



BReast CAncer gene (*BRCA*): snapshot of the Middle East

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Background

Breast cancer (BC) is the most common cancer in the world, accounting for approximately 23% of all cancers that affect females worldwide, and remains the most common cause of mortality in women globally (1). About 5–10% of all BC cases (2) and more than 23% of all ovarian cancers (3) are thought to be hereditary. Hereditary breast and ovarian cancer is commonly caused by an autosomal dominant BReast CAncer gene (*BRCA*) germ line mutation which causes a higher than normal incidence of ovarian and BC in genetically related families (4).

Women in the Arab world are diagnosed with BC at more advanced stages, with the incidence rates in this region increasing over the last three decades (5-10).

BRCA data

BRCA gene mutations have been identified as the most commonly linked germ-line mutations (11). Pathogenic mutations in both *BRCA1* and *BRCA2* increase the risk of developing BC up to 85% and ovarian cancer up to 54% during woman's lifetime (12). *BRCA* mutation occurrences are known to differ between populations and ethnic groups. Some studies also describe significant differences in the spectrum of *BRCA1* compared with *BRCA2* mutations, and in the *BRCA1/2* variants of uncertain significance (VUS) (13,14). For instance, from a sample of 46,276 women of non-Ashkenazi Jewish ancestry, females with African ancestry had the highest prevalence of VUS [16.5% vs. 5.7% Western European; odds ratio (OR): 3.2, 2.8–3.7] (13), while *BRCA2* mutations were reported to be more frequent than those of *BRCA1* in the Asian population (15). Furthermore, population-specific mutations have also

been described among Ashkenazi Jews (16) and patients of Spanish ancestry (17).

Founder *BRCA1* and *BRCA2* mutations have also been found in several European populations in Austria, Slovenia, Italy, France, Spain, Portugal, Belgium, the Netherlands Germany, the Czech Republic, Slovakia, Hungary, Greece, Cyprus, Denmark, Sweden, Norway, Finland, Iceland, the United Kingdom, Ireland, Poland, Latvia, Lithuania, Estonia, Belarus, and Russia (18).

In Saudi Arabian women, BC is ranked first among all cancers, accounting for 27% of all newly diagnosed malignancies. While the majority of BC cases are sporadic, familial susceptibility to BC constitutes 25% of all cases (16).

Although the population in Saudi Arabia is largely homogeneous and consanguinity is very common, especially in the central, eastern, and southern regions of the country, the prevalence of *BRCA1* and *BRCA2* mutations and the characteristics of BC have not been extensively studied. Available data are conflicting and inconclusive, as they are based on retrospective analyses from small heterogeneous groups of Saudi and non-Saudi patients (19-24).

In this paper, we present a snapshot of the *BRCA* studies that have been conducted in Arab countries in the Middle East. The *BRCA* studies examined included those involving both *BRCA1* and *BRCA2*. *Table 1* shows the summary of studies included in this paper.

Six countries with varying incidence rates and types of *BRCA* mutations were included: Saudi Arabia, Lebanon, Jordan, Qatar, Egypt, and Syria. The sample sizes ranged between 50 and 800 patients and the mean age at diagnosis ranged from 22 to 75 years. The type of testing employed varied and included multiple techniques. Mutation types were mostly deleterious.

Table 1 *BRCA* mutations among breast and/or ovarian cancer patients in Arab countries

Author	Year	Country	Sample size	Age at diagnosis (range or mean)	Test type	Mutation type
Bu	2016	Saudi Arabia	818	41.9	PCR, CS/SS4, and TCS	Deleterious
El Saghir	2015	Lebanon	250	40.8	MLPA	Deleterious, VUS
Abdel-Razeq	2018	Jordan	100	22–75	BART	Deleterious, suspected-deleterious
Bujassoum	2017	Qatar	82	<50	MLPA	Deleterious
Jalkh	2012	Lebanon	72	41	Fluorescent DS	Deleterious, VUS
Abulkhair	2018	Saudi Arabia	310	–	PCR	Deleterious
Ibrahim	2010	Egypt	60	43.5	SSCP, HAC	Deleterious
Khalil	2018	Syria	50	36	PCR	Deleterious

BART, comprehensive BRCAAnalysis and BRCAAnalysis Rearrangement Test; PCR, polymerase chain reaction; CS, capture sequencing; SS, sanger sequencing; TCS, targeted capture sequencing; MLPA, multiple ligation-dependent probe amplification; SSCP, single-strand conformation polymorphism assay; HAC, heteroduplex assay confirmation; DS, direct sequencing; VUS, variants of uncertain significance.

There was a variability in the prevalence of *BRCA* mutations in patients at high risk of having hereditary BC between 5.6% to 20% between different countries of the Arab world (11,19,25,26). These differences might be explained by either biological differences in *BRCA* gene prevalence (27) or differences in the age at onset in the study population (28,29). Studies have also suggested that there is a variation of *BRCA* prevalence among different ethnicities (16) while others found that the prevalence of these mutations is the same across different ethnicities (13). Family history of breast or ovarian cancer emerged as a significantly strong predictor for *BRCA* gene mutations (30).

Conclusions

Understanding population-specific *BRCA* gene distributions is critical, as this knowledge can be helpful in devising appropriate risk-assessment strategies to reduce the risk of cancer emergence and developing cost-effective strategies for genetic testing for *BRCA* mutations (24).

High-quality large-sample studies are necessary to better understand and recognize the impact of *BRCA* gene mutations and their role in breast and ovarian cancer incidence, risk and prognosis, surveillance, management, and outcome in this part of the world where cancer incidence is steadily increasing.

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