Pathology of Breast and Ovarian Cancers among BRCA1 and BRCA2 Mutation Carriers: Results from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA)


Authors' Affiliations: 1Centre for Cancer Genetic Epidemiology, Depart-ment of Public Health and Primary Care, University of Cambridge, Cam-bridge, United Kingdom; 2Fred A. Litwin Center for Cancer Genetics, Samuel Lunenfeld Research Institute, Mount Sinai Hospital; 3Departments of Medicine, Surgery, and Epidemiology-Biostatistics, Memorial Sloan-Kettering Cancer Center; 4Department of Epidemiology, Columbia University, New York, New York; 5Department of Molecular Genetics and 6Laboratory Medicine and Pathobiology, University of Toronto; 7St Michael’s Hospital, Toronto, Ontario, Canada; 8Center for Clinical Epidemiology and Biostatistics and Abramson Cancer Center, University of Pennsylvania; 9Laboratory Medicine and Pathology, IRRP, National Centre of Scientific Research “Demokritos”, Athens, Greece; 10Division of Cancer Prevention and Genetics, Istituto Europeo di Oncologia (IEO), Milan, Italy; 11Faculty of Medicine, University of Southampton, Southampton University Hospitals, NHS Trust, Southampton, United Kingdom; Departments of Obstetrics and Gynecology, 12Pathology, and 13Clinical Genetics, Helsinki University Central Hospital, Helsinki, Finland; 14Women’s Cancer Program at the Samuel Oschin Cancer Institute and Division of Gynecologic Oncology, Department of Obstetrics and Gynecology, Cedars Sinai Medical Center, Los Angeles, California; 15Queensland Institute of Medical Research, Brisbane, Queensland, Australia; 16Hormonal and Reproductive Epidemiology Branch, 17Clinical Genetics Branch, Division of Cancer Epidemiology and Genetics, National Cancer Institute, Rockville, Maryland; 18Department of Health Sciences Research, 19Laboratory Medicine and Pathology, and 20Department of Medical Genetics, Mayo Clinic, Rochester, Minnesota; 21Institute for Medical Informatics, Statistics and Epidemiology, University of Leipzig, Leipzig, Germany; 22Institute of Genetic Constitution of the Fréjus Cancers, Centre Hospitalier Universitaire de Lyon/Centre Léon Bérard; 23INSERM U1032, CNRS UMR2586, Université Lyon 1, Cancer Research Center of Lyon; 24Cancer Genetics Network “Groupe Génétique et Cancer”, Fédération Nationale des Centres de Lutte Contre le Cancer, Lyon, France; 25Genetic Epidemiology Laboratory, Department of Pathology, University of Melbourne, Victoria, Australia; 26Department of Dermatology, University of Utah School of Medicine, Salt Lake City, Utah; 27Department of Epidemiology, Cancer Prevention Institute of California, Fremont, California; 28Departments of Molecular and Regenerative medicine, Hematology, Oncology and Transfusion Medicine Center, Vrije Universiteit University Hospital Santarinius Clinics, Vilnius, Lithuania; 29Genetic Epidemiology Laboratory, Hospital Clinico San Carlos, Madrid, Spain; 30Department of Dermatology, University of Utah School of Medicine, Salt Lake City, Utah; 31Department of Epidemiology, University of Melbourne, Victoria, Australia; 32Department of Dermatology, University of Utah School of Medicine, Salt Lake City, Utah; 33Latvian Biomedical Research and Study Centre, Riga, Latvia; 34Genomic Medicine, Department of Clinical Biochemistry, Rigshospitalet, Copenhagen University Hospital; 35Department of Clinical Genetics, Rigshospitalet, Copenhagen University, Denmark; 36Human Genetics Group, Human Cancer Genetics Programme, Spanish National Cancer Research Centre and Spanish Network on Rare Diseases (CIBERER); 37Molecular Oncology Laboratory, Hospital Clinico San Carlos, Madrid, Spain; 38Molecular Diagnostics Laboratory, IRRP, National Centre of Scientific Research “Demokritos”, Athens, Greece; 39Unit of Medical Genetics, 40Unit of Molecular Bases of Genetic Risk and Genetic Testing, Department of Preventive and Predictive Medicine, Fondazione IRCCS Istituto Nazionale Tumori (INT); 41Division of Cancer Prevention and Genetics, Istituto Europeo di Oncologia (IEO); 42Fondazione Istituto FIRC di Oncologia Molecolare, Milan, Italy; 43Department of Genetics, Biology and Biochemistry, University of Turin, Turin; 44Cancer Immunotherapy Unit, Centro di Riferimento Oncologico, IRCCS, Aviano (PN); 45Department of Clinical Physiopathology, University of Florence, Florence; 46Department of Molecular Medicine, “Sapienza” University of Rome, Rome, Italy; 47Molecular Genetics of Breast Cancer, Deutsches Krebsforschungszentrum (DKFZ); 48Institute of Human Genetics, Department of Human Genetics, Heidelberg University Hospital, Heidelberg, Germany; 49Department of Basic Sciences, Shaukat Khanum Memorial Cancer Hospital & Research Centre, Lahore, Pakistan; 50Family Cancer Epidemiology, Biomarkers & Prevention

December 5, 2011; DOI: 10.1158/1055-9965.EPI-11-0775

Downloaded from cebp.aacrjournals.org on August 9, 2021. © 2012 American Association for Cancer Research.
Abstract

**Background:** Previously, small studies have found that BRCA1 and BRCA2 breast tumors differ in their pathology. Analysis of larger datasets of mutation carriers should allow further tumor characterization.

**Methods:** We used data from 4,325 BRCA1 and 2,568 BRCA2 mutation carriers to analyze the pathology of invasive breast, ovarian, and contralateral breast cancers.

**Results:** There was strong evidence that the proportion of estrogen receptor (ER)-negative breast tumors decreased with age at diagnosis among BRCA1 (P-trend = 1.2 × 10^{-5}), but increased with age at diagnosis among BRCA2, carriers (P-trend = 6.8 × 10^{-6}). The proportion of triple-negative tumors decreased with age at diagnosis in BRCA1 carriers but increased with age at diagnosis of BRCA2 carriers. In both BRCA1 and BRCA2 carriers, ER-negative tumors were of higher histologic grade than ER-positive tumors (grade 3 vs. grade 1; P = 1.2 × 10^{-13} for BRCA1 and P = 0.001 for BRCA2). ER and progesterone receptor (PR) expression were independently associated with mutation status [ER-positive odds ratio (OR) for BRCA2 = 9.4, 95% CI: 7.0–12.6 and PR-positive OR = 1.7, 95% CI: 1.3–2.3, under joint analysis]. Lobular tumors were more likely to be BRCA2-related (OR for BRCA2 = 3.3, 95% CI: 2.4–4.4; P = 4.4 × 10^{-14}), and medullary tumors BRCA1-related (OR for BRCA2 = 0.25, 95% CI: 0.18–0.35; P = 2.3 × 10^{-15}). ER-status of the first breast cancer was predictive of ER-status of asynchronous contralateral breast cancer (P = 0.0004 for BRCA1; P = 0.002 for BRCA2). There were no significant differences in ovarian cancer morphology between BRCA1 and BRCA2 carriers (serous: 67%; mucinous: 1%; endometrioid: 12%; clear-cell: 2%).

**Conclusions/Impact:** Pathologic characteristics of BRCA1 and BRCA2 tumors may be useful for improving risk-prediction algorithms and informing clinical strategies for screening and prophylaxis.
Introduction

The tumor suppressor genes BRCA1 and BRCA2 are associated with high risks of breast, ovarian, and contralateral breast cancer. Tumors arising in BRCA1 and BRCA2 mutation carriers display characteristic pathologic features (1–3). Cancers occurring among BRCA1 carriers are more frequently classified as medullary (1, 4, 5) and exhibit higher grade and mitotic count than sporadic controls (2, 6–8). Numerous studies have linked the estrogen receptor (ER)-negativity of breast tumors with BRCA1 mutation carrier status (6, 9–16). In addition, tumors arising in BRCA1 carriers tend to lack progesterone receptors (PR) and HER2, and therefore, display the “triple negative” (TN) phenotype (6, 10). The majority of BRCA1 tumors express basal cytokeratins (17) and fall into the ‘basal’ subtype in gene expression studies (18).

Breast cancers arising in BRCA2 mutation carriers tend to be more heterogeneous than those arising in BRCA1 mutation carriers (19). They exhibit higher grade than tumors from age-matched sporadic controls (6, 7, 20). Several investigators have reported similar prevalence of ER-positive tumors in BRCA2 carriers compared with sporadic controls (6, 9, 16, 17), although in 1 study (20) BRCA2 tumors were more often ER-positive. BRCA2 tumors are less likely to be HER2 overexpressing/amplified compared with sporadic tumors (6, 17). However, most studies of BRCA2 mutation carriers have been small, and detailed tumor pathology information from BRCA2 carriers has been sparse.

Similarly, pathology studies conducted on contralateral breast cancer (21) and ovarian cancer (22–24) arising in BRCA1 and BRCA2 mutation carriers have been small in size. In this study, we report pathology data from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA), which is the largest collaborative study of BRCA1 and BRCA2 mutation carriers of its kind. We assessed the morphology, grade, and pathologic markers in breast tumors arising in BRCA1 or BRCA2 carriers, and estimated age-specific distributions of the different disease subtypes. Where possible, these distributions were compared with published data for the general population. In addition, we compared the pathology of tumors arising in BRCA1 and BRCA2 mutation carriers to identify characteristics that could distinguish between BRCA1 and BRCA2 mutation carriers. Such information is relevant for developing algorithms that predict mutation carrier status or breast cancer risk. For ovarian cancer, we assessed grade and morphologic features of tumors. For contralateral breast cancer, we examined the relationship between pathology of the second and first invasive breast cancer. The size of the present dataset allowed the study of smaller subsets of disease, such as ER-positive tumors in BRCA1 mutation carriers or TN tumors in BRCA2 mutation carriers and the estimation of age-specific proportions of tumor subtypes in BRCA1 and BRCA2 mutation carriers, which are currently imprecise. One of the aims of this work was to replicate findings on the basis of single reports or much smaller studies. The results of these analyses should be useful for improving breast cancer risk-prediction algorithms and may inform screening practices for, and prophylaxis of, cancers arising in BRCA1 and BRCA2 mutation carriers.

Materials and Methods

Study participants

Eligibility to CIMBA is restricted to female BRCA1 or BRCA2 pathogenic mutation carriers who are 18 years or older (25). Thirty-seven groups from North America, Australia, and Europe submitted data for this analysis (Supplementary Table S1). Information collected included year of birth, age at diagnosis of breast and/or ovarian cancer, age at last observation, family membership, race/ethnicity, and information on bilateral prophylactic mastectomy and oophorectomy. All centers obtained informed consent from study participants and the protocols were approved by local ethical review committees.

The present analysis was restricted to mutation carriers who had been diagnosed with breast or ovarian cancer for whom information on tumor pathologic characteristics was available, and to women of self-reported white European ancestry. The number of mutation carriers of non-European ancestry with data on tumor pathology was too small to allow a meaningful analysis. Information on at least 1 tumor characteristic was available for 4,325 BRCA1 and 2,968 BRCA2 mutation carriers.

Tumor pathology data

Data on pathology were derived from medical, pathology, or tumor registry records or confirmed by pathologic review. For some cases, tumor pathology was based on immunohistochemical staining and scoring of tissue microarrays (TMA). The sources of the data collected by each center are shown in Supplementary Table S1. For approximately 1,000 cases, detailed information on breast cancer pathology, for example, staining intensity or proportion of cells staining, accompanied the summary result in the pathology records. This information was cross-checked against the marker status provided. In case of any discrepancies, the most widely used definitions for the receptor status, shown in Supplementary Table S2, were used. Grades 1, 2, and 3 represent well-differentiated, moderately differentiated, and poorly undifferentiated tumors, respectively. However, no information was available on the tumor grading system used at each center. Data were analyzed by individual hormone receptor status, joint expression of ER and PR, and HER2.

Mutation class and position

Mutations in the BRCA1 and BRCA2 genes can be classified according to their potential functional effect (26–28). Class 1 mutations are loss-of-function mutations, expected to result in a reduced transcript or protein level because of mRNA nonsense-mediated decay and/or degradation or instability of truncated proteins, translation
re-initiation but no production of stable protein, or the absence of expression because of the deletion of transcription regulatory regions. Class 2 mutations are those likely to generate potentially stable mutant proteins that might have dominant negative action, partially preserved normal function, or loss of function. Class 2 mutations include missense substitutions, in-frame deletions and insertions, as well as truncating mutations with premature stop codons occurring in the last exon. Mutations whose consequences at the transcript or protein level could not be inferred were not considered for this classification.

Mutations occurring in the central portion of the BRCA2 gene (NG_012772), previously referred to as the "ovarian cancer cluster region" (OCCR), are associated with a higher ratio of ovarian: breast cancer versus mutations outside this region (29, 30). We used the definition of the OCCR determined by Thompson and Easton (30), as bounded by nucleotides corresponding to regions c.2831 to c.3847, and c.6275 to c.6401 according to the HGVS nomenclature. As there is uncertainty in defining precise boundaries, the wider region c.2831 to c.6401 was used.

Statistical methods

Logistic regression was used to assess the association between pathologic characteristics and BRCA mutation carrier status. For assessment of continuous or ordered variables such as grade and age, tests for trend were also carried out. When comparing the pathologic characteristics of BRCA1 and BRCA2 mutation carriers, cases from countries where the mutation carriers had a mutation exclusively in either BRCA1 or BRCA2 (e.g., Iceland) were excluded. All analyses were adjusted for age at diagnosis and for country of origin. A robust variance approach was used to allow for dependencies between related individuals. All analyses were carried out with Stata v10 software.

Results

Pathologic characteristics of breast tumors arising in BRCA1 and BRCA2 mutation carriers

The analysis was based on 3,797 BRCA1 mutation carriers and 2,392 BRCA2 mutation carriers diagnosed with invasive breast cancer. Median age at diagnosis of invasive breast cancers was 40 years [interquartile range (IQR): 12.3] among BRCA1 and 43 years (IQR: 13) among BRCA2 mutation carriers. The majority of invasive breast cancers arising in both BRCA1 and BRCA2 carriers were ductal/no special-type carcinomas (Table 1). Furthermore, 78% of tumors arising in BRCA1 carriers were ER-negative, 79% were PR-negative, 90% HER2-negative, and 69% were TN. However, 23% of tumors arising in BRCA2 mutation carriers were ER-negative, 36% were PR-negative, 87% were HER2-negative, and 16% were TN. Age-specific proportions of invasive breast tumors arising in BRCA1 and BRCA2 mutation carriers that were of histologic grades 1, 2, or 3 are shown in Fig. 1. The number

<table>
<thead>
<tr>
<th>Table 1. Pathology of invasive breast cancer in BRCA1 and BRCA2 mutation carriers and ORs for predicting BRCA2 mutation carrier status</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Morphology</strong></td>
</tr>
<tr>
<td>----------------</td>
</tr>
<tr>
<td>Invasive ductal</td>
</tr>
<tr>
<td>Invasive lobular</td>
</tr>
<tr>
<td>Medullary&lt;sup&gt;d&lt;/sup&gt;</td>
</tr>
<tr>
<td>Other</td>
</tr>
<tr>
<td>ER, PR, HER2, TN</td>
</tr>
<tr>
<td>ER-positive</td>
</tr>
<tr>
<td>PR-positive</td>
</tr>
<tr>
<td>HER2-positive</td>
</tr>
<tr>
<td>Non-TN (vs. TN)</td>
</tr>
<tr>
<td>Grade</td>
</tr>
<tr>
<td>Grade 1</td>
</tr>
<tr>
<td>Grade 2</td>
</tr>
<tr>
<td>Grade 3</td>
</tr>
</tbody>
</table>

<sup>a</sup>Number of tumors (n) of each morphology type or tumor grade, or number of receptor-positive tumors, and as percentage (%) of all BRCA1- or BRCA2-related tumors.

<sup>b</sup>ORs for BRCA2 mutation carrier status, compared with BRCA1 mutation carrier status, associated with tumor morphology, receptor-positive tumors, or grade 2 versus grade 1, and grade 3 versus grade 1 tumors; analyses were adjusted for country and age at diagnosis.

<sup>c</sup>Analyses adjusted for country, age at diagnosis, and tumor grade; ORs for analysis of grade, adjusted for country, age at diagnosis, and ER status.

<sup>d</sup>Includes atypical medullary carcinomas.
of women included in these analyses is shown in Supplementary Table S3. Age at diagnosis was associated with grade in BRCA1 mutation carriers, in whom grade decreased with increasing age (ordered logistic regression, \( P\)-trend = \(1.4 \times 10^{-13}\)). There was no evidence of a similar trend among BRCA2 mutation carriers (ordered logistic regression, \( P\)-trend = \(0.07\)); however, the ratio of grade 1 to grade 3 tumors increased with increase in age (\( P = 6 \times 10^{-8}\)).

Age-specific proportions of ER-negative, PR-negative, HER2-negative, and TN invasive breast tumors arising in BRCA1 and BRCA2 mutation carriers are shown in Fig. 2. The frequency of ER-negative tumors decreased with the age at breast cancer diagnosis in BRCA1 mutation carriers (\( P\)-trend = \(1.2 \times 10^{-5}\)), and increased with the age at diagnosis in BRCA2 mutation carriers (\( P\)-trend = \(6.8 \times 10^{-4}\)). The distribution of PR status showed similar trends, decreasing with age at diagnosis in BRCA1 (\( P\)-trend = \(0.02\)) and increasing with age at diagnosis in BRCA2 (\( P\)-trend = \(6.1 \times 10^{-5}\)) carriers. There was no evidence of variation in the distribution of HER2 status by age at diagnosis (\( P\)-trend = \(0.8\) and \( P = 0.9\) for BRCA1 and BRCA2 mutation carriers, respectively). However, the number of tumors with HER2 information was limited at the extreme age groups. The proportion of TN tumors decreased with age at breast cancer diagnosis in BRCA1 mutation carriers (\( P\)-trend = \(0.01\)), and increased with age at diagnosis in BRCA2 carriers (\( P\)-trend = \(0.001\)).

The analyses described above were adjusted for grade; analyses without this adjustment yielded similar results. In addition, the associations were not confounded by calendar time of diagnosis. For example, after adjusting for 5-year cohorts based on calendar year of diagnosis, the associations between ER status and age at diagnosis were still significant for both BRCA1 and BRCA2 mutation carriers (\( P\)-trend = \(2 \times 10^{-5}\) and \( P\)-trend = \(1.2 \times 10^{-5}\), respectively).

For both BRCA1 and BRCA2 mutation carriers, there were significant differences in the distribution of tumor grade by ER status (Table 2; Fig. 3) ER-negative tumors were associated with higher grade than ER-positive tumors. For example, in BRCA1 mutation carriers, grade 3 tumors were less likely to be ER-positive than grade 1 tumors (odds ratio (OR) for ER-positivity 0.12; 95% CI: 0.07–0.21; \( P = 1.2 \times 10^{-11}\)). For BRCA2 mutation carriers, grade 3 tumors were less likely to be ER-positive compared with grade 1 tumors (OR for ER-positivity, 0.33; 95% CI: 0.17–0.63; \( P = 0.001\)). The distribution of tumor morphology by ER status is also shown in Table 2.

We tested the hypothesis that mutation class or intra-genic position influences tumor characteristics. Approximately 66% of BRCA1 mutation carriers harbored Class 1 mutations and 25% had Class 2 mutations. Class 2 mutations were infrequent among BRCA2 mutation carriers. There were no significant differences between class of BRCA1 mutation and tumor pathology of BRCA1-related tumors. There were also no differences in characteristics of BRCA2-related tumors according to whether the mutation was within the OCCR region (32% of mutation carriers) or outside the OCCR (68% of mutation carriers; results not shown).

Information was also available on a small number of preinvasive, ductal carcinomas in situ (DCIS). Compared with invasive breast tumors, a higher proportion of DCIS arising in BRCA1 and BRCA2 mutation carriers were ER-positive (Supplementary Table S4).

Comparison of BRCA1 and BRCA2 tumors

We compared the morphologic characteristics of tumors arising in BRCA1 and BRCA2 mutation carriers. There were significantly more lobular carcinomas among BRCA2 carriers than among BRCA1 carriers (\( P = 4.4 \times 10^{-15}\), and significantly more medullary or atypical medullary carcinomas among BRCA1 mutation carriers than among BRCA2 carriers (\( P = 2.3 \times 10^{-15}\); Table 1).

Logistic regression analysis, treating receptor status (positive/negative) as the explanatory variable and BRCA1/BRCA2 mutation status as the outcome variable, was used to test association between tumor characteristics
and BRCA mutation carrier status. ER-positive tumors were more likely to arise in BRCA2 than BRCA1 (Table 1; OR for BRCA2 = 11.4; 95% CI: 9.8–13.2) and this was true in all morphologic categories (OR for BRCA2 = 10.2; 95% CI: 8.2–12.6 among ductal/no special-type carcinoma tumors; OR = 26.6; 95% CI: 4.4–159 among lobular carcinoma tumors; and OR = 5.6; 95% CI: 1.8–17.2 among medullary carcinoma tumors). PR-positive (OR = 6.8; 95% CI: 5.8–7.9), HER2-positive (OR = 1.5; 95% CI: 1.1–2.1) and non-TN tumors (OR = 11.0; 95% CI: 8.8–13.8)

Table 2. Distribution of grade and morphology of ER-positive and ER-negative tumors in BRCA1 and BRCA2 mutation carriers

<table>
<thead>
<tr>
<th>Type</th>
<th>BRCA1 Mutation Carriers</th>
<th>BRCA2 Mutation Carriers</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>ER-Negative, n (%)a</td>
<td>ER-Positive, n (%)</td>
</tr>
<tr>
<td>Grade</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Grade 1</td>
<td>18 (1.2)</td>
<td>28 (6.9)</td>
</tr>
<tr>
<td>Grade 2</td>
<td>191 (13.1)</td>
<td>170 (41.6)</td>
</tr>
<tr>
<td>Grade 3</td>
<td>1,246 (85.7)</td>
<td>210 (51.5)</td>
</tr>
<tr>
<td>Morphology</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ductal</td>
<td>1,353 (58.8)</td>
<td>385 (86.5)</td>
</tr>
<tr>
<td>Lobular</td>
<td>16 (2.7)</td>
<td>21 (4.7)</td>
</tr>
<tr>
<td>Medullaryc</td>
<td>141 (23.5)</td>
<td>17 (3.8)</td>
</tr>
<tr>
<td>Other</td>
<td>91 (15)</td>
<td>22 (5)</td>
</tr>
</tbody>
</table>

aNumber of tumors (n) of each grade or morphology type by ER-status as a percentage (%) of all ER-negative or ER-positive tumors where this information is available.
bOR and 95% CI are for ER-positive versus ER-negative disease in grade 2 or grade 3 tumors compared with grade 1 tumors. These analyses were adjusted for age at diagnosis of breast cancer and country of origin.
cIncludes medullary and atypical medullary tumors.
were also more likely to be BRCA2 than BRCA1 (Table 1). The associations remained significant after adjusting for tumor grade, with the exception of HER2. Tumors arising in BRCA1 mutation carriers were of significantly higher histologic grade than those arising in BRCA2 mutation carriers (Table 1). However, this difference was not significant when the analysis was adjusted for ER status.

Although ER and PR are highly correlated, expression of these hormone receptors is discordant in a small proportion of tumors. The tumors were, therefore, analyzed by joint ER and PR status (Supplementary Table S5). PR-positivity was associated with BRCA2 mutation carrier status in ER-negative tumors. In addition, PR-positivity was associated with BRCA2 mutation carrier status in the ER-positive subset of tumors (OR for BRCA2 = 1.5; 95% CI: 1.1–2.0; \(P = 0.01\)). There was no statistically significant difference in the distribution of HER2 among BRCA1 and BRCA2 mutation carriers when ER- and/or PR-positive tumors were analyzed separately, but TN tumors were significantly associated with BRCA1 carrier status when compared with HER2-positive–ER-negative–PR-negative tumors (Supplementary Table S5). In a model incorporating the joint effects of ER, PR, and HER2 in predicting BRCA2 versus BRCA1 mutation carrier status, both ER and PR remained significant although HER2 status was not (ER: \(OR = 9.4; 95\% \text{ CI}: 7.0–12.6\); PR: \(OR = 1.7; 95\% \text{ CI}: 1.3–2.3\); HER2: \(OR = 1.1; 95\% \text{ CI}: 0.7–1.6\)).

**Pathologic characteristics of first and contralateral breast tumors**

Information on pathology was available for 720 BRCA1 and 302 BRCA2 mutation carriers diagnosed with invasive contralateral breast cancer (CBC). The median time interval between first breast cancer and CBCs was 5.2 years (IQR: 7.5) for BRCA1 and 5.0 years (IQR: 9.3) for BRCA2 carriers. The median age at diagnosis of asynchronous CBC occurring more than 1 year after diagnosis of the first breast cancer, was 46 years (IQR: 13.6) for BRCA1 and 51
years (IQR: 13.9) for BRCA2 mutation carriers. Morphology, grade, and ER and PR status of the first invasive and asynchronous cancers are summarized in Supplementary Tables S6–S9. For BRCA1 mutation carriers, 91% of women with ER-negative first breast cancer developed ER-negative asynchronous CBC occurring more than a year after the first cancer, whereas 70% of women with ER-positive first cancer developed ER-negative asynchronous CBC. For BRCA2 mutation carriers, 52% of women with ER-negative first cancer developed ER-negative asynchronous CBC and 12% of women with ER-positive first cancer developed ER-negative asynchronous CBC. Logistic regression analysis, treating receptor status (positive/negative) of the second cancer as the outcome variable and receptor status of the first cancer as the explanatory variable, indicated that the ER status of the first breast cancer was predictive of ER status of the CBC for BRCA1 mutation carriers (OR = 5.8; 95% CI: 2.8–11.7; P = 1.2 × 10⁻⁶; Supplementary Table S8) as well as for BRCA2 mutation carriers (OR = 11.0; 95% CI: 4.3–28.6; P = 7.8 × 10⁻⁷). The conclusions were similar when the analyses were restricted to asynchronous contralateral cancers (OR = 4.3; 95% CI: 1.9–9.7; P = 0.0004 for BRCA1; and OR = 6.4; 95% CI: 2.0–20.9; P = 0.002 for BRCA2 carriers; Supplementary Table S8). There were smaller numbers of carriers with information on both ER status and grade. When adjusted for grade, the association remained significant in BRCA1, but was attenuated in BRCA2 carriers; however, the OR estimate was in the same direction (Supplementary Table S8). In addition, PR status of the first breast cancer was also associated with PR status of the second cancer (data not shown).

**Pathologic characteristics of ovarian cancers**

This dataset included 838 BRCA1 mutation carriers and 281 BRCA2 mutation carriers who had been diagnosed with ovarian cancer. The distribution of pathologic characteristics of the ovarian cancers are shown in Table 3. The majority (67%) of all cancers (BRCA1 and BRCA2) were serous. More than 70% of ovarian cancers in BRCA1 mutation carriers were classified as grade 3. There was no association between grade and age at cancer diagnosis (P = 0.4). In BRCA2 carriers, the proportion of grade 3 tumors increased slightly with age, whereas the proportion of grade 1 tumors decreased (ordered logistic regression, P-trend = 0.03). Furthermore, 310 BRCA1 and 105 BRCA2 mutation carriers had developed breast cancer before developing ovarian cancer. History of breast cancer did not influence morphology or grade of ovarian cancer (data not shown). There were no significant differences in ovarian cancer morphology or grade between BRCA1 and BRCA2 mutation carriers (P > 0.05, for all tests).

**Discussion**

We analyzed data on the pathology of breast and ovarian tumors arising in a large series of women with BRCA1 and BRCA2 mutations from the CIMBA consortium. Previous studies that have assessed tumor pathology in mutation carriers have been limited by small numbers, particularly among BRCA2 carriers. The present analysis of more than 4,000 BRCA1 and 2,000 BRCA2 carriers is the largest of its kind and allowed for accurate assessment of tumor pathology in mutation carriers, and more powerful comparisons between BRCA1 and BRCA2-related tumors.

We confirmed that the majority of BRCA1 breast cancers are ER-negative and TN tumors. We calculated age-specific proportions of tumors expressing pathologic markers including ER, PR, and HER2. The proportion of ER-positive and PR-positive tumors increased with age among BRCA1 mutation carriers, and decreased with age among...
BRCA2 mutation carriers. Analyses adjusting for grade or for calendar year of diagnosis to allow for changes in screening patterns over time yielded similar results.

Tung and colleagues (8) as well as Foulkes and colleagues (12) reported higher prevalence of ER-positive tumors among BRCA1 carriers diagnosed with breast cancer at an older age. Foulkes and colleagues found that, at every age group, the proportion of ER-negative tumors was higher in BRCA1 mutation carriers than non-carriers (12). We made similar observations comparing with the publicly available SEER data (31). We further confirmed differences in the distribution of grade between ER-positive and ER-negative BRCA1 tumors previously seen in smaller studies (8, 12). Tung and colleagues also reported differences in pathology between sporadic ER-positive tumors and ER-positive tumors arising in BRCA1 carriers (8). More recently, they reported that a similar percentage (80%) of ER-positive and ER-negative BRCA1-associated tumors showed loss of heterozygosity with loss of the wild-type BRCA1 allele (32). They suggested that ER-positive tumors in BRCA1 carriers could be a heterogeneous group, in some cases developing from complete loss of BRCA1 function, whereas in others, they developed with intact BRCA1 (8). Lakhan and colleagues further proposed that environmental exposures together with predisposition of the cells to genomic instability could result in the same cell populations producing different tumor subtypes (33). However the cell (or cells) of origin of BRCA1-related tumors have not been determined. These data suggest that ER-positive cancers in BRCA1-carriers are related to mutation carrier status rather than being incidental. A more definitive resolution of this question could be obtained by comparing the incidence of ER-positive tumors in BRCA1 mutation carriers with the incidence of ER-positive tumors in the general population. This is not yet possible reliably; however, in future prospective studies of cancer incidence, it should be possible to stratify analyses by tumor subtype.

Several investigators have reported similar prevalence of ER- and PR-positive disease in BRCA2 carriers compared with sporadic controls (6, 9, 16, 17). Bane and colleagues reported higher prevalence of ER-positive tumors in a series of 64 BRCA2 mutation carriers compared with age-matched non-carrier controls (20). We found a statistically significant decrease in the proportion of ER-positive tumors with age at diagnosis of breast cancer in BRCA2 mutation carriers, consistent with observations in a few much smaller studies (12, 34). Compared to the publicly available SEER data from the United States, the proportion of ER-negative tumors in BRCA2 mutation carriers appeared to be somewhat higher than that in women of the same age group in the general population (31). Although we could not directly compare the distribution of pathologic markers in mutation carriers and non-carriers in this dataset, this observation contrasts with the well-established increase in the relative incidence of ER-positive as compared with ER-negative breast cancers at older ages observed in the general population (35). A number of risk-prediction models have recently been extended to include tumor pathology information (36–38). In most of these models, variation in the expression of pathologic markers with age at breast cancer diagnosis was not taken into account. Our results indicate that using age-specific pathologic data in risk-prediction models may provide more accurate mutation carrier predictions. Furthermore, precise characterization of the distribution of tumor pathology in mutation carriers may influence prophylactic and treatment strategies. For example, although it is known that TN status is associated with BRCA1 mutations, in our study 16% (and up to 25% in women in the age group of 50–60 years) of tumors in BRCA2 mutation carriers were TN. Consistent with the above observations on ER status, we also found that the proportion of TN tumors in BRCA2 carriers increased with age at diagnosis of breast cancer. This confirms the observation of Tung and colleagues (8) as well as Foulkes and colleagues (12), and contradicts the assumption that a diagnosis of TN disease is ‘synonymous’ with BRCA1 carrier status. TN tumors would be expected to have poorer prognosis than ER-positive tumors and require chemotherapy. In addition, knowing the likelihood of developing a TN tumor in a BRCA1 or BRCA2 mutation carrier may influence the decision to undergo prophylactic surgery.

We confirmed that there are significant differences in the distribution of ER status between BRCA1 and BRCA2 breast cancers, and also found that PR is independently associated with mutation carrier status. Our results also suggest that ER-positive, PR-negative tumors were less likely to be BRCA2-related than double-positive tumors, and ER-negative, PR-positive tumors were more likely to be BRCA2-related than double-negative tumors. The ER-negative and PR-positive subset of tumors, previously considered a technical artifact, has now been shown in the general population to exhibit unique clinical characteristics, indicating that it is a distinct biologic entity (39). We found no significant association between HER2 status and BRCA1 or BRCA2 mutation carrier status. However, the number of HER2-overexpressing tumors may have been too small to address this reliably. TN tumors are more likely to be BRCA1 rather than BRCA2. In addition, we confirmed data showing that high-grade cancers are more frequent among BRCA1 carriers and that these women have a higher percentage of medullary cancers. By contrast, lobular cancers are substantially more frequent among BRCA2 carriers.

We found no difference in the distribution of tumor characteristics of BRCA1 mutation carriers by mutation category, defined by their functional effects. This analysis may be confounded by the fact that tumor characteristics may be used (together with other factors) to infer pathogenicity of a small subset of missense Class 2 BRCA1 mutations. In this dataset, only 2% of all BRCA1 mutations would have been in this category. In addition, we found no difference in the distribution of tumor characteristics of
BRCA2 carriers by mutation position (OCCR vs. non-OCCR). Establishing tumor pathology associated with mutations in BRCA1 and BRCA2 will further aid in the evaluation of unclassified variants.

We further assessed the pathology of invasive CBCs occurring in mutation carriers. Weitzel and colleagues reported strong concordance in ER status between first and CBC in a study of 211 BRCA1 and 75 BRCA2 carriers (21). These investigators did not detect a relationship between history of tamoxifen use or risk-reducing salpingo-oophorectomy and ER status of CBC in BRCA1/2 mutation carriers (21). However, Swain and colleagues found that patients in the general population with an ER-positive primary cancer receiving tamoxifen exhibited lower concordance rate with fewer ER-positive CBCs (40). In our study, we confirmed the association between ER and PR status of first invasive breast tumors and CBC, indicating that second breast cancers arising against the same genetic and environmental background are of similar pathology. However, the majority (70%) of BRCA1 mutation carriers diagnosed with ER-positive first breast cancers developed ER-negative CBC. Future CIMBA studies will aim to compare the tumor pathology of cancers occurring after RRSO.

In agreement with other reports, most ovarian cancers arising in BRCA1 and BRCA2 mutation carriers in our series were invasive epithelial cancers of serous histology, and we found no significant difference in morphology and grade of BRCA1 and BRCA2-related tumors (22–24). CIMBA, an international collaboration, was represented by more than 37 groups from more than 20 countries in the present study. Tumor pathology data were collected through several mechanisms, including medical records, pathology reports, and TMA. Laboratory methods for tissue preparation, immunohistochemistry, and biochemical assays, scoring systems and data interpretation vary widely (Supplementary Table S1). However, data collated by CIMBA are more representative of typical assessment of pathology conducted in routine practice, and the distributions of ER and PR status across different study centers and countries in CIMBA were generally consistent. There was some variation in the distribution of HER2 status across centers. This could perhaps be explained by technical issues relating to testing of HER2 and differences in the definition of HER2 status between centers. In addition, there was some variation in the distribution of grade and morphology across countries. Unfortunately, details of scoring for all mutation carriers were not available to standardize definitions across centers. Furthermore, data on the methods of detection of each tumor or treatment before pathologic analysis were not available, and these factors may influence the distribution of tumor subtypes detected (41). Future CIMBA studies will aim to collect TMA data and fixed tissue samples for rapid analysis of other markers, such as basal cytokeratins, p53, or novel candidates, and to further standardize collation of information on established markers.

A further limitation of our study is that CIMBA collects data only BRCA1 and BRCA2 mutation carriers. Therefore, we were unable to contrast the tumor characteristics in mutation carriers against the characteristics of breast cancers from the general population or from breast cancer patients without BRCA1 and BRCA2 mutations. Such an analysis would require careful selection of control subjects from the same populations who are sampled under similar conditions as BRCA1 and BRCA2 mutation carriers.

The genetic factors underlying etiology of breast cancer subtypes are still not fully understood. Previous studies have reported that ER-negative tumors arising in BRCA1 and BRCA2 mutation carriers presented higher genomic instability and patterns of genomic alteration than ER-positive tumors (42, 43). Many of the common breast cancer susceptibility alleles identified through GWAS are predominantly associated with either ER-positive or ER-negative disease. The pattern of association with ER-positive and ER-negative disease parallels those observed in BRCA2 and BRCA1 mutation carriers, respectively (44), indicating that common mechanisms underlie the phenotype of tumors in both mutation carriers and the general population. Recently, associations between the common breast cancer susceptibility alleles and separate disease subtypes in BRCA1 and BRCA2 mutation carriers were assessed, using data on the tumor subtype distributions presented here (47). Mulligan and colleagues showed differences in the associations of genetic modifiers with the risk of developing ER-positive or ER-negative breast cancer in BRCA1 and BRCA2 mutation carriers. These associations mirror similar differences in genetic susceptibility to ER-positive or ER-negative disease seen in the general population (45, 46). The apparent differences in single-nucleotide polymorphisms (SNP) associations between BRCA1 and BRCA2 carriers, and non-carriers observed previously, may be explained by differences in the prevalence of tumor subtypes.

The present CIMBA study is the largest of its kind, allowing more accurate characterization of the pathology of BRCA1 and BRCA2 tumors. As participants were collated from diverse countries and study centers, the findings should be widely applicable. We were able to calculate precise age-specific distributions of markers expressed, and replicate findings reported in only a few small studies to date. This information should be helpful for improving the performance of breast cancer risk-prediction models that calculate BRCA1 and BRCA2 mutation carrier probabilities, or for developing algorithms that predict the risk of specific breast cancer subtypes for mutation carriers. These may be of clinical use in guiding screening and prophylactic practices for mutation carriers.

Disclosure of Potential Conflicts of Interest

Timothy R. Rebbeck is the Editor-in-Chief of Cancer, Epidemiology, Biomarkers & Prevention. In keeping with the AACR’s editorial policy, the paper was peer reviewed and a member of the AACR’s Publications Committee rendered the decision with regard to acceptability. The content of this manuscript does not necessarily reflect the views or policies of the National Cancer Institute or any of

www.aacjrournals.org Cancer Epidemiol Biomarkers Prev; 21(1) January 2012 143
the collaborating centers in the Breast Cancer Family Registry (BCFR), nor does
mention of trade names, commercial products, or organizations imply endorse-
ment by the US Government or the BCFR.

Study-Specific Acknowledgments

Breast Cancer Family Registry (BCFR)

Samples from the FCCC, ICL and CPIC were processed and distributed by the
Coriell Cell Repositories through cooperative agreements.

Breast Cancer Family Registry (BCFR)—Ontario site

The authors thank Gord Glendon, Teresa Selander, Mona Gill, Lucille Collins,
Nayana Weeraratna, and members of the Ontario Familial Breast Cancer Registry
for their contributions to the study.

Baltic Familial Breast Ovarian Cancer Consortium (BFBOCC)

The authors thank the Genome Database of Latvian Population, Latvian
Biomedical Research and Study Center for providing data and DNA samples.

Copenhagen Breast Cancer Study (CBCS)

The authors thank Bent Jørlensen for providing clinical data.

Spanish National Cancer Center (CNIO)

The authors thank R.M. Alonso, G. Pita, and R.M. Milne for their assistance.

The Hereditary Breast and Ovarian Cancer Research Group
Netherlands (HEBON)

HEBON Collaborating Centers: Coordinating center: Netherlands Cancer
Institute, Amsterdam, NL; F.B.L. Hogervorst, S. Verhoef, M. Verheus, L.J. van
’t Veer, F.E. van Leeuwen, M.A. Bokkoos; Erasmus Medical Center, Rotterdam,
NL; M. Colte, A.M.W. van den Ouweland, A. Jager, M.J. Hooning, M.M.A.
Tulans, Linthorst, C. Seynaeve; Leiden University Medical Center, NL; Leiden:
C.J. van Asperen, J.T. Wijnken, M.P. Vreeswijk, R.A. Tollenaar, P. Devilee;
Radboud University Nijmegen Medical Center, Nijmegen, NL; M.J. Lignenberg,
N. Hoogerbrugge; University Medical Center Utrecht, Utrecht, NL; M.G.
Ausems, R.B. van de Luijt; Amsterdam Medical Center, NL: C.M. Aalst, T.
A. van Os; VU University Medical Center, Amsterdam, NL: J.P. Gille, Q.
Waisfisz, H.E.J. Meijers-Heijboer; University Hospital Maastricht, Maastricht,
NL: E.B. Gomez-Garcia, C.E. van Roosendaal, Marinus J. Blok, B. Caenen;
University Medical Center Groningen University, NL: J.C. Oosterwijk, A.H. van
der Hout, M.J. Mourtzis; The Netherlands Foundation for the detection of
hereditary tumors, Leiden, NL; H.F. Vasen.

Epidemiological study of BRCA1 and BRCA2 mutation carriers (EMBRACE)

Douglas Easton is the principal investigator of the study. EMBRACE Collab-
orating Centers are: Coordinating Centre, Cambridge; Susan Froock, Debra Frost,
Steve Ellis, Elena Fineberg, North of Scotland Regional Genetics Service, Aber-
deen; Zosia Miedzybrodzka, Helen Gregory, Northern Ireland Regional Genetics
Service, Belfast; Patrick Morrison, Lisa Jeffrey, West Midlands Regional Clinical
Genetics Service, Birmingham; Trevor Cole, Kai-ren Ong, Jonathan Hoffman,
South West Regional Genetics Service, Bristol; Alan Donaldson, Margaret James,
East Anglian Regional Genetics Service, Cambridge; Joan Paterson, Sarah Down-
ing, Amy Taylor. Medical Genetics Services for Wales, Cardiff: Alexander Murray,
Mark T. Rogers, Emma McCann, St James’s Hospital, Dublin & National Centre
for Medical Genetics, Dublin; M. John Kennedy, David Barton. South East of
Scotland Regional Genetics Service, Edinburgh: Mary Porteous, Sarah Drum-
mond, Peninsular Clinical Genetics Service, Exeter: Carole Brewer, Emma Kirova,
Anne Searle, Selina Goodman, Kathryn Hill, West of Scotland Regional Genetics
Service, Glasgow; Rosemarie Davidson, Victoria Murday, Nicola Bradshaw,
Lesley Snaddon, Mark Longmuir, Catherine Watt, Sarah Gibson, Eshka Hague,
Ed Tobias, Alexis Duncan, South East Thames Regional Genetics Service, Guy’s
Hospital London: Louise Iatrt, Chris Jacobs, Caroline Langman, Anna Whaitie.
North West Thames Regional Genetics Service, Harrow: Huw Dorkins, Leicester-
shire Clinical Genetics Service, Leicester: Julian Barwell. Yorkshire Regional
Genetics Service, Leeds: Julian Adlard, Carol Chu, Julie Miller, Cheshire &
Merseyside Clinical Genetics Service, Liverpool: Ian Ellis, Catherine Houghton.
Manchester Regional Clinical Genetics Service, Manchester: D. Gareth Evans, Fiona
Lalloo, Jane Taylor. North East Thames Regional Genetics Service, NE Thames,
London: Lucy Side, Alison Male, Cheryl Berlin. Nottinghamb Centre for Medical
Genetics, Nottingham: Jacqueline Eason, Rebecca Collier. Northern Clinical
Genetics Service, Newcastle: Fiona Douglas, Oonagh Clarke, Irene Johnson, Oxford
Regional Genetics Service, Oxford: Lisa Walker, Diane McLeod, Dorothy Halliday,
Sarah Durell, Barbara Stayner. The Institute of Cancer Research and Royal
Marsden NHS Foundation Trust, London: Bruce Felber, Susan Stanley, Naeemeh Rahman,
Richard Houlston, Elizabeth Bancroft, Licia D’Mello, Elizabeth Page, Audrey
Arden-Jones, Kelly Kohut, Jennifer Wiggins, Elena Castro, Anita Mitra, Lisa
Robertson. North Trent Clinical Genetics Service, Sheffield: Jackie Cook, Oliver
Quarrill, Cathryn Bardlsy. South West Thames Regional Genetics Service,
London: Shirley Hodgson, Sheila Goff, Glen Brice, Lizzie Winchester, Charlotte
Eddy, Vishakha Tripathi, Virginia Attard. Wessex Clinical Genetics Service,
Princess Anne Hospital, Southampton: Amanda Eccles, Anneke Lucassen, Gillian
Crawford, Deanna McBride, Sarah Smalley.

Fox Chase Cancer Center (FCCC) Fox Chase Cancer Center
Biosample Repository

The authors thank M. Pat Gilroy, Lesley Cruz, Diane Faison, Barbara Detettore,
Mary Donovan, and Meghan Butler for their help in collecting patient data and
samples.

University of Kansas Medical Center (KUMC)

The author, A.K. Godwin, thanks the support from The University of Kansas
Cancer Center and the Kansas Bioscience Authority Eminent Scholar Program.
A.K. Godwin is the Chancellor’s Distinguished Chair in Biomedical Sciences-
endowed Professor.

Genetic Modifiers of cancer risk in BRCA1/2 mutation carriers (GEMO) study

The GEMO study was conducted at Cancer Genetics Network ’Groupe
Génétique et Cancer’, Fédération Nationale des Centres de Lutte Contre le
Cancer, Lyon, France. The authors thank all the GEMO Collaborating centers for
their contribution to this study. GEMO Collaborating Centers are: Coordinating
Centres, Unite Mixte de Génétique Constitutionnelle des Cancers Fréquents,
Centre Hospitalier Universitaire de Lyon/Centre Léon Bérard, & Equipe
« Génétique du cancer du sein », Centre de Recherche en Cancérologie de Lyon:
Olga Smirnokova, Sylvie Mazoyer, Laure Barjoux, Carole Venn-Pierre, Sophie
Giraud, Mélanie Léone; and Service de Génétique Oncologique, Institut Curie,
Paris: Dominique Stoppa-Lyonnet, Marion Gauthier-Villars, Bruno Bucher,
Claude Houdayer, Viviane Moncomite, Mariel Belorti, Corine Perez, Antoine
de Pauly, Institut Gustave Roussy, Villejuif; Brigitte Bressac-de Paillerets, Audrey
Rennenmieres, Véronique Byrde, Olivier Caron, Gilien仑q, Nancy Unhammer,
Centre Léon Bérard, Lyon; Christine Lasset, Valerie Bonadonna, Centre Francais des
Cancer Frequent, Centre Hospitalier Universitaire Paris/Centre Léon Bérard, ‘Equipe
Génétique du cancer du sein’, Centre de Recherche en Cancérologie de Lyon:
Olga Smirnokova, Sylvie Mazoyer, Laure Barjoux, Carole Venn-Pierre, Sophie
Giraud, Mélanie Léone; and Service de Génétique Oncologique, Institut Curie,
Paris: Dominique Stoppa-Lyonnet, Marion Gauthier-Villars, Bruno Bucher,
Claude Houdayer, Viviane Moncomite, Mariel Belorti, Corine Perez, Antoine
de Pauly, Institut Gustave Roussy, Villejuif; Brigitte Bressac-de Paillerets, Audrey
Rennenmieres, Véronique Byrde, Olivier Caron, Gilien仑q, Nancy Unhammer,
Centre Léon Bérard, Lyon; Christine Lasset, Valerie Bonadonna, Centre Francais des
Cancer Frequent, Centre Hospitalier Universitaire Paris/Centre Léon Bérard, ‘Equipe
Génétique du cancer du sein’, Centre de Recherche en Cancérologie de Lyon:
Olga Smirnokova, Sylvie Mazoyer, Laure Barjoux, Carole Venn-Pierre, Sophie
Giraud, Mélanie Léone; and Service de Génétique Oncologique, Institut Curie,
Paris: Dominique Stoppa-Lyonnet, Marion Gauthier-Villars, Bruno Bucher,
Claude Houdayer, Viviane Moncomite, Mariel Belorti, Corine Perez, Antoine
de Pauly, Institut Gustave Roussy, Villejuif; Brigitte Bressac-de Paillerets, Audrey
Rennenmieres, Véronique Byrde, Olivier Caron, Gilien仑q, Nancy Unhammer,
Centre Léon Bérard, Lyon; Christine Lasset, Valerie Bonadonna, Centre Francais des
Cancer Frequent, Centre Hospitalier Universitaire Paris/Centre Léon Bérard, ‘Equipe

the Clinical Follow Up Study for their contributions to this resource, and the many families who contribute to kConFab.

Memorial Sloane Kettering Cancer Center (MSKCC)

Swedish Breast Cancer Study (SWE-BRCA)

UK and Gilda Radner Familial Ovarian Cancer Registries (UKGRFOCR)
The authors thank Paul Pharoah, Carole Pye, Patricia Harrington, and Eva Wozniak for their contributions toward the UKFOCR. The authors would like to acknowledge the Roswell Park Alliance Foundation for their continued support of the Gilda Radner Ovarian Family Cancer Registry. GRFOCR would like to acknowledge Kirsten Moyisch (Department of Cancer Prevention and Control).

Grant Support
This work was supported by Cancer Research UK grants CI2292/A11174 and CI287/A11018. The research leading to these results has received funding from the European Community’s Seventh Framework Programme under grant agreement no 223175 (HEALTH-F2-2009-223175). NM was funded by a scholarship from the Medical Research Council. ACA is a CR-UK Senior Cancer Research Fellow. DFE is a CR-UK Principal Research Fellow.

BCFR
This work was supported by the National Cancer Institute, NIH, under RFA-CA-06-503 and through cooperative agreements with members of the Breast Cancer Family Registry and Principal Investigators, including Cancer Care Ontario (U01 CA69467), Columbia University (U01 CA69398), Fox Chase Cancer Center (U01 CA69631), Huntsman Cancer Institute (U01 CA69446), Cancer Prevention Institute of California (U01 CA69417), University of Melbourne (U01 CA69638), and Research Triangle Institute Informatics Support Center (RFP No. N02PC-60522-46).

BCFR—Ontario site
This work was supported by Cancer Care Ontario and the U.S. National Cancer Institute, NIH, under RFA-CA-06-503 and through cooperative agreements with members of the Breast Cancer Family Registry (BCFR) and principal investigators.

BFBOCC
Lithuania: This work is financially supported by the Research Council of Lithuania grant 1LGI-19-2010 to R. Janavicius, Latvia: I. Tihomirova was financially supported by LSC grants 05.0023.04 and 10.0010.08.

CBCS
The authors thank LEYE Foundation for financial support

Spanish National Cancer Center (CNIO)
This study was partially supported financially by the Fundación Mutua Madrileña, Asociación Española Contra el Cáncer and the Spanish Ministry of Science and Innovation (FIS PI08 1120). This was funded, in part, by the Basque Foundation for Health Innovation and Research (BIOEF): B1007/CA/006.

DKFZ study
The DKFZ study was supported by the DKFZ.

HEBON
The HEBON study is supported by the Dutch Cancer Society grants NKI1998-1854, NKI2004-3088, and NKI2007-3756 and the ZonMW grant 91190924.

EMBRACE
EMBRACE is financially supported by Cancer Research UK Grants CI287/A10118 and CI287/A11990. D.G. Evans and F. Laloue are financially supported by an NHRI grant to the Biomedical Research Centre, Manchester, UK. The investigators at The Institute of Cancer Research and The Royal Marsden NHS Foundation Trust are financially supported by an NIHR grant to the Biomedical Research Centre at the Institute of Cancer Research and the Royal Marsden NHS Foundation Trust. R. Eeles, E. Bancroft, and L. D’Mello are also financially supported by a Cancer Research UK grant C3047/A8385.

KUMC
A.K. Godwin was funded by U01CA69631, 5U01CA111396, and the Eileen Stein Jacoby Fund.

GC-HBMC
GC-HBMC is financially supported by a grant of the German Cancer Aid (grant 199076) the Centre of Molecular Medicine Cologne (CMMC).

GEMO
This study was supported by The Ligue Nationale Contre le Cancer and The Association “Le cancer du sein, parons-en!” Award.

Georgetown University (GEORGETOWN)
C. Isaacs and B.N. Peshkin are supported by National Cancer Institute Grant (NCI P30 CA51008-12) and by the Fisher Center for Familial Cancer Research.

HEBCS
The HEBCS study has been financially supported by the Helsinki University Central Hospital Research Fund, Academy of Finland (132473), the Finnish Cancer Society, and the Sigrid Juselius Foundation.

Iceland Landspitali—University Hospital (ILUH)
The ILUH group was supported by the Icelandic Association “Walking for Breast Cancer Research” and by the Landspitali University Hospital Research Fund.

INHERIT BRCA
This work was supported by the Canadian Institutes of Health Research for the "CIHR Team in Familial Risks of Breast Cancer" program and by the Canadian Breast Cancer Research Alliance—grant #019511.

Istituto Oncologico Veneto—Hereditary Breast Ovarian Cancer Study (IOVHBOCS)
This study was supported by "Ministero della Salute" (grant numbers RFS 2006-5-341353, ACC2/R6.9 and "Progetto Tumori Femminili").

kConFab
kConFab is supported by grants from the National Breast Cancer Foundation, the National Health and Medical Research Council (NHMRC) and by the Queensland Cancer Fund, the Cancer Councils of New South Wales, Victoria, Tasmania and South Australia, and the Cancer Foundation of Western Australia (funded by NHMRC grants 145684, 288704, and 454588).

Mayo Clinic (MAYO)
The MAYO study was supported by NIH grants CA116167, CA128978, a Specialized Program of Research Excellence (SPORE) in Breast Cancer (CA116281), and awards from the Komen Foundation for the Cure and the Breast Cancer Research Foundation.

National Cancer Institute (NCI)
The research of Drs. P.L. Mai and M.H. Greene was supported by the Intramural Research Program of the U.S. National Cancer Institute
References


Tumor Pathology in BRCA1 and BRCA2 Mutation Carriers


Pathology of Breast and Ovarian Cancers among BRCA1 and BRCA2 Mutation Carriers: Results from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA)

Nasim Mavaddat, Daniel Barrowdale, Irene L. Androulis, et al.