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Identifying disparities in germline and somatic testing for ovarian cancer

Marilyn Huang [a,*], Priyanka Kamath [a], Matthew Schlumbrecht [a], Feng Miao [c], Devin Driscoll [d], Sean Oldak [d], Brian Slomovitz [a], Tulay Koru-Sengul [b], Sophia George [a]

[a] Division of Gynecologic Oncology, Department of Obstetrics & Gynecology, University of Miami School of Medicine, Sylvester Comprehensive Cancer Center, Miami, FL, United States of America
[b] Division of Biostatistics, Department of Public Health Sciences, University of Miami School of Medicine, Sylvester Comprehensive Cancer Center, Miami, FL, United States of America
[c] Sylvester Comprehensive Cancer Center, University of Miami Miller School of Medicine, Miami, FL, United States of America
[d] University of Miami Miller School of Medicine, Miami, FL, United States of America

HIGHLIGHTS

- Genetic testing in a large cohort of minority women did not demonstrate discrepancy in completion of genetic testing.
- Disparities exist between genetic and somatic testing.
- Further investigation into lack of testing in both genetic and somatic testing among ovarian cancer patients are essential.

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ABSTRACT

Objective. Germline mutations occur in approximately 25% of patients with epithelial ovarian cancers while somatic BRCA mutations are estimated at 5–7%. The objectives of this study were to determine the rate of germline and somatic testing in women with ovarian cancer and to identify disparities in testing at a comprehensive cancer center (CCC) and a safety net hospital (SNH).

Methods. Patients treated for ovarian cancer from 2011 to 2016 were included. Clinicopathologic data were abstracted from the electronic medical records. Logistic regression modeling were performed to calculate odds ratios (OR) and corresponding 95% confidence intervals (95%CI).

Results. Out of 367 women, 55.3% completed germline testing; 27.0% received somatic testing. Women at the CCC were more likely to be tested for germline (60.4% vs 38.1%, $p \le 0.001$) and somatic (34.3% vs 2.4%, $p \le 0.001$) mutations than those at the SNH. Patients with Medicare (aOR = 0.51, 95%CI 0.28–0.94, $p = 0.032$) or Medicaid (aOR = 0.42, 95%CI 0.18–0.99, $p = 0.048$) were less likely to receive germline testing than those privately insured. Patients with Medicaid were less likely to receive somatic testing (aOR = 0.15, 95%CI 0.04–0.62, $p = 0.009$) than those privately insured. Women with disease recurrence had a higher likelihood of being tested for germline (OR = 3.64, 95%CI 1.94–6.83, $P < 0.001$) and somatic (OR = 7.89, 95%CI 3.41–18.23, $p < 0.001$) mutations. There was no difference in germline or somatic testing by race/ethnicity.

Conclusions. Disparities in both germline and somatic testing exist. Understanding and overcoming barriers to testing may improve cancer-related mortality by allowing for more tailored treatments as well as for improved cascade testing.

1. Background

In the United States, ovarian cancer is the leading cause of death for women with 14,070 deaths in 2018 [1,2]. To date, there are no effective screening methods, with the majority of patients diagnosed at an advanced stage and eventually dying of disease. Identifying mutations in cancer susceptibility genes can influence therapeutic and preventative recommendations in women with ovarian cancer. Inherited germline mutations in *BRCA1* and *BRCA2* mutations account for approximately 17–18%, while other mutations in the homologous recombination (HR) pathway make up the remaining 7–8% [3,4]. Current consensus guidelines published by the National Comprehensive Cancer Network (NCCN), American College of Obstetricians and Gynecologists (AGOG), Society for Gynecologic Oncology (SGO), and American Society of Clinical Oncology (ASCO) all endorse germline testing for women diagnosed with non-mucinous epithelial ovarian cancer [5–7]. Multi-gene panels can identify mutations in not only *BRCA1* and *BRCA2*, but also other

* Corresponding author at: Division of Gynecologic Oncology, Department of Obstetrics & Gynecology, Sylvester Comprehensive Cancer Center, University of Miami School of Medicine, 1121 NW 14th St, Room 345E, Miami, FL 33136, United States of America.
E-mail address: m.huang@med.miami.edu (M. Huang).

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cancer susceptibility genes (*RAD51C/D, PALB2, BRIP1*, and Lynch syndrome genes) that are associated with at least a moderate risk for developing ovarian cancer. Guidelines also recommend for consideration of risk-reducing surgery in women carrying these pathogenic mutations [5].

Somatic mutations are acquired genetic aberrations for which the prevalence in ovarian cancer has not been well characterized, but is estimated at 5–7% [8–14]. Somatic molecular testing with next generation sequencing can identify patients with HR deficiency and other mutations, for which targeted, personalized therapies such as poly ADP ribose polymerase [PARP] inhibitors are now available [13,14]. For women with recurrent ovarian cancer, 2018 NCCN guidelines now suggest molecular testing on the most recent available tumor specimen prior to initiation of therapy [15].

Despite strong recommendations from national professional societies, uptake for genetic testing remains low at approximately 20–30% [11,12,16,17]. In a recent SGO White paper, authors identified multiple obstacles to genetic testing and broadly grouped factors into four primary categories: provider-mediated, payor-associated, system-associated, and patient-associated [12]. Substantiating the White paper, pooled cross-sectional data from three Cancer Control Modules of the National Health Interview Survey among women with a history of ovarian cancer demonstrated only 10.5% of women underwent testing [18]. Furthermore, another study demonstrated women of color and those with public insurance had lower referral rates for genetic testing [19]. Identifying women at risk for developing ovarian cancer due to a heritable cause is currently the only successful method for cancer prevention and is a health disparity. Differences in genetic testing, particularly among minority populations, as well as in acquisition of somatic testing, are not well described in the literature. Our university-based health system is comprised of both a comprehensive cancer center (CCC) and a safety net hospital (SNH). Across both hospitals, 67% of the patient population is self-identified ethnic or racial minorities. The objectives of this study were to (1) determine rate of germline and somatic tumor testing and (2) to identify disparities in either germline and/or somatic testing in women diagnosed with ovarian cancer, with specific consideration for differences between institutions.

2. Methods

All patients treated for a diagnosis of non-mucinous epithelial ovarian, fallopian tube, or primary peritoneal cancer from January 1, 2011 to December 31, 2016 were identified through the tumor registry at the University of Miami Hospitals. We excluded patients with incomplete treatment histories (largely comprised of patients presenting for a second opinion consultation and returning to their treating oncologist for further treatment). Abstracted data from the electronic medical record (EMR) included age of diagnosis, race/ethnicity, medical history, stage at diagnosis, histology, cancer treatment histories, recurrence status, genetic counseling, genetic testing results, and molecular tumor profiling results. Molecular tumor testing was defined as next generation sequencing performed by either Caris Molecular Intelligence or Foundation Medicine. Patients with only immunohistochemistry analysis of mismatch repair proteins, microsatellite instability analysis, or homologous recombination deficiency analysis were excluded from the somatic testing cohort. Tumor tissue submitted for somatic testing could be from original surgical specimen or from a biopsy after recurrence. We acknowledged that genetic counseling had been performed if this was explicitly documented in the patient's chart by the treating oncologist or genetic counselor. Patient race and ethnicity were classified as either non-Hispanic White, Hispanic White, Black and other/unknown. Stage at diagnosis was classified as early (Stage I-II) or advanced (Stage III-IV). Recurrence was confirmed by either provider documentation or imaging documentation.

Clinical data was summarized by mean, standard deviation, and median values for continuous variables and by frequencies and percentages for categorical variables. Differences in proportions were tested by chi-square or Fisher's exact test for categorical variables. To account for national guideline updates in mid-2014 recommending germline testing in all women diagnosed with epithelial ovarian cancer, patients were grouped based on the date of diagnosis: prior to 2015 or after 2015. Multivariable logistic regression modeling approach was performed surrounding two different clinical scenarios: the performance of germline testing, and the performance of somatic testing. Adjusted odds ratios (aOR) with 95% confidence interval (95%CI) and *p*-values were calculated. Type-I error rate was set to 5%, where p-values<0.05 were considered statistically significant. Statistical analyses were performed with SAS v9.4 (SAS Institute Inc., Cary, NC, USA). Institutional review board approval was obtained at both the CCC and the SNH.

3. Results

We identified 504 women diagnosed and treated for ovarian cancer between January 1, 2011 and December 31, 2016 of which 367 patients met inclusion criteria. The demographic, clinical, and treatment characteristics of the study population are summarized in Table 1.1 The study population consisted of 45.2% Hispanic women, 39.2% non-Hispanic White women, 10.9% non-Hispanic Black women, and 4.6% unknown. The median age at diagnosis of all women was 59 years. The majority of women (283, 77.1%) were treated at the CCC while 84 (22.9%) were treated at the SNH. Most women were diagnosed with high grade serous histology (78.2%) and were stage III or IV at the time of diagnosis (76%). At the time of data abstraction, 35.4% of women were receiving or had completed their first line of treatment while the remaining 64.6% had received two or more lines of treatment. Table 1.2 suggests that there are significant relationships between medical treating center and patient's characteristics such as age ($p = 0.007$), race/ethnicity ($p < 0.001$), insurance type ($p < 0.001$), family ($p < 0.001$) or personal ($p = 0.006$) history of cancers, year of diagnoses ($p < 0.001$), lines of treatment ($p < 0.001$), type of patient ($p < 0.001$) or counseling performed ($p < 0.001$).

Of the entire cohort, 224 (61%) received genetic counseling either by genetic counselor or provider and 55.3% of women underwent germline testing. Table 2 summarizes patient characteristics by germline testing. Women treated at the CCC were significantly more likely to receive germline testing than those treated at the SNH (60.4% vs 38.1%, $p \leq 0.001$). Only 40% of non-Hispanic Black women underwent germline testing compared to 56.6% of Hispanic women and 59.7% of non-Hispanic White women ($p = 0.093$). Patients with private insurance (68.1%) more frequently underwent germline testing compared to those with Medicare (48.5%),Medicaid (36.7%), uninsured (35%) or self-pay (25%) patients (65.7% vs. 45.1%, $p < 0.001$). As expected, germline testing was performed more frequently in patients with a family history of cancer (63.2% vs 42.5% $p < 0.001$) or a personal history of another primary cancer (75.4% vs 51.6%, $p < 0.001$). Testing rates were significantly higher in patients who had received multiple lines of treatment compared to those who had received just one line of treatment ($p = 0.004$). Significantly more women in 2015 or later completed germline testing ($p < 0.001$).

Approximately a quarter (27%) of the women had molecular tumor (somatic) testing performed. Table 3 summarizes patient characteristics by somatic testing. A significantly higher proportion of women at the CCC had somatic testing than those treated at the SNH (34.3% vs 2.4%, $p < 0.001$). Privately insured patients (39%) were significantly more likely to receive somatic testing compared to Medicare (25.7%), Medicaid (3.3%), or uninsured patients ($p < 0.001$). Multiple prior lines of therapy corresponded to higher likelihood of somatic testing when compared to one prior line ($p < 0.001$). Similarly, patients presenting for a second opinion were more likely to undergo somatic testing when compared to patients who initiated care at the university health system ($p < 0.001$). There was no difference in somatic testing based

Table 1.1
Demographics and clinical characteristics.

	All patients	
	N	Col%
All	367	100.00
Age		
<65	253	68.94
≥65	114	31.06
Median (min, max)	59 (18, 91)	
Race/ethnicity		
Black	40	10.90
HW	166	45.23
NHW	144	39.24
Other/unknown	17	4.63
Treating medical center		
CCC	283	77.11
SNH	84	22.89
Insurance type		
Medicaid	60	16.35
Medicare	101	27.52
Private	182	49.59
Self-pay	4	1.09
Uninsured	20	5.45
Family history of cancers		
No	139	37.87
Yes	228	62.13
Personal history of cancers		
No	310	84.47
Yes	57	15.53
Year of diagnoses		
2015 and after	108	29.43
Before 2015	259	70.57
Lines of treatment		
1	130	35.42
2	80	21.80
>2	157	42.78
Histology		
Serous high grade	287	78.20
Serous low grade	31	8.45
Endometrioid	14	3.81
Clear cell	8	2.18
Carcinosarcoma	11	3.00
Mixed	14	3.81
Small cell	1	0.27
Transitional (malignant)	1	0.27
FIGO stage		
Low (I-II)	54	14.71
High (III-IV)	279	76.02
Unknown	34	9.26
Type of patient		
Full care	140	38.15
Second opinion	227	61.85
Counseling performed		
No	143	38.96
Yes	224	61.04

Table 1.2
Demographics and clinical characteristics by treating medical center.

	Treating medical center				
	CCC		SNH		
	N	Row%	N	Row%	p-Value
All	283	77.11	84	22.89	
Age					
<65	185	73.12	68	26.88	0.007
≥65	98	85.96	16	14.04	
Median (min, max)	60 (18, 91)		58.5 (21, 84)		
Race/ethnicity					
Black	21	52.50	19	47.50	<0.001
HW	116	69.88	50	30.12	
NHW	134	93.06	10	6.94	
Other/unknown	12	70.59	5	29.41	
Insurance type					
Medicaid	17	28.33	43	71.67	<0.001
Medicare	90	89.11	11	10.89	
Private	172	94.51	10	5.49	
Self-pay	4	100.00	–	–	
Uninsured	–	–	20	100.00	
Family history of cancers					
No	91	65.47	48	34.53	<0.001
Yes	192	84.21	36	15.79	
Personal history of cancers					
No	231	74.52	79	25.48	0.006
Yes	52	91.23	5	8.77	
Year of diagnoses					
2015 and after	71	65.74	37	34.26	<0.001
Before 2015	212	81.85	47	18.15	
Lines of treatment					
1	82	63.08	48	36.92	<0.001
2	60	75.00	20	25.00	
>2	141	89.81	16	10.19	
FIGO stage					
Low (I-II)	43	79.63	11	20.37	0.802
High (III-IV)	215	77.06	64	22.94	
Unknown	25	73.53	9	26.47	
Type of patient					
Full care	88	62.86	52	37.14	<0.001
Second opinion	195	85.90	32	14.10	
Counseling performed					
No	95	66.43	48	33.57	<0.001
Yes	188	83.93	36	16.07	

on age, race/ethnicity, family history of cancer, personal history of cancer, and stage at diagnosis.

In multivariable logistic regression analysis, only insurance status, number of prior therapies, family history of cancer, and personal history of cancer remained significant factors for receiving germline testing (Fig. 1). Patients with Medicare (aOR = 0.51, 95%CI 0.28–0.94, $p = 0.032$) or Medicaid (aOR =0.42, 95% CI 0.18–0.99, $p = 0.48$ were less likely to receive germline testing those privately insured. Patients with a personal (aOR = 2.33, 95%CI 1.14–4.77, $p = 0.021$) or family history of cancer (aOR = 1.80, 95%CI 1.09–2.95, $p = 0.021$) were more likely to have germline testing performed. Patients diagnosed in 2015 or later were more likely to have genetic testing performed compared to patients diagnosed prior to 2015 (aOR = 4.69, 95%CI 2.49–8.83, $p < 0.001$). Patients who had received three or more lines of therapy were also more likely to have genetic testing compared to patients with only one prior line of therapy (aOR = 3.64, 95%CI 1.94–6.83, $p < 0.001$).

Multivariable logistic regression analysis for somatic testing (Fig. 2) also showed that patients with Medicaid were much less likely to undergo testing than patients with private insurance (aOR = 0.15, 95%CI 0.04–0.62, $p = 0.009$). Patients treated at the CCC were significantly more likely to have molecular testing performed to guide treatment planning than patients treated at the SNH (aOR 5.78, 95%CI 1.35–24.76, $p = 0.018$). Patients diagnosed in 2015 or later were more likely to have somatic testing performed than patients diagnosed prior to 2015 (aOR = 2.75, 95%CI 1.32–5.74, $p = 0.007$). The rate of tumor testing also increased significantly at the time of first recurrence (aOR = 4.82, 95%CI 2.00–11.63, $p < 0.001$) and after three or more lines of therapy (aOR = 7.89, 95%CI 3.41–18.23, $p < 0.001$). Somatic testing was also noted to be more common in patients presenting for a second opinion compared to those who had received full care within our health system (aOR = 2.18, 95%CI 1.15–4.13, $p = 0.016$).

4. Discussion

Germline mutations are common in ovarian cancers but current literature suggests only about a third are receiving genetic testing [12,17]. Identification of hereditary cancer susceptibility genes assists clinicians in prioritizing therapeutic options, carry prognostic implications, and play a paramount role for cancer prevention through cascade testing [20–23]. Somatic tumor testing may provide further guidance in selecting subsequent therapies, such as with PARP inhibitors based on FDA approvals the first of which occurred in 2014 with subsequent

Table 2
Population characteristics and completion of germline testing.

	Germline testing performed				
	No		Yes		
	N	Row%	N	Row%	p-Value
All	164	44.69	203	55.31	
Age					
<65	107	42.29	146	57.71	0.169
≥65	57	50.00	57	50.00	
Median (min, max)	60 (24, 87)		58 (18, 91)		
Race/ethnicity					
Black	24	60.00	16	40.00	0.093
HW	72	43.37	94	56.63	
NHW	58	40.28	86	59.72	
Other/unknown	10	58.82	7	41.18	
Treating medical center					
CCC	112	39.58	171	60.42	<0.001
SNH	52	61.90	32	38.10	
Insurance type					
Medicaid	38	63.33	22	36.67	<0.001
Medicare	52	51.49	49	48.51	
Private	58	31.87	124	68.13	
Self-pay	3	75.00	1	25.00	
Uninsured	13	65.00	7	35.00	
Family history of cancers					
No	80	57.55	59	42.45	<0.001
Yes	84	36.84	144	63.16	
Personal history of cancers					
No	150	48.39	160	51.61	<0.001
Yes	14	24.56	43	75.44	
Year of diagnoses					
2015 and after	30	27.78	78	72.22	<0.001
Before 2015	134	51.74	125	48.26	
Lines of treatment					
1	72	55.38	58	44.62	0.004
2	36	45.00	44	55.00	
>2	56	35.67	101	64.33	
FIGO stage					
Low (I-II)	25	46.30	29	53.70	0.095
High (III-IV)	118	42.29	161	57.71	
Unknown	21	61.76	13	38.24	
Type of patient					
Full care	63	45.00	77	55.00	0.924
Second opinion	101	44.49	126	55.51	
Counseling performed					
No	131	91.61	12	8.39	<0.001
Yes	33	14.73	191	85.27	

Table 3
Population characteristics and completion of somatic testing.

	Somatic testing performed				
	No		Yes		
	N	Row%	N	Row%	p-Value
All	268	73.02	99	26.98	
Age					
<65	186	73.52	67	26.48	0.751
≥65	82	71.93	32	28.07	
Median (min, max)	59 (21, 91)		60 (18, 82)		
Race/ethnicity					
Black	29	72.50	11	27.50	0.425
HW	126	75.90	40	24.10	
NHW	99	68.75	45	31.25	
Other/unknown	14	82.35	3	17.65	
Treating medical center					
CCC	186	65.72	97	34.28	<0.001
SNH	82	97.62	2	2.38	
Insurance type					
Medicaid	58	96.67	2	3.33	<0.001
Medicare	75	74.26	26	25.74	
Private	111	60.99	71	39.01	
Self-pay	4	100.00	–	–	
Uninsured	20	100.00	–	–	
Family history of cancers					
No	107	76.98	32	23.02	0.183
Yes	161	70.61	67	29.39	
Personal history of cancers					
No	229	73.87	81	26.13	0.394
Yes	39	68.42	18	31.58	
Year of diagnoses					
2015 and after	78	72.22	30	27.78	0.823
Before 2015	190	73.36	69	26.64	
Lines of treatment					
1	118	90.77	12	9.23	<0.001
2	55	68.75	25	31.25	
>2	95	60.51	62	39.49	
FIGO stage					
Low (I-II)	43	79.63	11	20.37	0.287
High (III-IV)	198	70.97	81	29.03	
Unknown	27	79.41	7	20.59	
Type of patient					
Full care	118	84.29	22	15.71	<0.001
Second opinion	150	66.08	77	33.92	

approval of two additional PARP inhibitors in 2016 for recurrent ovarian cancer [24–27]. Furthermore, maintenance olaparib following platinum-based chemotherapy in newly diagnosed ovarian cancer patients with germline *BRCA1/2* mutations provided a substantial benefit in progression free survival [28]. Minority and underserved populations are at substantial risk for further divide in health equity if obstacles are not identified and addressed.

There are few studies examining the prevalence of *BRCA1/2* mutations in non-White high risk women referred for genetic testing. In one data repository study, reported rates were 14.5% Latin American, 15.6% African, 12.7% Asian and 13.2% Native American [29]. Among breast cancer patients, multiple studies have demonstrated that Black women are less likely to undergo genetic testing compared to White women [30]. In contrast, there is much less published literature regarding disparities in genetic testing among ovarian cancer patients. In Ontario, through the Ministry of Health, genetic testing is available to all women with invasive ovarian cancer; however, only 19% of eligible women completed testing [16]. Other studies have reported similar rates of genetic testing among ovarian cancer patients (10.5–33%) [16–18]. Furthermore, Black women with ovarian cancer were less likely to be referred for genetic counseling compared to White or Hispanic women [11]. These findings are consistent with prior studies demonstrating unequal cancer care delivery by race and socioeconomic status [31,32].

In our study, 224 (61%) of women received genetic counseling and germline testing was completed in 191 (85.3%) patients, which is higher than previously reported data. While there was a trend towards lower frequency of genetic testing among Black women, this was not statistically significant ($p = 0.212$). Interestingly, in our cohort comprised of nearly 50% Hispanic women, there was no difference in completion of genetic testing compared to Non-Hispanic White women. This differs from a prior study by Manriquez et al., who reported a genetic testing rate of 33% with rates differing by race, English language, and private or Medicare insurance being associated with completion of testing [19]. A potential discrepancy between the studies is the patient population, with 45.2% Hispanic White and 10.9% Black in our cohort compared to a largely non-Hispanic White (57.7%) group with only 14% Hispanic and 4% Black in the Manriquez et al. study. Our study is one of the largest to date reporting on rate of genetic testing among Hispanic women with ovarian cancer and demonstrates no discrepancy in completion of genetic testing.

We also found that privately insured patients were significantly more likely to complete genetic testing and there was greater adherence to completing genetic testing among women with a personal history of cancer, having a family history of cancer, and having received at least three prior lines of therapy. The rapidly evolving technology incorporating multigene panels and next generation sequencing modalities as well as the development of targeted therapies for germline mutation carriers have contributed to improved testing rates. Our improved testing rates based on personal cancer history and increasing

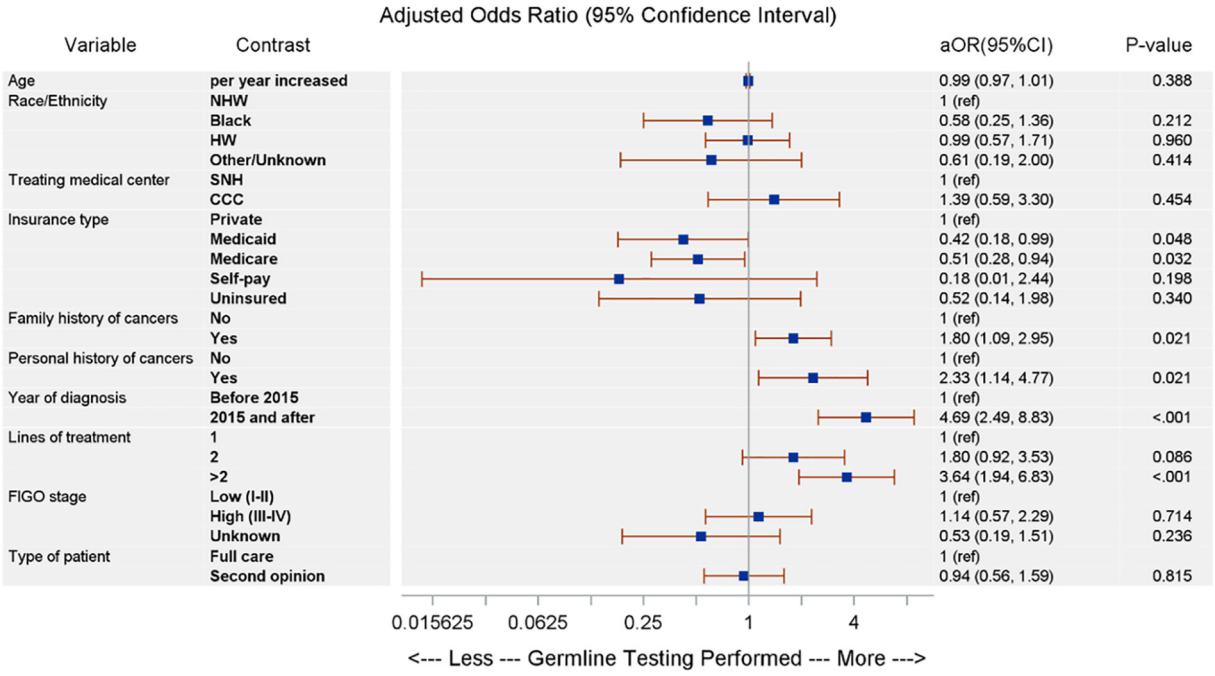

Fig. 1. Logistic regression: the probability of germline testing performed.

prior lines of therapy are likely a reflection of temporal bias as well as the advancing field of precision medicine with the FDA approval of three PARP inhibitors. This may further highlight disparate care as cancer prevention and improved treatment options become standard.

Reported barriers to testing include the lack of awareness of testing, lack of recognition of risk (partly due to incomplete family history), lack of provider recommendation for testing, and lack of support for obtaining counseling and testing, particularly in resource-limited settings [33–35]. In our cohort, increased rates of genetic testing may be a reflection of improved access to health information by way of technology (internet) bridging gaps in knowledge for both patients and family members. The internet has also increased access for providers with up to date guidelines and resources readily available. Not uncommonly, patients are overwhelmed at the time of initial diagnosis and this may account for some delay in germline testing. Our results suggests that the importance for germline testing was progressively recognized by providers since NCCN guideline updates in 2015 as well as prioritizing for somatic testing after recurrence.

There are additional missed opportunities to perform germline testing at the time of diagnosis. Potential impedance to genetic counseling referrals may be due to the limited number of available appointments with counselors due to national shortage, multiple appointments to receive multi-modality therapy (surgery and chemotherapy) coupled with emotional, physical, and financial strain, and lack of prioritization

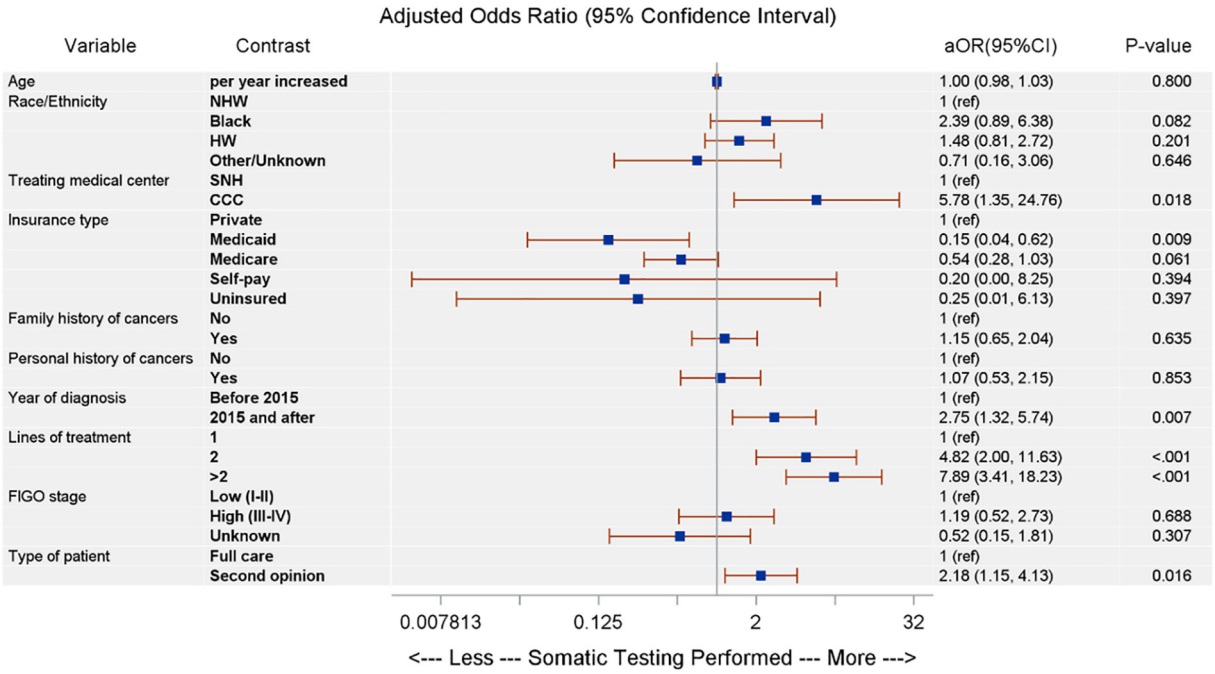

Fig. 2. Logistic regression: the probability of somatic testing performed.

by providers [36]. In our population, genetic testing was completed by 60% of patients at the CCC while only by 40% at the SNH. This difference is largely due to the implementation of genetic counseling and testing within the gynecologic oncology clinics at the CCC in mid-2015 due to shortage of genetic counselors, with referral to genetic counselors with positive test results. Identified barriers at the SNH include limited resources in terms of scheduling appointments, availability of appointments (frequently scheduling 6–8 months out), insurance coverage, need for separate appointment, overall lengthy process, and ill-defined cultural barriers. A potential consideration to improve germline testing in the SNH is to offer germline testing in the gynecologic oncology clinic, thereby eliminating scheduling challenges. The ENGAGE study recently demonstrated an oncologist-led testing strategy that shortened turnaround times and was highly accepted among patients and providers [37]. This is similar to the approach utilized by our practice due to limitation of genetic counseling appointments at the CCC. However, so far, oncologist-led testing has not been feasible at the SNH due to lack of testing coverage despite expanded insurance programs, more competitive pricing, and the development of free testing initiatives. Efforts to assist patients in low resource hospital systems, such as with navigator programs, are effective yet costly and unsustainable, highlighting need for alternative strategies [38,39].

There have been very few studies investigating the rate of somatic testing or disparities in testing. Yusuf et al. examined attitudes towards somatic testing in women with breast cancer, noting that even when testing was financially covered, non-White participants were less willing to undergo molecular testing to guide therapy. Reasons for their reluctance to testing were not clearly defined. However, the authors did highlight that income and education levels were not statistically associated with willingness to undergo testing [40]. Our overall rate of somatic testing was 27.1% but was performed significantly more for patients treated at the CCC with private insurance. In March 2018, the Centers for Medicaid and Medicare Services (CMS) approved coverage for all FDA approved tumor next-generation sequencing tests. Our patients more frequently had somatic testing performed corresponding to multiple prior lines of therapy, suggesting that testing was performed later to guide subsequent treatment in the course of disease. Furthermore, FDA approval of PARP inhibitors also likely contributed to the increase in rate of somatic testing during the study timeframe. Discrepancies in molecular tumor testing were multi-factorial in our population, though primarily driven by lack of insurance coverage, particularly at the SNH. Another important consideration is that during the study period, next generation sequencing with commercial platforms were still being introduced. As such, somatic testing through Caris Life Sciences for our uninsured and Medicaid patients was possible, but likely minimizes differences between CCC and SNH. Since the end of the study period, somatic testing is no longer available for uninsured patients at SNH. Somatic testing is not a surrogate for germline testing, but rather a tool to further guide treatment strategies. As somatic testing improves with shorter turnaround times, real-time decision-making regarding treatment selection may be possible in the future.

There are several strengths of this study. Our university medical campus with both a CCC and a county SNH provided a distinct opportunity to effectively evaluate for the presence of disparities in genetic and somatic molecular testing. The patient population was cared for by the same group of gynecologic oncologists, limiting substantial practice pattern variation that may impact survival outcomes. Unlike other disparity studies in ovarian cancer, our population is diverse with considerable minority representation. To our knowledge, this is the first study to investigate disparities in somatic molecular testing and one of a few studies investigating disparities in genetic testing in a diverse population with ovarian cancer.

The retrospective nature of this study confers limitations. The electronic medical record system is different between CCC and SNH such that data abstraction may be inaccurate with a degree of information bias. For example, genetic testing results at the CCC were delivered directly to the ordering physician, whereas at the SNH, results were delivered to the genetic counselor's clinic. As a referral center, many patients presented as second opinion for cancer care, possibly with testing performed elsewhere. There is also a subset of women who were referred for germline testing but did not complete the visit for various reasons. We were also unable to subclassify race and ethnicity which may have revealed discrepancies in testing between certain groups, such as English/Creole speaking Afro-Caribbean and Hispanic Black. Additional variables that may have been significant but not analyzed in our cohort were socioeconomic status, preferred language, and educational status.

Improving genetic testing to identify hereditable causes for cascade testing is the only effective strategy to prevent ovarian cancer. As the era of targeted therapy escalates the need for universal testing in all women with non-mucinous epithelial ovarian cancer is paramount. Identifying existing disparities to genetic and somatic testing is essential to develop effective strategies to foster equitable access. Routine utilization of combined testing platforms will allow for faster, more tailored therapy to improve outcomes in ovarian cancer patients. Future directions in our program will be aimed at improving genetic testing at time of diagnosis and to increase cascade testing in affected families. Additionally, quality initiative approaches to expand both genetic and somatic testing rates at the county SNH are being planned.

Conflict of interest statement

All authors note that they have no conflicts of interest.

Author contribution section

Priyanka Kamath – data collection, data interpretation, manuscript writing.

Sophia George – data collection, data interpretation, manuscript writing, critique of manuscript, final approval of manuscript.

Matthew Schlumbrecht – critique of manuscript, final approval of manuscript.

Feng Miao – data analysis, manuscript writing, final approval of manuscript.

Devin Driscoll – data collection, final approval of manuscript.

Sean Oldak – data collection, final approval of manuscript.

Brian Slomovitz – critique of manuscript, final approval of manuscript.

Tulay Koru-Sengul—data analysis, manuscript writing, final approval of manuscript.

Marilyn Huang – concept and design of the study, data interpretation, manuscript writing, manuscript critique, final approval of manuscript.

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