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Observational Study

Germline mutations in Thai patients with nonmucinous epithelial ovarian cancer

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Abstract

BACKGROUND

Genetic testing is widely recommended for all epithelial ovarian cancer (EOC) patients. However, an increased probability of identifying germline mutations has been reported in selected patients with risk factors such as a family history or personal history of cancer and high-grade serous carcinoma (HGSC) subtype. HGSC has been reported to be the most common subtype of EOC worldwide (approximately 70%). However, this subtype is less prevalent in Thai patients (reported as only 20%). The difference in the distribution of various subtypes of EOC may reflect the incidence of germline mutations in Thai EOC patients.

AIM

To evaluate the frequencies of germline mutations in EOC patients and to compare the frequencies in those with and without clinical risk factors for hereditary ovarian cancer.

METHODS

This cross-sectional study included 112 nonmucinous EOC patients who underwent primary surgery at our tertiary care hospital. Clinical risk factors for hereditary ovarian cancer were defined as follows: Age below 40 years, a significant family history of cancer, synchronous ovarian and endometrial cancer, and HGSC. Comprehensive germline mutations were detected by next-generation sequencing.

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RESULTS

Of a total of 112 patients, 82 (73.2%) patients had ≥ 1 risk factor and 30 (26.8%) patients had no risk factors. Germline mutations were detected in 26 patients: 20 (17.8%) patients had *BRCA1/2* mutations, but 6 (5.4%) patients had mutations in other genes, including 1 in *MLH1*, 1 in *MSH2*, 1 in *RAD51C*, 2 in *ATM* and 1 in *CDH1*. Germline mutations were only detected in patients with risk factors (26 of 82, 31.7%), not in patients without risk factors ($P < 0.001$). A significant family history of cancer and HGSC were the only two significant risk factors associated with a higher proportion of germline mutations (56.3% *vs* 10% for those with and without a history of cancer, respectively, 40.8% *vs* 9.5% for those with and without HGSC). Germline *BRCA* mutations were detected in 38.8% of patients with HGSC but in only 1.6% of those with non-HGSC. An age below 40 years, personal history of breast cancer, and synchronous ovarian and endometrial cancer were not significant factors (14.3% *vs* 23.5%, 33.3% *vs* 21%, 22.2% *vs* 22.3%).

CONCLUSION

Approximately one-third of EOC patients with risk factors had germline mutations. Almost all germline *BRCA* mutations were found in patients with the HGSC subtype. Selected patients with HGSC and a family history of cancer should be initially considered for genetic analysis in Thailand.

Key words: *BRCA* mutation; Epithelial ovarian cancer; Germline mutation; Thai

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Core tip: Germline mutations could not be detected in any epithelial ovarian cancer patients without risk factors such as age below 40 years, significant family or personal history of cancer, and high-grade serous subtype. Mutations were detected in approximately one-third of patients with these risk factors: 25% had *BRCA1/2* mutations, 5% had mutations in other homologous recombination genes, and 2.5% had *MMR* mutations. Significantly more germline mutations were found in patients with a family history of cancer, especially ovarian cancer. Germline *BRCA* mutations were detected in 38.8% of patients with the high-grade serous subtype but in only 1.6% of those with a non-high-grade serous subtype. Selected patients with the high-grade serous subtype or a significant family history of cancer should initially be considered for genetic analysis in limited resource settings.

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INTRODUCTION

Although most epithelial ovarian cancers (EOCs) are sporadic, at least 10% of EOC patients have a genetic predisposition^[1]. Risk assessment has been previously used to identify patients at risk for hereditary ovarian cancers and to offer genetic counseling and testing. These risk factors are as follows: Early age of onset, personal history of breast cancer, family history of breast, ovarian cancer, endometrial and colon cancer, and specific histologic subtype such as high-grade serous carcinoma (HGSC)^[2]. HGSC has been reported to increase the risk of germline mutations. It has also been reported that approximately 20% of HGSCs harbor *BRCA* mutations^[3]. Recently, the recommendation for genetic testing in EOC patients has changed. Various national professional societies such as the American College of Obstetricians and Gynecologists, the Society of Gynecologic Oncologists, and the National Comprehensive Cancer Network have recommended offering genetic counseling and testing for all women with EOC including fallopian tube cancers and primary peritoneal cancers irrespective of risk factors^[4,5]. Firstly, some patients with germline

mutations will be missed if the testing is based on these current risk factors. Secondly, genetic results can predict treatment outcomes. Patients with *BRCA*-mutated EOC have increased platinum sensitivity response rates and significant improvement in survival rate compared with those with non-*BRCA*-mutated EOC^[6]. Thirdly, novel targeted therapy with Poly (ADP-ribose) polymerase inhibitors has been reported to be a promising targeted therapy for *BRCA*-mutated cancers including homologous recombination (HR) gene-deficient ovarian cancers^[7].

The frequency of germline mutations varies across different countries and ethnicities. The incidence of *BRCA* mutations has been reported to range from 5.8%-24.8%^[8]. Our previous study reported that 11.4% of patients with nonmucinous EOC had *BRCA* mutations^[9]. However, that study included a small number of patients, and the mutations were reported only in selected patients with risk factors for hereditary ovarian cancers such as a family history or personal history of cancer and HGSC. Therefore, the incidence of *BRCA* mutations in unselected EOC patients could be even lower than this number. The incidence of HGSC is a major predictive variable. Although it has been reported as the most common subtype worldwide at approximately 70%^[3], only 20% of Thai patients have serous carcinoma^[9,10]. The difference in the distribution of various subtypes of EOC between Thai patients and others worldwide may reflect the lower incidence of germline mutations in Thai EOC patients. The objective of this study is to evaluate the frequency of germline mutations in EOC patients and to compare the frequency in those with and without clinical risk factors for hereditary ovarian cancer.

MATERIALS AND METHODS

Ethic statements

This study was approved by the Institutional Review Board, Faculty of Medicine, Chulalongkorn University. This was a cross-sectional study conducted between November 2015 and February 2018.

Patients

Patients with EOC, fallopian tube or primary peritoneal cancer who underwent primary surgery and had a pathologically confirmed nonmucinous subtype were enrolled. Clinical risk factors for hereditary ovarian cancer are defined as follows: (1) Age at diagnosis below 40 years; (2) Significant family history (≥ 1 relative with ovarian cancer at any age, ≥ 1 relative with breast cancer or hereditary nonpolyposis colorectal cancer (HNPCC)-associated cancers such as colon cancer or endometrial cancer diagnosed before 50 years of age, ≥ 2 relatives with breast cancer or HNPCC-associated cancers diagnosed after 50 years of age; (3) Previous diagnosis of breast cancer; (4) Synchronous ovarian cancer and endometrial cancer; and (5) HGSC^[9]. All patients who agreed to participate in this study received genetic counseling by a geneticist and provided informed consent.

Germline mutation analysis

Comprehensive germline mutation analysis was performed using peripheral blood DNA samples analyzed by a GeneRead DNaseq Mix-n-Match Panel v2 (27-gene panel including *APC*, *ATM*, *AXIN2*, *BARD1*, *BMP1A*, *BRCA1*, *BRCA2*, *BRIP1*, *CDH1*, *CHEK2*, *EPCAM*, *MLH1*, *MLH3*, *MRE11*, *MSH2*, *MSH6*, *MUTYH*, *NBN*, *PALB2*, *PMS2*, *PTEN*, *RAD50*, *RAD51C*, *RAD51D*, *SMAD4*, *STK11*, and *TP53*) (Qiagen) and next-generation sequencing (NGS) (The Illumina MiSeq System; Illumina, San Diego, CA, United States). DNA was extracted from the patients' peripheral blood using a QIAamp DNA Blood Mini Kit. DNA quality was assessed using GeneRead DNA QuantiMIZE Kits according to the manufacturer's instructions (Qiagen, Germany). DNA library preparation and NGS were performed as previously described^[9]. Variant pathogenicity was classified based on the American College of Medical Genetics and Genomics and the American Society of Molecular Pathology standard and guidelines for the interpretation of sequence variants^[11]. Variant classification was listed as "Pathogenic", "Likely pathogenic", "Variant of Uncertain Clinical Significance", "Likely benign" or "Benign" in decreasing order of clinical importance. The pathogenic and likely pathogenic variants found in this study were confirmed using bi-directional Sanger sequencing.

Statistical analysis

SPSS version 22 (SPSS Inc., Chicago, IL, United States) was used for the statistical analysis. Comparisons of the proportions of germline mutations between two groups were analyzed by Chi-square or Fisher's Exact test. *P* values less than 0.05 were considered statistically significant.

RESULTS

Patient characteristics

Of the 112 patients, 97 were diagnosed with EOC, 4 with fallopian tube cancer, 2 with primary peritoneal cancer, and 9 with synchronous endometrial and ovarian cancer. The mean age was 52.8 ± 11.0 years. Patient characteristics are shown in Table 1. Eighty-two patients (73.2%) had at least one clinical risk factor, and 27 patients (24.1%) had more than one risk factor. Of the 82 patients, EOC was diagnosed in 67 patients (81.7%), fallopian tube cancer in 4 patients (4.9%), primary peritoneal cancer in 2 patients (2.4%), and synchronous endometrial and ovarian cancer in 9 patients (11.0%). The histologic subtypes in these patients were HGSC in 49 patients (59.8%), low-grade serous carcinoma in 4 patients (4.9%), endometrioid carcinoma in 15 patients (18.3%), clear cell carcinoma in 12 patients (14.6%), mixed endometrioid and clear cell carcinoma in 1 patient (1.2%), and adenocarcinoma in 1 patient (1.2%). Thirty patients (26.8%) had no clinical risk factors of hereditary ovarian cancer, all of whom were diagnosed with EOC. The histologic subtypes in these patients were endometrioid carcinoma in 13 patients (43.3%), clear cell carcinoma in 12 patients (40%), mixed endometrioid and clear cell carcinoma in 3 patients (10%) and low-grade serous carcinoma in 2 patients (6.7%).

Germline mutation analysis

Germline mutations were detected in 26 patients (23.2%), whereas 20 patients (17.8%) had *BRCA1* or *BRCA2* mutations, and 6 patients (5.4%) had mutations in other genes (Table 2). Germline mutations could not be detected in any of the 30 patients without risk factors. In contrast, all mutations were detected in 26 of 82 patients with ≥ 1 risk factor (31.7%, $P < 0.001$). The frequency of germline mutations according to various risk factors is shown in Table 3. Significantly more germline mutations were observed in patients with a significant family history of cancer compared with patients without a significant family history (56.3% and 10% for with and without a history of cancer, respectively, $P < 0.001$). Fourteen of 32 patients who had a family history of cancer had *BRCA* mutations (43.7%) and 3 patients (9.4%) had other gene mutations. In contrast, 6/80 (7.5%) patients without a family history of cancers had *BRCA* mutations and 2/80 (2.5%) had other gene mutations (1 *ATM* and 1 *CDH1*). Significantly higher frequencies of germline mutations were observed in patients with a family history of ovarian cancer (70% vs 17.6% for those with and without a family history of ovarian cancer, respectively, $P = 0.001$) and in patients with a family history of breast cancer (40.9% vs 17.8% for patients with and without a family history of breast cancer, respectively, $P = 0.04$). Patients with a family history of ovarian cancer had a higher frequency of *BRCA* mutations than those with a family history of breast cancer (60% vs 40.9%). If other genes were included, the frequency of germline mutations was 70% and 40.9%, in those with family histories of ovarian and breast cancers, respectively. HGSC was also observed as another factor associated with a higher frequency of germline mutations (40.8% and 9.5%, $P < 0.001$). Nineteen patients with HGSC (38.8%) had *BRCA* mutations. Seven of 63 patients (11.1%) who had types other than HGSC had germline mutations; 1.6% had *BRCA* mutations and 7.9% had other gene mutations. A sub-analysis of 30 patients with HGSC without the other clinical risk factors revealed that the frequency of *BRCA* mutations was 16.7% (13.3% with *BRCA1* mutations and 3.3% with *BRCA2* mutations). The frequency of germline mutations in patients with other risk factors such as age below 40 years, personal history of breast cancer, and synchronous cancer was not significantly different (14.3% vs 23.5%, 33.3% vs 21%, 22.2% vs 22.3%; $P > 0.05$).

Germline *BRCA* mutations were found in 20/82 (24.4%) patients with risk factors (14 *BRCA1* mutations and 6 *BRCA2* mutations). MMR mutations (*MLH1* and *MSH2*) were found in 2 (2.4%) patients who were diagnosed with synchronous endometrial and ovarian cancer. Other gene mutations such as *RAD51C*, *ATM* and *CDH1* were detected in 4 (4.9%) patients. The proportion of germline mutations is shown in Figure 1. Among 20 patients with *BRCA* mutations, 14 patients (70%) had a family history of breast and/or ovarian cancer, 19 patients (95%) had HGSC, 3 patients (15%) had a personal history of breast cancer, and 7 patients (35%) were older than 60 years at diagnosis.

DISCUSSION

At least 10% of EOCs are hereditary, and most germline mutations are associated with *BRCA1* and *BRCA2*^[1]. A 10%-15% frequency of germline *BRCA* mutations has been reported in unselected EOC patients^[12-14]. However, mutations in MMR genes (*MLH1*,

Table 1 Patient characteristics of patients with and without clinical risk factors

Characteristics	Patients with risk factors (n = 82)	Patients without risk factor (n = 30)	P value
Mean age (yr)	51.8 ± 11.7	55.6 ± 8.3	0.06
Menopause, n (%)	39 (47.6)	17 (56.7)	0.52
Diagnosis, n (%)			
Epithelial ovarian cancer	67 (81.7)	30 (100)	0.10
Fallopian tube cancer	4 (4.9)	0	
Peritoneal cancer	2 (2.4)	0	
Synchronous ovarian and endometrial cancer	9 (11.0)	0	
Histologic subtype, n (%)			
High-grade serous	49 (59.8)	0	< 0.001
Low-grade serous	4 (4.9)	2 (6.7)	
Endometrioid	15 (18.3)	13 (43.3)	
Clear cell	12 (14.6)	12 (40.0)	
Mixed endometrioid and clear cell	1 (1.2)	3 (10.0)	
Adenocarcinoma	1 (1.2)	0	
Stage, n (%)			
1	27 (32.9)	13 (43.3)	0.06
2	10 (12.2)	8 (26.7)	
3	38 (46.3)	9 (30.0)	
4	7 (8.5)	0	
Platinum sensitivity, n (%)	66 (80.5)	23 (76.7)	0.73
Germline mutation, n (%)	26 (31.7)	0	< 0.001

MSH2, *MSH6*, *PMS2*) associated with Lynch or HNPCC syndrome and other genes in HR pathways have been implicated in inherited susceptibility to ovarian cancer. Approximately a quarter of EOC patients carry germline mutations in HR genes, including *BRCA1*, *BRCA2*, and other HR genes such as *ATM*, *BARD1*, *BRIP1*, *CHEK1*, *CHEK2*, *FAM175A*, *MRE11A*, *NBN*, *PALB2*, *RAD51C*, and *RAD51D*. Moreover, about 6% of patients carry germline mutations in other HR genes^[15,16]. The frequency of germline mutations in this study has been reported to be 31.7% in selected EOC patients with risk factors. Of these patients, 24.4% carried *BRCA1* or *BRCA2* mutations and 7.3% had mutations in other genes. Other mutations found in this study include those in the *RAD51C*, *ATM*, *CDH1*, *MLH1*, and *MSH2* genes. The *RAD51C* and *ATM* genes are involved in DNA repair mechanisms similar to the *BRCA1* and *BRCA2* genes. These genes have been reported to increase the risk of developing breast and ovarian cancer^[17]. Germline *CDH1* mutations are known to cause hereditary diffuse gastric cancer syndrome, which increases the lifetime risk of gastric, breast, and colon cancer. However, down-regulation of *CDH1* gene expression is involved in cancer invasion and metastasis in many cancers, including ovarian cancer^[18]. Mutations in *MMR* genes are associated with Lynch syndrome or HNPCC, which both increase the lifetime risk of colorectal, endometrial and ovarian cancer. The frequency of *MMR* mutations in this study was 1.8% (2/112 patients), which was slightly higher than that reported in previous studies (0.5%)^[14]. A family history or personal history of Lynch syndrome-associated cancers was considered a risk factor in this study. Furthermore, our previous study reported that endometrioid carcinoma was the most common histological subtype among Thai EOC patients^[10]. EOC patients with germline *MMR* mutations usually have the endometrioid subtype. These different subtypes might affect the different frequency of germline mutations in *MMR* genes in this study.

The selection criteria for germline testing in EOC patients included young age, a family or personal history of cancer, HGSC, and specific ethnicity. Using these criteria, 27.5% of patients with germline *BRCA* mutations might not have been selected for genetic testing^[8]. Although germline *BRCA* mutations are rarely found in patients aged over 60 years, one-third to half of all *BRCA* mutations are found in this group of women^[1]. Furthermore, a significant family history of cancer is absent in 27%-56% of patients with germline *BRCA* mutations^[1]. Our study showed that 35% of patients with germline *BRCA* mutations were older than 60 years at diagnosis and 30% had no significant family history of cancer. In addition, each patient might have overlapping risk factors. Therefore, other risk factors such as HGSC or a personal history of cancer in these patients might explain the germline *BRCA* mutations.

Table 2 Details of epithelial ovarian cancer patients with germline mutations

Age (yr)	Gene	Mutation			Variant classification	Cancer	Family history of cancer	Synchro-nous cancers	Histology
		Nucleotide change	Protein change	Type					
63	<i>BRCA1</i>	c.1889delA	p.Asn630IlefsTer2	Frameshift	Pathogenic	Ovarian cancer IIIC	Ovarian cancer (sister)	-	High-grade serous
64	<i>BRCA1</i>	c.981_982delA T	p.Cys328Ter	Frameshift	Pathogenic	Ovarian cancer IIIB	Ovarian cancer (sister)	-	High-grade serous
56	<i>BRCA1</i>	c.5072C>A	p.Thr1691Lys	Missense	Likely pathogenic	Fallopian tube cancer IIA	-	-	High-grade serous
52	<i>BRCA1</i>	c.3748G>T	p.Glu1250Ter	Nonsense	Pathogenic	Peritoneal cancer IIIC	Breast cancer (mother) ovarian cancer (sister)	-	High-grade serous
46	<i>BRCA1</i>	c.2059C>T	p.Gln687Ter	Nonsense	Pathogenic	Ovarian cancer IIIC	Ovarian cancer (grandmother)	-	High-grade serous
72	<i>BRCA1</i>	c.3049G>T	p.Glu1017Ter	Nonsense	Pathogenic	Ovarian cancer IIIA	Breast cancer (2 sisters) endometrial cancer (mother)	-	High-grade serous
57	<i>BRCA1</i>	c.3770_3771delAG	p.Glu1257GlyfsTer9	Frameshift	Pathogenic	Ovarian cancer IIIC	Breast cancer (aunt)	-	High-grade serous
51	<i>BRCA1</i>	c.1426delC	p.His476MetfsTer2	Frameshift	Pathogenic	Ovarian cancer IVB	Breast cancer (niece)	-	High-grade serous
35	<i>BRCA1</i>	c.3020C>A	p.Ser1007Ter	Nonsense	Pathogenic	Ovarian cancer IIIC	Breast cancer (mother)	-	High-grade serous
63	<i>BRCA1</i>	c.3181delA	p.Ile1061Ter	Frameshift	Pathogenic	Tubal cancer IVB	-	-	High-grade serous
69	<i>BRCA1</i>	c.1155G>A	p.Trp385Ter	Nonsense	Pathogenic	Tubal cancer IC	-	-	High-grade serous
45	<i>BRCA1</i>	c.3049G>T	p.Glu1017Ter	Nonsense	Pathogenic	Ovarian cancer IVB	-	-	High-grade serous
62	<i>BRCA1</i>	c.4327C>T	p.Arg1443	Frameshift	Pathogenic	Peritoneal cancer IIB	Breast cancer (daughter) Breast and ovarian cancer (sister) endometrial cancer (sister)	-	High-grade serous
59	<i>BRCA1</i>	c.981_982delA T	p.Cys328Ter	Frameshift	Pathogenic	Ovarian cancer IIIC	Breast cancer (sister)	-	High-grade serous
49	<i>BRCA2</i>	c.4126G > T	p.Gly1376Ter	Nonsense	Pathogenic	Ovarian cancer IIIC	Breast cancer (sister) Prostate cancer (uncle) Colon cancer (uncle)	-	High-grade serous
56	<i>BRCA2</i>	c.7558C > T	p.Arg2520Ter	Nonsense	Pathogenic	Ovarian cancer IIIC	-	-	High-grade serous
60	<i>BRCA2</i>	c.3109C > T	p.Gln1037Ter	Nonsense	Pathogenic	Ovarian cancer IVB	Breast cancer (2 sisters)	Breast cancer	High-grade serous
49	<i>BRCA2</i>	c.1367_1368delAG	p.Lys457GluTer4	Frameshift	Pathogenic	Ovarian cancer IIIC	Ovarian cancer (mother)	Breast cancer	High-grade serous
40	<i>BRCA2</i>	c.22_23delAG	p.Arg8AlafsTer4	Frameshift	Pathogenic	Ovarian cancer IIIC	Breast cancer (sister)	-	Clear cell carcinoma
63	<i>BRCA2</i>	c.1405_1406delIGA	p.Asp469	Nonsense	Pathogenic	Ovarian cancer IIB	-	Breast cancer	High-grade serous

46	<i>MLH1</i>	c.109G > A	p.Glu37Lys	Nonsense	Likely pathogenic	Ovarian cancer IIC and endometrial cancer IAG1	Colon cancer (grandfather, father and uncle)	-	Well differentiated serous and well differentiated endometrioid
48	<i>MSH2</i>	c.1183C > T	p.Gln395Ter	Nonsense	Pathogenic	Ovarian cancer IA and endometrial cancer IAG1	Endometrial cancer (aunt)	Endometrial cancer	Endometrioid
48	<i>CDH1</i>	c.1118C > T	p.Pro373Leu	Missense	Likely pathogenic	Ovarian cancer IC and endometrial cancer IAG3	-	Endometrial cancer	Endometrioid with clear cell
54	<i>RAD51C</i>	c.905-2A > C	Not applicable	Splice site loss	Likely pathogenic	Ovarian cancer IIIC	Ovarian cancer (mother)	-	High-grade serous
67	<i>ATM</i>	c.1402_1403delAA	p.Lys468Glufs Ter18	Frameshift	Likely pathogenic	Ovarian cancer IA	-	Breast cancer (Triple-negative)	Clear cell
52	<i>ATM</i>	c.8431_8432delAA	p.Lys2811Valfs Ter3	Frameshift	Likely pathogenic	Ovarian cancer IIIC	Colon cancer (mother, aunt) liver cancer (aunt)	-	Clear cell

The frequency of germline *BRCA* mutations in EOC patients with a significant family history of breast/ovarian cancer was 43.7% in this study, which was comparable with that found in previous studies (33%-55%)^[12,19-21]. A family history of ovarian cancer increases the chance of identifying germline *BRCA* mutations compared with a family history of breast cancer (60% *vs* 40.9%). This finding is consistent with previous studies in Korea and Australia, which reported incidences of *BRCA* mutations of 55%-63% and 15%-35% for a family history of ovarian and breast cancers, respectively^[13,21].

Germline *BRCA* mutations are particularly frequent in HGSC and have been reported as 11%-23%^[12-14]. Our study reported a higher frequency of 38.8%. As mentioned previously, it is likely that each patient has overlapping risk factors. The frequency of germline *BRCA* mutations was 16.7% in patients with HGSC without other risk factors. Most patients (95%) with germline *BRCA* mutations had HGSC, which is somewhat higher than the 73.2% reported in a previous study^[8]. In contrast, only 1.6% of patients with non-HGSC had *BRCA* mutations, and 7.9% of these patients had germline mutations in other genes. This finding is in agreement with that of a previous study, which reported that germline *BRCA* mutations were detected in less than 10% of endometrioid carcinomas and had a very low frequency in clear cell carcinoma^[1].

The incidence rates of EOC differ according to various geographic locations. Rates are highest in Western countries and lowest in Asian countries^[22]. The age-standardized incidence rate in Thailand has been reported at approximately 6.2 per 100000 people in 2018^[22]. Thus, the incidence of germline mutations in EOC may vary by ethnicity and country. Germline *BRCA* mutations were identified in 13% of Malaysian, 13% of Japanese and 17% of Taiwanese^[23-25]. A higher frequency has been reported in 23% of Indian patients, and even higher frequencies have been reported in Korean and Chinese patients (up to 26% and 28.5%, respectively)^[25-27]. Different proportions of histologic subtypes are also a major variable. HGSC is the most common subtype worldwide with an incidence rate of 70%^[3], but it is much less prevalent in Thai patients (20%-22%). The endometrioid and clear cell carcinoma subtypes are observed more frequently (up to 60%)^[9,10]. The reason for the high prevalence of endometrioid and clear cell carcinoma in Thai patients is unknown. Geographic differences may be a possible explanation, as clear cell carcinoma is more prevalent in Asia than in Western countries^[27].

In this study, the frequency of germline mutations in patients with risk factors was 31.7% overall and 24.4% for *BRCA* mutations but was 0% in patients without risk factors. According to our previous study, 30% of EOC patients were classified as high-risk for hereditary ovarian cancer^[9]. Most of our patients had non-HGSC and did not have other clinical risk factors. Therefore, the weighted estimated overall frequency of germline mutations in unselected patients should be only 9.5% overall and only 7.3% for *BRCA* mutations. This number is lower than reported in previous studies from Western countries and some countries in Asia. A much higher proportion of EOC patients who had no clinical risk factors, and HGSC, might be a plausible explanation

Table 3 Frequency of germline mutations according to various clinical risk factors

Risk factors	Number of patients	<i>BRCA1</i> , n (%)	<i>BRCA2</i> , n (%)	Other genes, n (%)
None	30	0	0	0
Family history of cancers (breast/ovary/endometrium/colon)	32	10 (31.2)	4 (12.5)	4 (12.5) (1 <i>ATM</i> , 1 <i>RAD51C</i> , 1 <i>MLH1</i> , 1 <i>MSH2</i>)
Family history of breast cancer	22	6 (27.3)	3 (13.6)	0
Family history of ovarian cancer	10	5 (50.0)	1 (10.0)	1 (10.0) (<i>RAD51C</i>)
Personal history of breast cancer	12	0	3 (25.0)	1 (8.3) (<i>ATM</i>)
Two primary ovarian and endometrial cancer	9	0	0	3 (33.3) (1 <i>MLH1</i> , 1 <i>MSH2</i> , 1 <i>CDH1</i>)
High-grade serous carcinoma	49	14 (28.6)	5 (10.4)	1 (2.1) (<i>RAD51C</i>)
Young age (< 40 yr)	14	1 (7.1)	1 (7.1)	0

for the lower incidence of germline *BRCA* mutations in this study. In general, if the estimated probability of harboring germline mutations is more than 10%, genetic testing is considered cost-effective^[28,29]. Nonetheless, genetic testing is rather uncommon in many countries including Thailand because of cost considerations, reimbursement and availability. Since the estimated frequency of germline mutations in unselected patients is below 10%, genetic testing in all EOC patients may not be cost-effective.

The strength of this study was that reliable and comprehensive NGS techniques were used to analyze *BRCA* genes and other genes associated with HR pathways. The limitation of this study was that not all EOC patients during the study period were included and not all were offered genetic testing. Selection bias might affect the reversed proportion between patients with and without risk factors in this study (73% *vs* 27%). The overall frequency of germline mutations in this study was presumed and estimated based on the 30% of patients with risk factors. Moreover, *BRCA* dysfunction by epigenetic silencing was not analyzed. Further studies with larger numbers of patients and multicenter trials should be conducted to better represent the incidence of germline mutations in the Thai population.

In conclusion, approximately one-third of EOC patients with risk factors for hereditary ovarian cancer had germline mutations (24.4% had *BRCA* mutations and 7.3% had mutations in other genes). However, patients without risk factors did not have germline mutations. The weighted estimated overall frequency of germline mutations in unselected EOC patients was less than 10% and only 7.3% for *BRCA* mutations. Selected patients with the high-grade serous subtype or a significant family history of ovarian/breast cancers should be initially considered for further genetic analysis and intervention in countries with limited resources.

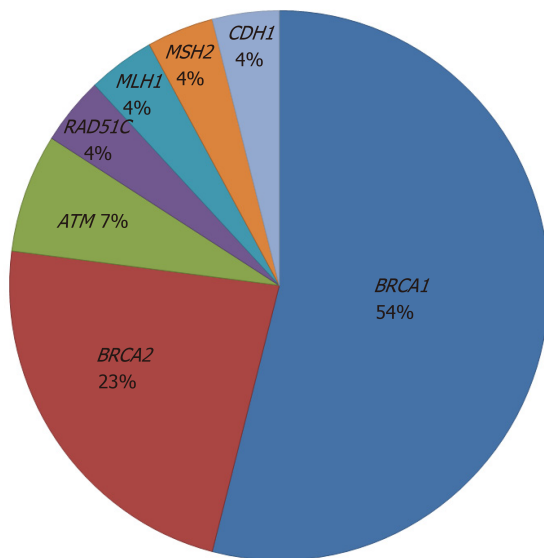


Figure 1 Proportion of germline mutations in patients with epithelial ovarian, fallopian tube, or peritoneal cancers.

ARTICLE HIGHLIGHTS

Research background

Genetic testing is widely recommended for all patients with epithelial ovarian cancer (EOC) including fallopian tube and primary peritoneal cancers. A 10%-15% incidence of germline *BRCA* mutations has been reported in unselected EOC patients. However, universal genetic testing in all patients may not be cost-effective if the estimated probability of harboring germline mutations is less than 10%. The incidence of germline mutations may vary across different countries and ethnicities. Different common histologic subtypes in various countries may be significant variables. The high-grade serous subtype is the most common subtype worldwide (approximately 70%), whereas it is less common in Thai EOC patients (rate of only 20%). Per this result, the incidence of germline mutations might be lower in unselected Thai EOC patients.

Research motivation

Different incidences of germline mutations in EOC patients among various countries may guide different recommendations for genetic testing. Universal genetic testing in all EOC patients may not be cost-effective in Thailand. The risk factors associated with the increased likelihood of having germline mutations should be evaluated.

Research objectives

The objective of this study was to evaluate the frequency of germline mutations in EOC patients and to compare the frequency in those with and without clinical risk factors for hereditary ovarian cancer.

Research methods

This cross-sectional study was conducted on 112 nonmucinous EOC patients including those with fallopian tube and primary peritoneal cancers who underwent primary surgery at our tertiary care hospital between November 2015 and February 2018. Patients were divided into two groups based on clinical risk factors for hereditary ovarian cancer as follows: Age below 40 years, significant family history of cancer, synchronous ovarian and endometrial cancer, and high-grade serous carcinoma (HGSC). All patients who agreed to participate in this study received genetic counseling by a geneticist and provided informed consent. Comprehensive germline mutations were detected using next-generation sequencing.

Research results

Germline mutations were detected in 26 of 112 patients (23.2%); 20 patients (17.8%) had *BRCA1* or *BRCA2* mutations, but 6 patients (5.4%) had mutations in other genes including 1 with an *MLH1*, 1 with an *MSH2*, 1 with a *RAD51C*, 2 with an *ATM* and 1 with a *CDH1* mutation. All mutations were detected in 26 of 82 patients with ≥ 1 risk factor (31.7%), but none were detected in the 30 patients without risk factors ($P < 0.001$). A significantly higher frequency of germline mutations was found in patients with a significant family history of cancer (56.3% and 10%, $P < 0.001$). Patients with a significant family history of ovarian cancer had a higher frequency of *BRCA* mutations than those with a family history of breast cancer (60% and 40.9%, respectively). HGSC was also associated with a higher frequency of germline mutations (40.8% and 9.5%, $P < 0.001$). Germline *BRCA* mutations were detected in 38.8% of patients with HGSC but in only 1.6% of those with non-HGSC. Other risk factors such as age below 40 years, personal history of breast cancer, and synchronous ovarian and endometrial cancer were not significantly different

in terms of germline mutations (14.3% *vs* 23.5%, 33.3% *vs* 21%, 22.2% *vs* 22.3%, $P > 0.05$).

Research conclusions

A significant family history of cancer and HGSC were the only two significant risk factors associated with a higher frequency of germline mutations. Germline *BRCA* mutations were detected in 38.8% of patients with HGSC but in only 1.6% of those with non-HGSC. According to the reverse proportion of histologic subtypes in Thai patients, the estimated overall frequency of germline mutations in unselected EOC patients should be only 9.5% overall and only 7.3% for *BRCA* mutations. These findings suggest the consideration of genetic testing in selected EOC patients in Thailand.

Research perspectives

Although universal genetic testing in all EOC patients is recommended by various national professional societies, it may not apply in every country. The narrow availability of genetic testing, the high cost when not reimbursed, and the limited number of geneticists are major obstacles in Thailand. Selected EOC patients should initially be considered for genetic analysis. As the number of patients in this study is still small and since the study was conducted in only one tertiary hospital, it may not fully represent the Thai population. Further prospective studies with multicenter trials should be conducted. The incidence of germline mutations should be studied in unselected EOC Thai patients to identify significant risk factors. Furthermore, *BRCA* genes should not be the only focus of germline mutation studies, but these studies should also be expanded to include other homologous recombination and MMR genes.

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