Gynecologic Oncology 190 (2024) 250–254

Contents lists available at ScienceDirect

Gynecologic Oncology

journal homepage: www.elsevier.com/locate/ygyno

Timely targeted testing for hereditary cancer syndromes – Importance of clinician-facilitated cascade testing in the first year post-diagnosis

Benjamin Grant [a,*], Alex Raghunandan [a], Emily Epstein [b], Jesse T. Brewer [b], Isabelle Chandler [b], Taylor Larosa [c], Alissa Kalyan [c], Sarah Schulman [c], Ashley Llenas [c], Eloise Chapman-Davis [b], Charlene Thomas [d], Paul Christos [d], Steven M. Lipkin [e], Ravi N. Sharaf [f,g,1], Melissa K. Frey [b,1]

[a] Weill Cornell Medical College of Weill Cornell Medicine, New York, NY, USA
[b] Department of Obstetrics and Gynecology, Division of Gynecologic Oncology, Weill Cornell Medicine, New York, NY, USA
[c] Department of Obstetrics and Gynecology, Weill Cornell Medicine, New York, NY, USA
[d] Department of Population Sciences, Weill Cornell Medicine, New York, NY, USA
[e] Department of Medicine, Division of Genetic Medicine, Weill Cornell Medicine, New York, NY, USA
[f] Division of Gastroenterology, Department of Medicine, Weill Cornell Medicine, New York, NY, USA
[g] Division of Epidemiology, Department of Population Health Sciences, Weill Cornell Medicine, New York, NY, USA

ARTICLE INFO

Article history:
Received 6 July 2024
Received in revised form 30 August 2024
Accepted 1 September 2024
Available online xxxx

Keywords:
Hereditary cancer syndromes
Genetics
Cascade testing
Pathogenic variant

ABSTRACT

Objective. Cascade testing for hereditary cancer syndromes allows relatives to estimate cancer risk and pursue prevention and early detection strategies. The current paradigm relies on patient coordinated care, resulting in only one-third of relatives successfully completing testing. Studies suggest that team-based approaches, where clinicians facilitate testing, can increase uptake. As institutions consider implementing such programs, understanding patient characteristics associated with interest is crucial for resource allocation. We aim to assess interest in clinician-facilitated testing and evaluate barriers.

Methods. Patients with cancer-associated pathogenic variants seen at a gynecologic oncology clinic were offered clinician-facilitated cascade testing. Patient interest and demographic variables were recorded and patients that declined were interviewed regarding the decision.

Results. From 11/2023–4/2024, 139 patients were offered clinician-facilitated cascade testing. Median patient age was 43 years (IQR 17), 97 (69.8 %) self-identified as White and 101 (72.7 %) as non-Hispanic. Fifty-six (40.3 %) patients harbored a BRCA1 pathogenic variant, 37 (26.6 %) BRCA2, and 46 (33.1 %) other cancer-associated genes. Fifty-seven (41.0 %) patients expressed interest in the intervention. Interested patients were more likely to have been diagnosed in the prior year vs. patients who were not interested on univariate (OR 4.6, 95 % CI 2.0–10.2, $P = 0.0002$) and multivariable analyses (adjusted OR 3.8, 95 % CI 1.622–9.009, $P = 0.0022$).

Conclusions. Our study demonstrates that patients are almost five time more likely to be interested in cascade genetic testing within the first year of diagnosis of a pathogenic variant. Given the utility of such programs and their resource requirements, targeting this population could maximize effectiveness and uptake of cascade services.

1. Introduction

Germline pathogenic variants in cancer-associated genes confer an increased lifetime risk for developing cancer. For patients diagnosed with a pathogenic variant (probands), cascade testing, or the process of extending genetic services to relatives of the proband, is highly encouraged [1]. Cascade testing is considered a tier one genetic application for Hereditary Breast and Ovarian Cancer Syndrome and Lynch syndrome by the Centers for Disease Control and Prevention, demonstrating significant potential for positive impact on public health [1]. Appropriate and timely completion of cascade testing can result in

* Corresponding author at: 1300 York Ave, New York, NY, 10021, USA.
E-mail addresses: bjg4001@med.cornell.edu (B. Grant), alr4017@med.cornell.edu (A. Raghunandan), eme4004@med.cornell.edu (E. Epstein), jesse.t.brewer@kp.org (J.T. Brewer), irc4005@med.cornell.edu (I. Chandler), tal2009@med.cornell.edu (T. Larosa), alk4042@med.cornell.edu (A. Kalyan), sas4066@med.cornell.edu (S. Schulman), ajl4004@med.cornell.edu (A. Llenas), elc9120@med.cornell.edu (E. Chapman-Davis), cht2028@med.cornell.ed (C. Thomas), pac2001@med.cornell.edu (P. Christos), stl2012@med.cornell.edu (S.M. Lipkin), ras9030@med.cornell.edu (R.N. Sharaf), mkf2002@med.cornell.edu (M.K. Frey).
[1] Co-Senior authors.

https://doi.org/10.1016/j.ygyno.2024.09.001
0090-8258/

cancer prevention and early stage cancer detection, improving cancer-related morbidity and mortality [2].

The current paradigm of cascade genetic testing relies on patients to facilitate cascade family testing. Studies suggest that only approximately one-third of relatives complete cascade testing when the process is mediated by the patient [3,4]. There are numerous barriers that likely contribute to low uptake of genetic testing, including but not limited to: family communication/dynamics, fear of genetic discrimination, cost, result anxiety, and limited genetics knowledge [5,6]. Barriers to cascade testing may be even more pronounced in certain racial and ethnic minority groups [7,8].

A team-based approach, whereby the clinical team facilitates relative contact and cascade testing, has been cited as a promising and feasible intervention to increase uptake of cascade testing and improve equity [4,9,10]. We sought to prospectively review a clinician-facilitated cascade testing intervention. With the reality of limited healthcare resources, we sought to assess patient characteristics associated with interest to optimize and determine how to best target the intervention in a real-world setting.

2. Methods

2.1. Intervention

The study was approved by the Weill Cornell Medicine Institutional Review Board. Over a predefined six-month period (November 2023 to April 2024),139 patients with pathogenic variants at an urban gynecologic oncology clinic were approached and offered participation in a clinician-facilitated cascade testing trial. Patient were approached a single time, those that declined where not re-approached. Patients who were interested in the intervention completed informed consent. Patients provided the contact information for all family members that they designated for contact. Patients agreed to contact their relatives first to inform them of the familial pathogenic variant and trial participation prior to relative contact by the clinical team. The clinical team consisted of an attending physician specialized in gynecologic oncology, licensed social worker, research assistant, and medical student, all of whom were trained to contact designated family members. The clinical team called patient-approved family members to review the pathogenic variant present in their family member, review the increased risk for the specific hereditary cancer syndrome, explain the process of cascade testing, and for those interested in assistance, help coordinating genetic testing (scheduling genetics appointments, identifying local genetics providers, and sharing options for direct-to-patient mailed saliva kit testing) (Fig. 1).

Patients who declined clinician-facilitated cascade testing were asked for reasons why they were not interested in participation. Responses were recorded and coded by two independent reviewers who utilized the *Socio-Ecological Framework* to assess barriers to cascade testing [11,12]. Demographic information for all approached patients was abstracted from the electronic medical record.

2.2. Measures & outcomes

The primary outcome of our study was to assess patient characteristics associated with interest in clinician-facilitated cascade testing. Interest was defined as patients indicating that they would like the clinical team to contact their family members. Lack of interest was defined as patients indicating that they did not want the study team to contact any family members regarding cascade genetic testing.

We also aimed to assess barriers to cascade testing within the context of our intervention. Patient responses were categorized according to the *Socio-Ecological Model*. The broadest category was "societal" and referred to any barriers that resulted from social constructs and/or policy. "Healthcare community" referred to barriers that existed because of processes within the healthcare system such as cost of testing and access to care. "Interpersonal Relationships" referred to barriers that resulted from dynamics between probands and their family members, either positive or negative. "Individual" referred to barriers that stemmed from personal beliefs and experiences of the proband [11,12]. "Other" was used to categorize any patient that reported all family members had already been tested.

2.3. Statistical analyses

Statistical analyses were conducted using R Studio (New York, NY). Wilcoxon two-sample rank-sum test, Fisher's exact test, and the chi-squared statistical tests were used, where appropriate, to evaluate for associations between patient characteristics and interest in the intervention. Wald confidence limits were utilized to calculate 95 % confidence intervals for odds ratios. Youden index was utilized to determine the best time cut point to define recent and distant diagnoses. One year (365 days) was determined to be both the most statistically and clinically relevant time cut point for this designation. Probands with a diagnosis of a pathogenic mutation ≤365 days ago were considered a "recent" diagnosis while those with a diagnosis >365 days were considered a "distant" diagnosis. Multivariable logistic regression analysis model accounting for patient age, race, history of cancer, time since genetic testing, and specific pathogenic variant present was utilized to calculate adjusted odds ratios. All *p*-values were two-sided with statistical significance evaluated at the 0.05 alpha level.

3. Results

3.1. Patient characteristics

Of the 139 patients approached and offered clinician-facilitated cascade testing, 57 (41 %) were interested in the intervention. Median age

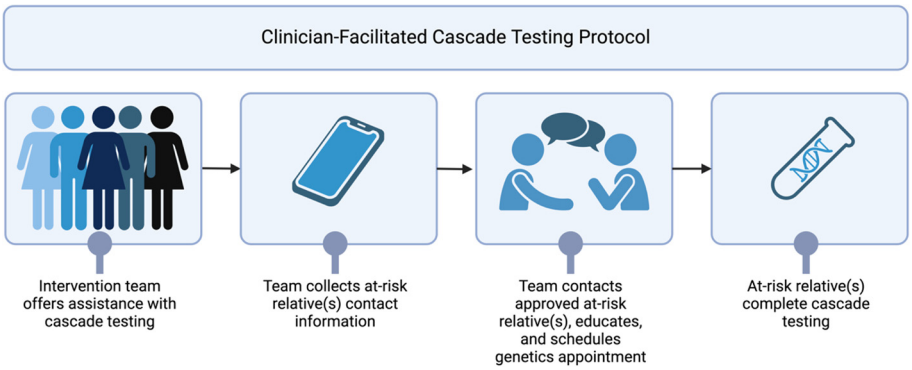

Fig. 1. Study workflow for clinician-facilitated cascade testing intervention.

for all approached patients was 43 years (IQR 17). Ninety-seven (69.8 %) patients self-identified as White, 5 (3.6 %) as Black, 1 (0.7 %) as Asian, 11 (7.9 %) as other, and 25 (18 %) did not report race. One hundred and one (72.7 %) identified as non-Hispanic, 9 (6.5 %) as Hispanic, and 29 (20.9 %) did not report ethnicity. Sixty-one (43.9 %) of patients were of Ashkenazi Jewish heritage. All 139 patients were female. Fifty-three patients (38.1 %) had a personal history of cancer. Thirty-seven (26.6 %) patients were diagnosed with a pathogenic variant within the last year (≤ 365 days since genetic testing results were reported). Forty-five (32.4 %) patients were nulliparous. Ninety-four (67.6 %) had at least one living child. The most common pathogenic variants present in the study were BRCA1 (56, 40.3 %) and BRCA2 (37, 26.6 %) (Table 1).

3.2. Primary outcome: patient associations

The median time since diagnosis of a pathogenic variant for patients who were interested in clinician-facilitated cascade testing was 583 days vs. 1152 days for patients who declined the intervention ($P = 0.002$). On univariate analysis, patients diagnosed with a pathogenic variant within the past year were significantly more likely to be interested in clinician-facilitated cascade testing compared to those with a distant diagnosis (67.6 % vs. 31.4 %, $P = 0.0001$). Patients with a BRCA1 pathogenic variant were least likely to be interested in the intervention (BRCA1–30.4 %; BRCA2–40.5 %, non-BRCA1/2 pathogenic variants 54.4 %, $P = 0.05$). Race, age, ethnicity, Ashkenazi Jewish heritage, personal history of cancer, and number of living children were not associated with interest in the intervention (P values: race = 0.130; age = 0.485; ethnicity = 0.087; Ashkenazi Jewish heritage = 0.163; history of cancer = 0.332; children = 0.592) (Table 2). Patients interested in clinician-facilitated cascade testing were 4.6 times more likely to have been diagnosed with their pathogenic variant within the past 365 days when compared to those who were not interested (OR 4.6, 95 % CI 2.0–10.2, $P = 0.0002$).

Table 1
Summary of patient characteristics for all collected demographic data.

Patient Characteristic	*N* (%)
Interested in Intervention?	
Yes	57 (41 %)
No	82 (59 %)
Age	
Median (IQR)	43 (17)
Race	
White	97 (69.8 %)
Black	5 (3.6 %)
Asian	1 (0.7 %)
Other	11 (7.9 %)
Declined	25 (18 %)
Ethnicity	
Hispanic	9 (6.5 %)
Non-Hispanic	101 (72.7 %)
Declined	29 (20.9 %)
Ashkenazi Jewish Heritage?	
Yes	61 (43.9 %)
No	78 (56.1 %)
Personal History of Cancer?	
Yes	53 (38.1 %)
No	86 (61.9 %)
Parity	
Nulliparous	45 (32.4 %)
≥1	94 (67.6 %)
Time Since Diagnosis	
Recent (≤365 days)	37 (26.6 %)
Distant (>365 days)	102 (73.4 %)
Pathogenic Variant Present	
BRCA1	56 (40.3 %)
BRCA2	37 (26.6 %)
Other[a]	46 (33.1 %)

[a] Combination of patients diagnosed with APC (2)/ATM (8)/BRIP1 (4)/CDH1 (1)/CFTR (1)/CHEK2 (3)/MLH1 (2)/MSH2 (3)/MSH6 (6)/MUTYH (1)/PALB2 (4)/PMS2 (6)/RAD51C (3)/RAD51D (1)/STK11 (1).

Table 2
Univariate associations between patient characteristics and interest in clinician-facilitated cascade testing.

	Interested $N = 57$ (41 %)	Not Interested $N = 82$ (59 %)	*P*-Value
Age			
Median (IQR)	44 (16)	42 (15)	0.485
Race			0.130
White (N = 97)	38 (39.2 %)	59 (60.8 %)	
Black (N = 5)	4 (80 %)	1 (20 %)	
Other[a] *(N = 12)*	7 (58.3%)	5 (41.7 %)	
Declined (N = 25)	8 (32 %)	17 (68 %)	
Ethnicity			0.087
Hispanic (N = 9)	7 (77.8 %)	2 (22.2 %)	
Non-Hispanic (N = 101)	38 (37.6 %)	63 (62.4 %)	
Declined (N = 29)	12 (41.4 %)	17 (58.6 %)	
Ashkenazi Jewish Heritage?			0.163
Yes (N = 61)	21 (34.4 %)	40 (65.6 %)	
No (N = 78)	36 (46.2 %)	42 (53.8 %)	
Personal History of Cancer?			0.332
Yes (N = 53)	19 (35.8 %)	34 (64.2 %)	
No (N = 86)	38 (44.2 %)	48 (55.8 %)	
Parity			0.592
Nulliparous (N = 45)	17 (37.8 %)	28 (62.2 %)	
≥ 1 (N = 94)	40 (42.6 %)	54 (57.4 %)	
Time Since Diagnosis			0.0001
Recent (N = 37)	25 (67.6 %)	12 (32.4 %)	
Distant (N = 102)	32 (31.4 %)	70 (68.6 %)	
Pathogenic Variant Present			0.050
BRCA1 (N = 56)	17 (30.4 %)	39 (69.6 %)	
BRCA2 (N = 37)	15 (40.5 %)	22 (59.5 %)	
Other[b] *(N = 46)*	25 (54.4 %)	21 (45.6 %)	

[a] Combination of "Other" and "Asian".
[b] Combination of all other reported pathogenic variants besides BRCA1 and BRCA2.

Multivariable analysis was conducted controlling for proband age, race, personal history of cancer, time since pathogenic variant diagnosis, and the specific pathogenic variant present. Type 3 analysis of effect demonstrated that only time since diagnosis was significant in this model (P values: age = 0.571, race = 0.389, personal history of cancer = 0.560, time since diagnosis = 0.0012, pathogenic variant present = 0.208) (Suppl. Table 1). In this model, the association between time since diagnosis and interest continued to be significant (adjusted OR 3.8, 95 % CI 1.622–9.009, $P = 0.0022$), while the association between BRCA1 and interest was no longer significant (adjusted OR 0.4, 95 % CI 0.178–1.092, $P = 0.0767$) (Table 3).

3.3. Secondary outcome: barriers to cascade testing

Of the 82 patients who did not express interest in the intervention, 1 (1.2 %) reported barriers at the Societal level, citing "fear of genetic discrimination" as a reason for declining. Six (7.3 %) patients reported

Table 3
Odds ratio estimates for interest in clinician-facilitated cascade testing in multivariable logistic regression model accounting for age, race, personal history of cancer, time since diagnosis, and pathogenic variant present.

Comparison	Adjusted Odds Ratio	95 % Wald Confidence Interval		P-Value
Age	1.0	0.972	1.030	0.9829
Black vs White	3.9	0.342	44.823	0.2722
Declined vs White	0.7	0.268	1.968	0.5294
Other[a] vs White	2.0	0.523	7.360	0.3182
Personal History of Cancer vs No Cancer	0.9	0.388	1.984	0.7542
Recent vs Distant Diagnosis	3.8	1.622	9.009	0.0022
BRCA1 vs Other[b]	0.4	0.178	1.092	0.0767
BRCA2 vs Other[b]	0.7	0.258	1.768	0.4245

[a] Combination of "Other" and "Asian".
[b] Combination of all other reported pathogenic variants besides BRCA1 and BRCA2.

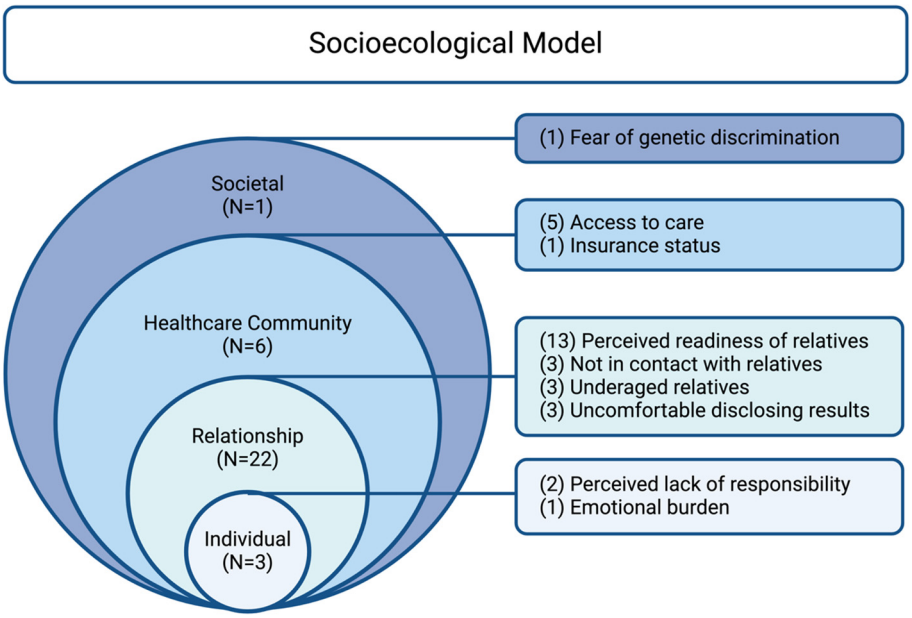

Fig. 2. Socioecological model analysis of patient reported barriers to clinician-facilitated cascade testing for those not interested in the intervention.

barriers at the Healthcare Community level citing "access to care" as the most common reason for declining. Twenty-two (26.8 %) patients reported barriers at the Relationship level citing "perceived readiness of relatives" as the most common reason for declining. Three (3.7 %) reported barriers at the individual level citing "perceived lack of responsibility" as the most common reason for declining (Fig. 2). Of the remaining 50 patients who declined the intervention, 48 (58.5 %) reported that "all family members had already completed genetic testing", and 2 (2.4 %) did not report a reason for declining.

4. Discussion

Cascade genetic testing is intended to efficiently diagnose pathogenic variants by leveraging familial relationships and trace germline pathogenic variants through a family tree [13]. Timely diagnosis of a pathogenic variant informs risk reducing interventions, screening frequency, and can have significant positive impact on morbidity and mortality [4,14]. However, even with its known potential benefits and cost-effectiveness, uptake of cascade testing is poor, frequently cited as only about a third of at-risk relatives [5,15–19]. Several strategies have been suggested to improve cascade testing uptake, such as team-based interventions through which clinicians contact probands' family members to offer testing [9].

Clinician-facilitated cascade testing is both a feasible and cost-effective means of improving uptake of testing and identification of high-risk individuals [18,19]. With limited resources in healthcare, targeting such interventions towards groups with high interest will be essential. To further improve uptake of genetic testing. Our data suggest that the first year following diagnosis with a pathogenic variant is the most opportune time to offer such an intervention as those interested in clinician-facilitated cascade testing were 4.6 times more likely to have received their diagnosis within the last 365 days.

While clinician-facilitated cascade testing is intended to reduce barriers to cascade services, patient interviews in the context of such an intervention demonstrated that numerous barriers persisted; particularly at the relationship levels (Fig. 2). The most cited barrier to intervention uptake was "perceived readiness of relatives" at the relationship level. Our evaluation of barriers in the context of such an intervention suggests that developing strategies to promote patient activation (i.e. motivating family members to undergo genetic testing to know their status) at the familial level could promote further testing uptake.

Future studies are needed to evaluate real-world impact of targeted clinician-facilitated cascade testing when efforts are focused on recently diagnosed patients. Studies are also needed to determine ways to improve access to care, particularly for patients who have family members that do not live within the United States, as facilitating testing for these individuals can be even more complicated. Lastly, evaluation of familial patient activation related to testing for hereditary germline pathogenic variants should be done to understand what limits family member uptake of testing after being contacted by an intervention team.

Our study holds numerous strengths. To our knowledge, this is the first of its kind to determine target groups and time intervals for clinician-facilitated cascade testing interventions. Furthermore, our patient interviews gave us significant insight into patient experiences and areas to improve for future interventions. In summation, our study not only determined a feasible and potentially significant way to improve these interventions, but it also identified areas for future improvement.

This study also has important limitations. Of note, our study population was limited to one urban gynecologic oncology clinic. Additionally, our sample size was modest, consisting of 139 total participants. Our study's endpoint was patient interest and not full intervention uptake. We selected this endpoint because interest is the first step in activating a cascade. Long-term follow-up of our population is underway to determine rates of completion of genetic testing among contacted family members and our prior pilot study demonstrated that once successfully contacted by the genetics team, 70 % of at-risk relatives completed genetic testing [9]. Finally, our study had limited patient diversity and further evaluation of such an intervention in racially and ethnically diverse clinical environments is greatly needed as racial disparities in cascade services have been documented extensively in the literature [8].

In summary, in the context of a clinician-facilitated cascade testing intervention, those interested in the intervention were more likely to have been recently diagnosed with a pathogenic variant. As medical institutions contemplate the implementation of facilitated-cascade programs, targeting such interventions towards patients newly diagnosed with a pathogenic variant may prove advantageous for increasing uptake and identification of at-risk relatives. Future studies are needed to evaluate the real-world utility and impact of targeted clinician-

facilitated cascade testing in large and diverse patient cohorts, particularly for patients diagnosed within the last year.

Funding

Steven M Lipkin was supported by NCI 272,688. Ravi N Sharaf was supported by the following grants: National Cancer Institute Grant # K07CA216326 and R01CA211723 and Patient Centered Outcomes Research Institute Grant # IHS-2017C3–9211. Melissa K Frey was supported by the following grant: American Association of Obstetricians and Gynecologists Foundation / American Board of Obstetrics & Gynecology (AAOGF/ABOG) Career Development Award. Paul J Christos and Charlene Thomas were supported by the following grant: Clinical and Translational Science Center at Weill Cornell Medical College (UL1TR002384).

CRediT authorship contribution statement

Benjamin Grant: Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Alex Raghunandan:** Writing – review & editing, Writing – original draft, Visualization, Methodology. **Emily Epstein:** Writing – review & editing, Resources, Project administration, Investigation. **Jesse T. Brewer:** Writing – review & editing, Project administration, Investigation. **Isabelle Chandler:** Writing – review & editing, Project administration, Investigation. **Taylor Larosa:** Writing – review & editing, Project administration. **Alissa Kalyan:** Writing – review & editing, Project administration. **Sarah Schulman:** Writing – review & editing, Project administration. **Ashley Llenas:** Writing – review & editing, Project administration. **Eloise Chapman-Davis:** Writing – review & editing, Supervision, Resources, Investigation, Conceptualization. **Charlene Thomas:** Data curation, Formal analysis, Writing – review & editing. **Paul Christos:** Data curation, Formal analysis, Writing – review & editing. **Steven M. Lipkin:** Writing – review & editing, Validation, Supervision, Conceptualization. **Ravi N. Sharaf:** Writing – review & editing, Validation, Supervision, Methodology, Data curation, Conceptualization. **Melissa K. Frey:** Writing – review & editing, Validation, Supervision, Methodology, Data curation, Conceptualization.

Data availability

Data that support the findings of this study are available from the corresponding author upon request.

Declaration of competing interest

The authors have no financial or personal conflicts of interest to disclose.

Acknowledgements

We thank our patients for allowing us to share their experiences with the hope that others, as a result, will benefit. All figures presented were created using BioRender.com.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ygyno.2024.09.001.

References

[1] Cascade Testing: Finding Family Members with Genetic Conditions|CDC. https://www.cdc.gov/genomics/disease/cascade_testing/cascade_finding.htm; 2022.
[2] M.K. Frey, et al., What happens in the long term: uptake of cancer surveillance and prevention strategies among at-risk relatives with pathogenic variants detected via cascade testing, Cancer 128 (2022) 4241–4250.
[3] M.D. Ahsan, et al., Do people with hereditary cancer syndromes inform their at-risk relatives? A systematic review and meta-analysis, PEC Innov. 2 (2023), 100138.
[4] M.K. Frey, et al., Cascade Testing for hereditary Cancer syndromes: should we move toward direct relative contact? A systematic review and Meta-analysis, J. Clin. Oncol. Off. J. Am. Soc. Clin. Oncol. 40 (2022) 4129–4143.
[5] R.M. Kahn, et al., Barriers to completion of cascade genetic testing: how can we improve the uptake of testing for hereditary breast and ovarian cancer syndrome? Fam. Cancer 22 (2023) 127–133.
[6] K.D. Whitaker, E. Obeid, M.B. Daly, M.J. Hall, Cascade genetic Testing for hereditary Cancer risk: an underutilized tool for Cancer prevention, JCO Precis. Oncol. (2021) https://doi.org/10.1200/PO.21.00163.
[7] S. Hesse-Biber, M. Seven, H. Shea, M. Heaney, A.A. Dwyer, Racial and ethnic disparities in genomic healthcare utilization, patient activation, and Intrafamilial communication of risk among females tested for BRCA variants: a mixed methods study, Genes 14 (2023) 1450.
[8] N.M. Kassem, et al., Racial disparities in cascade testing for cancer predisposition genes, Prev. Med. 172 (2023), 107539.
[9] M.K. Frey, et al., Prospective feasibility trial of a novel strategy of facilitated Cascade genetic Testing using telephone counseling, J. Clin. Oncol. 38 (2020) 1389–1397.
[10] R.N. Wilke, et al., Cascade genetic testing: an underutilized pathway to equitable cancer care? Fam. Cancer (2024), https://doi.org/10.1007/s10689-024-00367-2.
[11] Chapter 1: Models and Frameworks | Principles of Community Engagement. ATSDR, 2018. https://www.atsdr.cdc.gov/communityengagement/pce_models.html.
[12] Glanz, K., Rimer, B. K. & Viswanath, K. Theory, Research, and Practice. n.d.
[13] J. Chiang, J. Ngeow, The management of BRCA1 and BRCA2 carriers in Singapore, Chin. Clin. Oncol. 9 (2020) 62.
[14] E.L. Silver, M. Niell-Swiller, Should all patients undergoing genetic testing for hereditary breast cancer syndromes be offered a multigene panel? Curr. Opin. Obstet. Gynecol. 34 (2022) 36.
[15] K. Agiannitopoulos, et al., Only 32.3% of breast cancer families with pathogenic variants in cancer genes utilized cascade genetic Testing, Cancers 15 (2023) 5218.
[16] K.R. Muessig, et al., Retrospective assessment of barriers and access to genetic services for hereditary cancer syndromes in an integrated health care delivery system, Hered. Cancer Clin. Pract. 20 (2022) 7.
[17] E.M. Bednar, C.C. Sun, S. McCurdy, S.W. Vernon, Assessing relatives' readiness for hereditary cancer cascade genetic testing, Genet. Med. 22 (2020) 719–726.
[18] H.W. Tuffaha, et al., Cost-effectiveness analysis of germ-line BRCA testing in women with breast cancer and cascade testing in family members of mutation carriers, Genet. Med. 20 (2018) 985–994.
[19] S.D. Grosse, When is genomic Testing cost-effective? Testing for lynch syndrome in patients with newly-diagnosed colorectal cancer and their relatives, Healthcare 3 (2015) 860.