleton RN, Norton MA, Asmundson GJ. Fearing the unknown: a short version of the intolerance of uncertainty scale. J Anxiety Disord 2007;21(1):105–17.
[17] Hu L, Bentler PM. Cutoff criteria forfit indexes in covariance structure analysis: Conventional criteria versus new alternatives. Struct Equ Model 1999;6:1–55.
[18] Kline RB. Principles and practice of structural equation modeling. Methodology in the social sciences. The Guilford Press; 2015.
[19] Bartley N, Best M, Jacobs C, Juraskova I, Newson AJ, Savard J, et al. Cancer patients' views and understanding of genome sequencing: a qualitative study. J Med Genet 2020;57(10):671–6. https://doi.org/10.1136/jmedgenet-2019-106410.
[20] Solomon I, Harrington E, Hooker G, et al. Lynch syndrome limbo: patient understanding of variants of uncertain significance. J Genet Couns 2017;26:866–77.
[21] Hitch K, Joseph G, Guiltinan J, Kianmahd J, Youngblom J, Blanco A. Lynch syndrome patients' views of and preferences for return of results following whole exome sequencing. J Genet Couns 2014;23:539–51.
[22] Braithwaite D, Sutton S, Steggles N. Intention to participate in predictive genetic testing for hereditary cancer: the role of attitude toward uncertainty. Psychol Health 2002;17(6):761–72. https://doi.org/10.1080/0887044021000054764.
[23] Roger EM. Diffusion of Innovations, ed 5 (rev). New York: Free Press; 2003.