Prevalence of the BRCA1 c.68_69delAG (BIC: 185delAG) mutation in women with breast cancer from north-central Poland and a review of the literature on other regions of the country

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Introduction

Germline mutations in tumor suppressor genes BRCA1 and BRCA2 are strongly associated with breast cancer (BC) and ovarian cancer (OC). It was estimated that women carrying these mutations have 84% lifetime risk of BC and 27% of OC [1, 2].

The BRCA1 gene (MIM 113705), located on chromosome 17q21, is involved in cell cycle control, DNA repair pathways and regulation of apoptosis [3, 4]. The c.68_69delAG frameshift mutation occurs in codon 23, exon 2, and results in creation of the STOP codon in position 39. This alteration leads to premature termination of translation and significant truncation of the protein [5].

The c.68_69delAG mutation was first described in the Ashkenazi Jews and together with c.5266dupC (BIC: BRCA1 5382insC) and c.5946delT (BIC: BRCA2 6174delT) is one of the most frequent founder mutations in this population (0.9%, 0.13% and 1.52% frequency, respectively). Among Ashkenazi women diagnosed with BC, the incidence of c.68_69delAG is 4.16% [6–9].

The aim of this study was to investigate the frequency of the congenital c.68_69delAG mutation in women with BC inhabiting north-central Poland and to compare it to other authors’ findings in different regions of the country. The relationship between c.68_69delAG and the age at BC diagnosis was also investigated, as well as BC history of patients’ families.

Material and methods

Patients

Women with BC from north-central Poland were recruited to the investigation out of the women consecutively diagnosed in 2009–2010 at the Oncology Center in Bydgoszcz. The study group comprised 252 women in whom the presence of the most frequent BRCA1 founder mutations in the Polish population, i.e. c.5266dupC, c.181T>G (BIC: C61G) and c.4034delA (BIC: 4153delA), was excluded. The histological type of BC and family history of cancer were not qualifying criteria.

The median age at BC diagnosis was 45 years (range 18–55). One woman was diagnosed with bilateral BC – two primary cancers within two years (at the age of 41 and 42).

In the family with suspicion of hereditary c.68_69delAG mutation, molecular tests were performed (two close relatives of the BC patient agreed to be tested).
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79% of the tested women originated from families with at least one other cancer case in a first or second degree relative, most frequently breast, lung, colon, kidney and prostate cancer.

Pedigree analysis for recognition of families with suspicion of hereditary breast cancer syndrome (HBC-susp.) was performed using the following criteria:
• at least two first-degree relatives with BC (or second degree from the paternal side), at least one BC diagnosed before the age of 50;
• one BC diagnosed before the age of 40.

The control group consisted of 225 volunteers – healthy women from 21 to 60 years old (median age 47 years), unsolicited for cancer family history, originating from north-central Poland.

Medical records confirmed the BC diagnosis and the clinical history of all women. Informed consent was obtained from all patients and healthy persons. The study was approved by the Ethics Committee of Collegium Medicum, Nicolaus Copernicus University, Bydgoszcz, Poland.

Molecular analysis

The c.68_69delAG mutation was analyzed in DNA from peripheral blood leukocytes, extracted by the standard salting-out method. Molecular investigations were performed using ASO-PCR assay with specific primers described by Struwing et al. [10]. Mutation-positive cases were confirmed by sequencing analysis using primers as in the ASO-PCR and the BigDye Direct Cycle Sequencing Kit (Applied Biosystems, USA), and analyzed on the ABI-PRISM 3130 Genetic Analyzer (Applied Biosystems).

Results

The c.68_69delAG mutation was found in one woman out of the 252 tested (0.4%). The woman was diagnosed with BC at the age of 43. Sequence analysis confirmed the heterozygous character of the mutation (Fig. 1). Family investigations revealed the presence of c.68_69delAG also in the patient’s mother (BC diagnosed at age 68). In the patient’s healthy daughter (age at molecular diagnosis 19), c.68_69delAG was not found. In the sister of the patient’s mother, with kidney cancer (KC; age at diagnosis unknown), the mutation was not tested (Fig. 2). The results confirmed the hereditary character of the mutation in this family. No woman from the control group had the c.68_69delAG mutation.

The analysis of BC history in families of the 252 tested women revealed that 69 of them (27.4%) fulfilled the criteria of HBC-susp. The median age of BC onset in these women was 39 years (range 18-50). The family of the c.68_69delAG carrier was also taken into account; thus 1.4% frequency of this mutation was calculated among HBC-susp. families.

Discussion

The BRCA1 c.68_69delAG mutation belongs to the group of pathogenic mutations whose incidence varies among different populations and subpopulations, and is mainly associated with the founder effect [11].

In the first studies of BRCA1 mutations on a large group of 4000 people from the general Polish population, Górski et al. [12] found 0.4% incidence of c.5266dupC, 0.05% of c.181T>G and 0.03% of c.4034delA. The c.68_69delAG mutation was not tested. Recently, an extensive investigation of the Polish population was carried out by Brożek et al. [13]. Among 16 849 examined persons, the authors found 0.17% c.5266dupC carriers, among 3923 persons 0.1% c.3700_3704del5 (BIC: 3819del5) carriers, and in a group of 13 462 persons 0.08% were carriers of the c.181T>G mutation. None of the 12 485 persons investigated for the presence of c.68_69delAG had this mutation. These results sug-
gest a narrow spectrum of high frequency BRCA1 mutations, as well as a strong founder effect in the Polish population.

The BRCA1 mutations were also analyzed in Polish women with a family history of BC/OC. The first such study was performed by Sobczak et al. [14], who identified three pathogenic mutations, c.4034delA, c.314A>G (BIC: Tyr105Cys) and c.5510G>A (BIC: Trp1782X), each with 0.6% frequency. Among 200 families from various regions of the country with strong BC/OC aggregation, Górski et al. [15] found 34% frequency of c.5266dupC, 15.5% of c.181T>G and 6% of c.4034delA. The c.68_69delAG mutation was predominantly detected in the territory of Poland, beginning in the 10th–11th century. The occurrence of the c.68_69delAG mutation in the Polish population may be related to the settlement of the Ashkenazi Jews (i.e. Jews of Central-Eastern European ancestry) in the territory of Poland, beginning in the 10th–11th century. The c.68_69delAG mutation was predominantly detected in the Ashkenazi population, which suggested its common ancestor and a founder effect. It was estimated that c.68_69delAG arose about 46 generations ago, or around the early 1200s [24, 25]. In sporadic cases, this mutation was also reported in Jewish non-Ashkenazi families [6, 26, 27]. Bar-Sade et al. [27] hypothesized that a common ancient founder for c.68_69delAG emerged prior to the dispersion of the Jewish people in the Diaspora after the destruction of the Second Temple (about 70 AD).

Despite a very strong Jewish tradition of entering into marriage within their own ethnic group, the Polish and Jewish populations merged over the ages. After the Second World War, large groups of Polish and Ashkenazi descent migrated from various regions of the country, mainly Eastern territories belonging to Poland before 1939, to the contemporary Polish area, especially to the north, west and the highly industrialized region of Silesia. These are the parts of Poland where the highest frequencies of c.68_69delAG were found. Górski et al. [20] reported that the ancestors of two c.68_69delAG carriers identified by them lived in Łódź and in Lviv regions before the Second World War.

In the family burdened with c.68_69delAG, no carriers were identified in a group of 21 women from HBC-susp. families, while a more recent study revealed 2.2% incidence of c.68_69delAG in a larger group of such families [19, 20]. However, the highest frequencies of this mutation were reported in north-western (5.7%), northern (4.7%) and south-western (2.9%) parts of the country, in BC/OC families [21–23] (Table 1).

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In the family burdened with c.68_69delAG identified by us, vertical transmission of the disease in two successive generations, as well as anticipation occurred. The woman carrying c.68_69delAG was diagnosed with BC at 43 years of age, whereas her mother, also a carrier of this mutation, was diagnosed with BC at age 68. The age of BC onset in the second woman turned out to be relatively late. In some authors’ studies, cited in this paper, the age of BC onset in women carriers of c.68_69delAG ranged between 51 and 55

### Table 1. Prevalence of the BRCA1 c.68_69delAG mutation among BC/OC families from different regions of Poland

<table>
<thead>
<tr>
<th>Region of Poland</th>
<th>Family types</th>
<th>c.68_69delAG Carriers/ Total (%)</th>
<th>Age of BC/OC onset</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>Whole country</td>
<td>HBC-susp.</td>
<td>0/100 (0%)</td>
<td>ng</td>
<td>Górski et al., 2004 [15]</td>
</tr>
<tr>
<td></td>
<td>HBOC-susp.</td>
<td>1/100 (1%)</td>
<td>ng</td>
<td>Górski et al., 2000 [21]</td>
</tr>
<tr>
<td>North-western</td>
<td>HBC-susp.</td>
<td>2/35 (5.7%)</td>
<td>ng</td>
<td>Górski et al., 2000 [21]</td>
</tr>
<tr>
<td>(mainly city of Szczecin)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Northern</td>
<td>HBOC-susp.</td>
<td>3/64 (4.7%)</td>
<td>BC43, BC51, OC52</td>
<td>Ratajska et al., 2008 [22]</td>
</tr>
<tr>
<td>Upper Silesia</td>
<td>HBC-susp.</td>
<td>2/68 (2.9%)</td>
<td>BC51, BC-NG</td>
<td>Grzybowska et al., 2002 [23]</td>
</tr>
<tr>
<td>(south-western)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>North-eastern</td>
<td>HBC-susp.</td>
<td>1/46 (2.2%)</td>
<td>BC55</td>
<td>Perkowski et al., 2003 [20]</td>
</tr>
<tr>
<td>North-eastern</td>
<td>HBC-susp.</td>
<td>0/21 (0%)</td>
<td>–</td>
<td>Van der Looij et al., 2000 [19]</td>
</tr>
<tr>
<td>Western (city of Poznań)</td>
<td>HBC-susp.</td>
<td>2/123 (1.6%)</td>
<td>–</td>
<td>Jasińska and Krzyżosiak, 2001 [17]</td>
</tr>
<tr>
<td></td>
<td>(healthy women tested)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Central (city of Warsaw)</td>
<td>HBC-susp.</td>
<td>0/52 (0%)</td>
<td>–</td>
<td>Paszko et al., 2002 [18]</td>
</tr>
<tr>
<td>North-central</td>
<td>HBC-susp.</td>
<td>1/69 (1.4%)</td>
<td>BC43 (mother BC68)</td>
<td>present study</td>
</tr>
</tbody>
</table>

years, and was 43 years in one case (Table 1). Al-Mulla et al. [28], based on an analysis of 241 English women from 131 BC/OC families, estimated that the median age of BC onset among c.68_69delAG carriers is 55 years.

We conclude that in north-central Poland, the prevalence of c.68_69delAG among families with suspicion of hereditary BC is much lower than c.5266dupC (27%), c.1817+G (18%) and c.4034delA (2.2%, unpublished data) [16]. Therefore, it does not seem necessary to include this mutation in the primary BRCA1 screening test, containing the most frequent founder mutations (c.5266dupC, c.1817+G and c.4034delA).

However, women who are not burdened with these mutations, especially originating from HBC-susp. families, should be examined for c.68_69delAG. Late age at BC diagnosis does not seem necessary to include this mutation in the primary screening test, containing the most frequent founder mutations (c.5266dupC, c.1817+G and c.4034delA). Identification of families burdened with hereditary c.68_69delAG will make it possible to offer them genetic counseling and provide the carriers with a diagnostic program for early cancer detection.

The authors declare no conflicts of interest.

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