BRCA1 Wild-Type Allele Modifies Risk of Ovarian Cancer in Carriers of BRCA1 Germ-Line Mutations

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Abstract

Strong inter- and intrafamilial variation of penetrance of breast and ovarian cancer is observed in BRCA1 mutation carriers. The wild-type copy of the BRCA1 gene is a plausible candidate as a cancer risk modifier given that the residual function corresponding to the intact BRCA1 allele may influence the process of tumor formation in BRCA1 carriers. Indeed, growing evidence is now becoming available on impaired reparation of double-strand DNA breaks in cells heterozygous for BRCA1 mutations, implying an enhanced mutability of BRCA1*+/− cells. To determine whether certain variant forms of the wild-type BRCA1 allele are implicated in variation of the BRCA1-related cancer risk, their effect was studied in a panel of 591 women with BRCA1 germ-line mutations. We found that BRCA1 carriers with the wild-type BRCA1 copy bearing a common Gly1038 variant were at increased risk of ovarian cancer (hazards ratio, 1.50; 95% confidence interval, 1.03–2.19). The results of our study imply that a quite significant proportion of the interindividual variability in ovarian cancer penetrance in BRCA1 carriers may be explained by a common BRCA1 Gly1038 wild-type allele, given its high frequency (0.27).

Introduction

Carriers of mutations in the BRCA1 and BRCA2 genes have considerably increased susceptibility to develop breast and ovarian cancer as compared with the general population. Strong inter- and intrafamilial variation of penetrance of these cancers is observed in mutation carriers. Substantially different BRCA1 penetrance estimates have been reported depending on the method of family ascertainment: lifetime cancer risk of about 80% for breast cancer and 60% for ovarian cancer have been found in the studies of highly selected families with multiple cancer cases, whereas in population-based studies, these estimates appeared to be much lower (40–50% for breast cancer, 20–40% for ovarian cancer; Refs. 1–6). These differences suggest that genetic and/or nongenetic factors have influence on BRCA1-associated cancer risk. Several such factors have been suggested already (7). A number of hormonal aspects, mainly associated with a woman’s reproductive life, e.g., pregnancy, oral contraceptives use, breastfeeding, oophorectomy, were found to modify breast and ovarian cancer expression in mutation carriers (8–12). An effect of genetic modifiers was reported as well. The presence of at least one rare allele of the variable number of tandem repeats (VNTR) polymorphism in the downstream region of the HRAS1 proto-oncogene was found to be associated with an elevated risk of ovarian cancer in women carrying BRCA1 mutations (13). The progesterone receptor variant characterized by an intronic Alu insertion confers an increased ovarian cancer risk in BRCA carriers who never used oral contraceptives (14). The risk of breast cancer was increased in those carriers with at least one long allele (>28 CAG repeats) as compared with that with shorter alleles in the genes coding for the androgen receptor and the AIB1 steroid hormone receptor coactivator (15, 16). However, these modifier effects were not examined or were not replicated in independent studies (17).

Although not yet considered, the wild-type copy of the BRCA1 gene appears to be a plausible candidate for cancer risk
Table 1  BRCA1 mutation carriers included in the studya

<table>
<thead>
<tr>
<th>Ovarian cancer</th>
<th>Breast (BR)/Ovarian (OV) cancer</th>
<th>Breast cancer</th>
<th>Breast- and ovarian-cancer free</th>
</tr>
</thead>
<tbody>
<tr>
<td>BRCA1 carriers: 591 (388)</td>
<td>119 (84)</td>
<td>51 (43)</td>
<td>272 (175)</td>
</tr>
<tr>
<td>Mean age at diagnosis (yr)</td>
<td>47.5 (47.2)</td>
<td>BR: 43.4 (44.9)</td>
<td>OV: 51.6 (52.8)</td>
</tr>
<tr>
<td>Mean year of birth</td>
<td>1941 (1945)</td>
<td>1940 (1940)</td>
<td>1948 (1947)</td>
</tr>
<tr>
<td>Mean parity</td>
<td>2.8 (2.4)</td>
<td>2.2 (2.2)</td>
<td>1.9 (2.0)</td>
</tr>
</tbody>
</table>

a In bold, total of BRCA1 carriers; in parentheses, BRCA1 carriers independent for segregation of the wild-type BRCA1 allele.

b Mean current age.

modifier in BRCA1 mutation carriers given that the residual function corresponding to the intact BRCA1 allele may influence the process of tumor formation in BRCA1 carriers (18). This hypothesis is mainly based on the growing evidence of impaired repair of double-strand DNA breaks in cells heterozygous for BRCA1 mutations, implying an enhanced mutability of BRCA1+/− cells (19–22). To determine whether certain variant forms of the wild-type BRCA1 allele are implicated in variation of the BRCA1-related cancer risk, their effect was studied in a panel of women with BRCA1 germ-line mutations.

Materials and Methods

Study Participants. The study included 591 women belonging to 282 different families recruited and identified as carriers of BRCA1 germ-line mutations in the framework of research and counseling programs on hereditary breast and ovarian cancer in 15 centers in France, the United States, Canada, and Greece. Of these 591 women, 119 have been diagnosed with ovarian cancer, 272 with breast cancer, 51 with both breast and ovarian cancer, and 149 women as breast- and ovarian-cancer-free at the time of the last follow-up. Information available on study subjects included clinical characteristics, date of birth, current age or age at death, age at diagnosis of breast and/or ovarian cancer, age at prophylactic surgery (oophorectomy or mastectomy), and parity (Table 1).

BRCA1 Genotyping. The samples were genotyped for four coding bi-allelic single nucleotide BRCA1 polymorphisms: A1186G/Gln356Arg, G2196A/Asp693Asn, A3232G/Glu1038Gly, and A4956G/Ser1613Gly. DNA samples were available for 568 study participants. For 23 affected women whose samples were lacking, the BRCA1 genotype was established using DNA of their children and husband. Heteroduplex analysis, denaturing gradient gel electrophoresis (DGGE), denaturing high-precision liquid chromatography (DHPLC), enzymatic digestion (AlwI for A1186G, Hsp92II for G2196A, and NlaIV for A3232G and A4956G) and sequencing (ABI 3100; Applied Biosystems) were used for genotyping of the BRCA1 polymorphisms. These procedures were performed as described elsewhere (23–25). For each of the four BRCA1 polymorphisms studied, the corresponding BRCA1 amplicons of five individuals were sequenced (ABI 3100; Applied Biosystems), confirming the genotyping accuracy of the procedures used.

Identification of Polymorphic Variant Carried on BRCA1 Wild-Type Allele. In individuals heterozygous for the typed BRCA1 polymorphisms, it was necessary to determine which polymorphic variant was carried on the wild-type BRCA1 copy. This was done using genotype information in homozygous relatives when available. In four families with 5382insC-ter1828 the common mutual origin was established using haplotype data on several microsatellite markers surrounding the BRCA1 locus (D17S1185, D17S1320, D17S1321, D17S855, D17S1322, D17S1323, D17S1327, D17S1326, and D17S1325), permitting the phase identification of the BRCA1 polymorphisms in carriers in these families. BRCA1 PCR fragments encompassing both polymorphism and mutation sites were cloned in 41 mutation carriers from families in which only heterozygotes for the BRCA1 polymorphisms studied were detected. The cloning was performed with the use of the TOPO TA Cloning kit (Invitrogen) according to the manufacturer’s instructions. Cloned DNA was PCR amplified and sequenced (ABI 3100; Applied Biosystems). All of the carriers in whom the phase of the BRCA1 polymorphisms could not be determined by the above methods were excluded from the analysis. The proportion of such individuals was very similar in the groups of breast cancer patients, ovarian cancer patients, and unaffected carriers, varying between 0.012 and 0.014 for Gln356Arg, Asp693Asn, and between 0.033 and 0.051 for the Glu1038Gly and the Ser1613Gly polymorphisms.

Statistical Analysis. The data were analyzed by disease-free survival analysis using a Cox proportional hazards model to adjust for different periods of risk, given the strong variation in the age of the BRCA1 carriers included in the study. For the estimation of breast cancer risk, the women were followed until the diagnosis of breast cancer (mean age at diagnosis, 39.8 years), considering only the first malignancy in patients with multiple tumors. They were censored at the age of prophylactic mastectomy or oophorectomy, ovarian cancer diagnosis or death. The effect of the BRCA1 wild-type allele was also analyzed in the proportional hazards model after adjusting for these risk factors.

Results

Five hundred ninety-one female BRCA1 mutation carriers have been included in the study. Clinical characteristics, year of birth, and parity of carriers are presented in Table 1. The samples were genotyped for four coding BRCA1 SNPs. Two of them (A2322G/Glu1038Gly and A4956G/Ser1613Gly) have been reported to be in strong linkage disequilibrium with each other, as well as with at least six other polymorphisms in the BRCA1 gene, the frequency of the rare allele being about 0.30 (26, 27). The other two BRCA1 polymorphisms tested were

4 The abbreviations used are: SNP, single nucleotide polymorphism; HR, hazards ratio; CI, confidence interval.
A1186G/Gln356Arg and G2196A/Asp693Asn, with reported frequencies of the rare allele of about 0.06 (26, 27). Thus, the analyzed SNPs included all of the known BRCA1 polymorphisms with a frequency greater than 0.05, Gln1038Arg and Ser1613Gly having been chosen as tag SNPs corresponding to the above mentioned linkage disequilibrium block.

Analysis of each of the BRCA1 wild-type allele variants, considered independently, suggested an association of Gly1038 with an increased risk of ovarian cancer (HR, 1.39; 95% CI, 0.98–1.95). Results on the other variants tested were not significant. To account for the fact that a number of the analyzed subjects were related to one another, the survival analysis was undertaken in a group of carriers independent for segregation of the wild-type BRCA1 allele. Because an excess of sharing of the wild-type BRCA1 allelue only sisters and not other relationships (e.g., mother-daughter), the group of independent individuals included one carrier per sister-set selected according to the following priority criteria: (a) ovarian cancer case diagnosed at the youngest age; (b) the oldest unaffected carrier; and (c) breast cancer case diagnosed at the youngest age; a criteria: (d) the oldest affected carrier per sister-set selected according to the following priority

tion controls by Durocher et al. (26) and Dunning et al. (27). The study of Baldeyron et al. (22) demonstrated a reduced fidelity of double-strand breaks end-joining in BRCA1 wild-type carriers (8, 9). The magnitude of the estimated effect of Gly1038 wild-type allele on ovarian cancer risk was slightly reduced by adjustment for year of birth and for parity (HR = 1.35, 95% CI, 0.88–2.08).

A recent analysis of Thompson and Easton (29) using the largest series of BRCA1 breast/ovarian cancer families analyzed thus far for genotype/phenotype correlation, provided evidence that BRCA1 truncating mutations located in the central portion of the coding sequence (nucleotides 2401–4190) are associated with 30% reduction of breast cancer risk compared with mutations located outside of this region. This study also detected less ovarian cancers among carriers of 3’ mutations (nucleotides 4190–5711) than among those with mutations in the remaining part of the gene. We evaluated the effect of mutation position on breast and ovarian cancer risk in our sample and found no significant trend. The Gly1038-associated increase of ovarian cancer risk was similar in the groups of carriers of BRCA1 mutations in the 3’ region and in the rest of the gene (data not shown).

### Discussion

Our findings suggest that certain alleles of the wild-type copy of the BRCA1 gene modify the risk of ovarian cancer in women whose other BRCA1 copy is inactivated by a mutation. The difficulty of collecting samples from BRCA1 carriers affected with ovarian cancer, given the poor survival of these patients, didn’t allow us to perform our analysis on a very large set. Because of the rapidly growing number of newly identified BRCA1 mutation carriers, it will become easier in the future to gather samples to verify, in an independent set of carriers, the effect of the BRCA1 Gly1038 wild-type allele on ovarian cancer risk detected in our series. The biological rationale underlying this effect might be related to certain interactions of BRCA1 with its multiple cellular partners, reflecting the variety of the BRCA1 functions, and is expected in particular to be related to the role of BRCA1 in DNA damage-sensing mechanisms. Although these mechanisms have been primarily studied in BRCA1 nullizygous cells (reviewed in Ref. 18), growing evidence is becoming available on the impaired repair of double-strand DNA breaks in cells heterozygous for BRCA1 mutations, implying an enhanced mutability of BRCA1*+/− cells. An increased radio-sensitivity and high level of micronuclei formation were observed in BRCA1*+/− lymphoblasts, lymphocytes, or fibroblasts (19–21). The study of Baldeyron et al. (22) demonstrated a reduced fidelity of double-strand breaks end-joining in BRCA1*+/− cells compared with controls. Thus, the specific function of the protein encoded by the second, intact copy of the BRCA1 gene appears to be critical for accelerating or slowing down the accumulation of unrepaired DNA damage and chromosone aberrations in BRCA1*+/− cells. Therefore, functional variations between different polymorphic forms of the wild-type BRCA1 are likely to exist and would be expected to influence cancer penetrance in BRCA1 carriers.

This postulate might appear to contradict the tumor-suppressor two-hit model supported by the loss of the BRCA1 wild-type allele observed in most of the BRCA1-associated tumors studied (30, 31). However, the timing of this event

### Table 2  Effect of BRCA1 wild-type allele variants on breast and ovarian cancer penetrance in 388 independent BRCA1 mutation carriers

<table>
<thead>
<tr>
<th>BRCA1 wild-type allele variant</th>
<th>Breast cancer HR (95% CI)</th>
<th>Ovarian cancer HR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Arg356</td>
<td>0.78 (0.45–1.33)</td>
<td>0.82 (0.40–1.68)</td>
</tr>
<tr>
<td>Asn693</td>
<td>0.99 (0.60–1.66)</td>
<td>1.18 (0.57–2.43)</td>
</tr>
<tr>
<td>Gly1038</td>
<td>0.82 (0.60–1.12)</td>
<td>1.50 (1.03–2.19)</td>
</tr>
<tr>
<td>Gly1613</td>
<td>0.88 (0.65–1.18)</td>
<td>1.38 (0.93–2.03)</td>
</tr>
</tbody>
</table>
remains uncertain. It seems very plausible that BRCA1+/− cells accumulating DNA anomalies would be prone to acquire for their survival a mutation(s) in checkpoint gene(s) rather than loss of the second BRCA1 allele (18). Although no convincing data are available on the chronology of key genetic events in cancer-prone tissues in BRCA1 carriers, for BRCA2 heterozygotes, there is evidence of inactivation of the BRCA2 wild-type copy late in tumor progression (32).

Examples of inherited diseases of which the major gene penetrance is modified by the wild-type allele are being reported in the literature. Such a modifier effect has been described in the case of the dominant inherited disorder of heme biosynthesis, erythropoietic protoporphyria, caused by mutations in the FECH gene resulting in ferrochelatase deficiency (33). The intronic variant IVS3−48C of the wild-type FECH (allelic frequency, 0.11), associated with diminished expression because of increased efficiency of abnormal splicing was found to boost clinical expression of the disease. The severity of another hematological disorder, hereditary elliptocytosis, is also augmented by the presence in trans of the common Val1857/IVS45−12T/IVS46−12A allele of spectrin in heterozygote spectrin mutation carriers (34, 35). This polymorphic allele produces transcripts with partially skipped exon 46 coding for a motif involved in the formation of spectrin dimers, resulting in under-representation of wild-type spectrin dimers in erythrocyte membrane.

It is difficult to speculate about specific mechanisms of modulation of ovarian cancer risk by the wild-type BRCA1 Gly1038-carrying allele because no data are available on its functional evaluation. However, it is tempting to hypothesize that this allele might have tissue-dependent functional particularities (regarding transcript or protein stability, alternative splicing, interaction with tissue-specific partners, and so forth) rendering BRCA1+/− ovarian, but not breast cells more susceptible to malignant transformation. The fact that the Gly1038 allele is observed in BRCA1 carriers older than age 50 years suggests that certain latency period of DNA error accumulation might be necessary for the modifier effect to
become detectable. An alternative to this speculation is that the postmenopausal hormonal background might favor manifestation of variations of the BRCA1 function in estrogen-signaling pathways (36, 37).

Several studies compared the frequency of this BRCA1 allele between sporadic breast or ovarian cancer cases and controls; however, no statistically meaningful difference could be detected (26, 27, 38). These results suggest that the cancer risk associated with the Gly1038 allele might be minor and hardly detectable in the relatively small and heterogeneous samples studied (26, 38). Alternatively, this BRCA1 allele might have no effect in the absence of an inactivating mutation in the other BRCA1 copy (24). In conclusion, the results of our study imply that a quite significant proportion of the interindividual variability in ovarian cancer penetrance in BRCA1 carriers may be explained by a common BRCA1 Gly1038 wild-type allele, given its high frequency (0.27).

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