Gene panel testing of 5589 BRCA1/2-negative index patients with breast cancer in a routine diagnostic setting: results of the German Consortium for Hereditary Breast and Ovarian Cancer

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Abstract
The prevalence of germ line mutations in non-BRCA1/2 genes associated with hereditary breast cancer (BC) is low, and the role of some of these genes in BC predisposition and pathogenesis is conflicting. In this study, 5589 consecutive BC index patients negative for pathogenic BRCA1/2 mutations and 2189 female controls were screened for germ line mutations in eight cancer predisposition genes (ATM, CDH1, CHEK2, NBN, PALB2, RAD51C, RAD51D, and TP53). All patients met the inclusion criteria of the German Consortium for Hereditary Breast and Ovarian Cancer for germ line testing. The highest mutation prevalence was observed in the CHEK2 gene (2.5%), followed by ATM (1.5%) and PALB2 (1.2%). The mutation prevalence in each of the remaining...
Introduction

The prevalence of heterozygous BRCA1 and BRCA2 germ line mutations and their associated risks for breast cancer (BC) and ovarian cancer (OC) have been extensively studied [1]. Pathogenic BRCA1 and BRCA2 germ line mutations were found in approximately 17% of the index patients with BC who met the inclusion criteria of the German Consortium for Hereditary Breast and Ovarian Cancer (GC-HBOC) for germ line testing [2]. With the advent of next-generation sequencing (NGS), germ line testing for hereditary BC/OC could be extended beyond the analysis of the BRCA1 and BRCA2 genes [3]. However, gene panel sequencing and the testing of a number of potential risk genes are challenging, as international guidelines for the clinical management of patients carrying mutations in non-BRCA1/2 genes do not exist. Established non-BRCA1/2, BC/OC risk genes are rarely mutated [4–7], and data regarding their contribution to BC/OC risk are often controversial. Hence, verification is needed before the non-BRCA1/2 genes generally included in gene panel testing can be treated as confirmed BC/OC risk genes [8, 9]. Moreover, criteria that predict mutation probabilities in non-BRCA1/2 genes are largely unknown and may differ from those that predict mutation probabilities in BRCA1 and BRCA2.

The GC-HBOC established multi-gene panel testing in 2015. In addition to BRCA1 and BRCA2, eight genes were defined as “core genes” based on data available at the time of the gene panel design, that suggested their association with BC (ATM, CDH1, CHEK2, NBN, PALB2, and TP53) or OC (RAD51C and RAD51D) [10–13]. With a relative risk of 5.3 (90% CI: 3.0–9.4), deleterious mutations in the PALB2 gene appeared to confer high BC risk [14–17]. Lower relative risks were reported for mutations in the CHEK2 (3.0, 90% CI: 2.6–3.5) [18, 19] and ATM genes (2.8, 90% CI: 2.2–3.7) [3, 20–23]. The NBN gene was considered as a BC predisposition gene mainly based on the genotyping results of a common founder mutation, c.657_661del, p.(Lys219Asnfs*16). For this variant, a meta-analysis of 10 studies revealed a pooled OR of 2.66 (95% CI: 1.82–3.90; P < .001) [24]. Mutations in TP53 and CDH1 are associated with multiple cancer types, one of which is BC. For CDH1 mutations, a relative BC risk of 6.6 (90% CI: 2.2–19.9; P = .004) was reported [25], whereas reliable risk estimates for TP53 mutations are missing. Mutations in the RAD51C and RAD51D genes have shown clear evidence of an association with OC, whereas evidence of an association with BC is limited [10, 26, 27]. The aim of this study was to investigate the associations of germ line mutations in selected non-BRCA1/2 genes with BC risk and BC phenotype in a
sample of 5589 BRCA1/2 negative BC index patients who were recruited and counseled at university hospital-based centers of the GC-HBOC.

Patients and Methods

Patient sample

All patients met the inclusion criteria of the GC-HBOC for germline testing (Table S1). Of note, the GC-HBOC inclusion criteria are not restricted to familial cases and also consider patients with early-onset BC (age at first diagnosis [AAD] before 36 years), bilateral BC (AAD before 51 years), and patients affected by BC and OC even in the absence of a family history of BC and OC. In the absence of a patient with OC in a family, the available BC patient with the youngest AAD was defined as the index patient. In families with OC, a BC patient was defined as the index patient only when DNA derived from the OC patient was not available for genetic testing. Overall, 5589 female index patients with BC and without a personal history of OC were included in this study. All patients were counseled at a participating GC-HBOC center. Physicians qualified in genetic counseling recorded personal and family BC/OC history, information regarding age at first BC diagnosis and tumor receptor status. Written informed consent was obtained from all patients, and ethical approval was granted by the ethics committee of the University of Cologne (07-048). All patients were tested negative for pathogenic germ line variants in the BRCA1 and BRCA2 genes, including large genomic rearrangements (LGRs).

Control sample

Two publicly accessible control datasets (ExAC and FLOSSIES) and sequencing data from 2189 geographically matched female controls were used in this study (Table 1). From the Exome Aggregation Consortium (ExAC) [28], we requested a dataset of individuals of European, non-Finnish ancestry, excluding samples from The Cancer Genome Atlas (TCGA). This dataset comprises a total of 27,173 samples, which were analyzed by whole exome sequencing. The FLOSSIES project provides a dataset of 7325 women of European American ancestry (https://whi.color.com). All participating women have remained cancer-free until at least 70 years of age. Germ line DNA samples of all participants were screened for variants in 27 established or suggested BC predisposition genes, including the eight selected non-BRCA1/2 genes. In addition, we sequenced germ line DNA samples of 2189 female control individuals of German descent (geographically matched controls; GMCs) by NGS and analyzed these samples for variants in the eight selected non-BRCA1/2 genes. Healthy controls were recruited by a study on genetic factors of a noncancer, age-related phenotype, and a study on civilization diseases. The studies were approved by the local ethic committees, and all participants gave their written informed consent. At the time of blood draw, all GMCs were at least 40 years old (mean age 63, range 40–92) and cancer-free.

Gene panel analysis

Genomic DNA was isolated from venous blood samples. NGS and data analysis were carried out at each participating center using Illumina sequencing platforms, employing either the customized TruRisk® (Agilent or Illumina), a customized HaloPlex (Agilent, Santa Clara, California, USA), or the TruSight™ Cancer Sequencing Panel (Illumina, San Diego, California, USA) for target enrichment. All gene panels covered the eight selected non-BRCA1/2 core genes. The diagnostic pipelines of the labs involved have been successfully tested in European Molecular Genetics Quality Network (EMQN) schemes. Since LGRs cannot be detected reliably on the basis of NGS-data [29], this mutation type was not included in this study. All deleterious variants affecting canonical non-BRCA1/2 core gene transcripts (ATM, NM_000051.3; CDH1, NM_004360.3; CHEK2, NM_007194; NBN, NM_002485.4; PALB2, NM_024675.3; RAD51C, NM_058216.2; RAD51D, NM_002878.3; TP53, NM_0000546.5) were routinely verified by Sanger sequencing.

Variant classification

Variant classification was performed in accordance with the regulations of the international ENIGMA consortium [30] (Evidence-based Network for the Interpretation of Germ line Mutant Alleles; https://enigmaconsortium.org; version 1.1: 26 March 2015). All genetic variants were classified using a five-tier variant classification system as proposed by the Unclassified Genetic Variants Working Group of the International Agency for Research on Cancer (IARC) (deleterious = class 5, likely deleterious = class 4, variant of uncertain significance (VUS) = class 3, likely benign = class 2, and benign = class 1) [31]. According to the ENIGMA regulations [30], variants reported with a minor allele frequency (MAF) ≥1% in control reference groups (e.g., ExAC excluding TCGA, FLOSSIES) were generally considered benign (class 1). For simplification, class 4/5 variants were defined as “deleterious variants.” To investigate the associations of germ line mutations in selected non-BRCA1/2 genes with BC risk, only protein truncating variants (PTVs) were considered in patients and controls. PTVs were defined as nonsense, frameshift, or essential splice-site variants affecting the invariant splice sites or the last nucleotide of an exon. As suggested by Lilyquist et al., protein truncating variants in the last exon
or within the last 55 bp of the penultimate exon were classified as VUS, unless a known functional domain was disrupted [32]. For the identification of potentially damaging, rare missense variants we employed two in silico prediction tools (SIFT and MutationTaster). Missense variants were defined as potentially damaging when predicted deleterious by both tools (Alamut version 2.10; Interactive Biosoftware, Rouen, France) as of 30 November 2017.

**Statistical analysis**

We performed case–control analyses for the investigation of the association of variants with the BC phenotype and case–case analyses for comparison of molecular subgroups. Univariate logistic regression was performed to estimate odds ratios (OR) and 95% confidence intervals (95%CI) using SPSS Statistics, Version 25 (IBM, Armonk, New York, USA). Fisher’s exact test and the Student’s t-test (for aged-related analysis) were used to calculate levels of significance, with P-values <0.05 considered significant.

**Results**

**Associations of protein truncating variants in the selected core genes with BC**

Detailed information on the patient sample is given in Table 1. Only protein truncating variants (PTVs) were considered to investigate the associations of germ line mutations in selected non-BRCA1/2 genes with BC risk in patients and controls. A list of all PTVs identified in the study sample is provided in Table S2. Among 5589 index patients with BC, 274 patients (4.9%) carried PTVs in the selected non-BRCA1/2 genes. The overall occurrence of PTVs in the selected core genes was markedly lower in all three control datasets compared with BC index patients. In the ExAC control dataset, 389 out of 27,173 individuals (1.4%) carried PTVs, which was comparable to the hypernormal control datasets FLOSSIES (67 of 7325 women, 0.9%) and GMCs (33 of 2189 women, 1.5%). When comparing mutation prevalence in BC index patients with ExAC data on a gene-specific level, significant associations were observed for ATM (OR: 3.63, 95% CI 2.67–4.94; P < .0001), CHEK2 (OR: 2.93, 95% CI 2.29–3.75; P < .0001), PALB2 (OR: 9.53, 95% CI 6.25–14.51; P < .0001), CDH1 (OR: 17.04, 95% CI 3.54–82; P < .0001), and TP53 (OR: 7.30, 95% CI 1.22–43.68; P = .038) (Table 2). In contrast, we did not observe significant associations between PTVs in the NBN gene and BC (OR: 1.39, 95% CI 0.73–2.64; P = .363). When comparing the PTV prevalence in BC index patients with hypernormal controls (FLOSSIES, GMCs), higher ORs were observed for ATM, CHEK2, and PALB2 than were observed in comparison with ExAC data (Table 2). Again, no association between PTVs in the NBN gene and BC was observed. In contrast to the aforementioned genes, the analysis of RAD51C and RAD51D revealed ambiguous results. For RAD51C, a significant association with BC was observed when comparing PTV prevalence with FLOSSIES but not when compared with ExAC data or GMCs (Table 2). For RAD51D, ORs of 3.04 (vs. ExAC data) and 3.28 (vs. FLOSSIES) were observed, though both comparisons did not reach levels of significance (Table 2).

**Deleterious variants in non-BRCA1/2 genes in the overall patient sample**

Overall, heterozygous deleterious variants in at least one of the eight non-BRCA1/2 core genes were present in
Table 2. Prevalence of protein truncating variants (PTVs) in eight non-BRCA1/2 cancer predisposition genes in 5589 BC index patients compared with control datasets (ExAC, FLOSSIES, and GMCs). Percentages of individuals carrying a mutation in the respective datasets are shown in parentheses.

<table>
<thead>
<tr>
<th>Gene</th>
<th>BC n = 5589 (%)</th>
<th>ExAC n = 27,173 (%)</th>
<th>FLOSSIES n = 7,325 (%)</th>
<th>GMCs n = 2,189 (%)</th>
<th>BC vs. ExAC OR (95% CI, P*)</th>
<th>BC vs. FLOSSIES OR (95% CI, P*)</th>
<th>BC vs. GMCs OR (95% CI, P*)</th>
</tr>
</thead>
<tbody>
<tr>
<td>ATM</td>
<td>71 (1.27)</td>
<td>96 (0.35)</td>
<td>14 (0.19)</td>
<td>9 (0.41)</td>
<td>3.63 (2.67–4.94, &lt;0.0001)</td>
<td>6.72 (3.78–11.93, &lt;0.0001)</td>
<td>3.12 (1.56–6.25, 0.0004)</td>
</tr>
<tr>
<td>CDH1</td>
<td>7 (0.13)</td>
<td>2 (0.01)</td>
<td>0 (0.00)</td>
<td>0 (0.00)</td>
<td>17.04 (3.54–82, &lt;0.0001)</td>
<td>n.a. (n.a., 0.0028)</td>
<td>n.a. (n.a., 0.2020)</td>
</tr>
<tr>
<td>CHEK2</td>
<td>103 (1.84)</td>
<td>172 (0.63)</td>
<td>28 (0.38)</td>
<td>11 (0.50)</td>
<td>2.93 (2.29–3.75, &lt;0.0001)</td>
<td>4.87 (3.20–7.40, &lt;0.0001)</td>
<td>3.72 (1.99–6.94, &lt;0.0001)</td>
</tr>
<tr>
<td>CHEK2, c.1100del</td>
<td>79 (1.41)</td>
<td>127 (0.47)</td>
<td>22 (0.30)</td>
<td>8 (0.37)</td>
<td>3.02 (2.28–4.01, &lt;0.0001)</td>
<td>4.71 (2.93–7.56, &lt;0.0001)</td>
<td>3.91 (1.87–8.05, &lt;0.0001)</td>
</tr>
<tr>
<td>NBN</td>
<td>12 (0.21)</td>
<td>42 (0.15)</td>
<td>14 (0.19)</td>
<td>9 (0.41)</td>
<td>1.39 (0.73–2.64, 0.3630)</td>
<td>1.12 (0.53–2.43, 0.8438)</td>
<td>0.52 (0.22–1.24, 0.1466)</td>
</tr>
<tr>
<td>PALB2</td>
<td>64 (1.15)</td>
<td>33 (0.12)</td>
<td>7 (0.10)</td>
<td>2 (0.09)</td>
<td>9.53 (6.25–14.51, &lt;0.0001)</td>
<td>12.11 (5.55–26.45, &lt;0.0001)</td>
<td>12.67 (3.10–51.79, &lt;0.0001)</td>
</tr>
<tr>
<td>RAD51C</td>
<td>9 (0.16)</td>
<td>34 (0.13)</td>
<td>2 (0.03)</td>
<td>2 (0.09)</td>
<td>1.29 (0.62–2.69, 0.5409)</td>
<td>5.91 (1.28–27.34, 0.0129)</td>
<td>1.76 (0.38–8.17, 0.7384)</td>
</tr>
<tr>
<td>RAD51D</td>
<td>5 (0.09)</td>
<td>8 (0.03)</td>
<td>2 (0.03)</td>
<td>0 (0.00)</td>
<td>3.04 (0.99–9.30, 0.0558)</td>
<td>3.28 (0.64–16.91, 0.2512)</td>
<td>n.a. (n.a., 0.3308)</td>
</tr>
<tr>
<td>TP53</td>
<td>3 (0.05)</td>
<td>2 (0.01)</td>
<td>0 (0.00)</td>
<td>0 (0.00)</td>
<td>7.30 (1.22–43.68, 0.0378)</td>
<td>n.a. (n.a., 0.0810)</td>
<td>n.a. (n.a., 0.5640)</td>
</tr>
<tr>
<td>PTVs</td>
<td>274</td>
<td>389</td>
<td>67</td>
<td>33</td>
<td>n.a. (n.a., 0.0028)</td>
<td>n.a. (n.a., 0.0028)</td>
<td>n.a. (n.a., 0.0028)</td>
</tr>
<tr>
<td>Carriers</td>
<td>272 (4.87)</td>
<td>389 (1.43)</td>
<td>67 (0.91)</td>
<td>33 (1.51)</td>
<td>n.a. (n.a., 0.0028)</td>
<td>n.a. (n.a., 0.0028)</td>
<td>n.a. (n.a., 0.0028)</td>
</tr>
</tbody>
</table>

OR, odds ratio; CI, confidence interval.
*Fisher’s exact test.
#Two patients carried two PTVs (ATM and CHEK2; NBN and RAD51C).

339 of the 5589 BC index patients (6.1%, Table 3). The highest prevalence of deleterious variants was observed in the CHEK2 gene (138 carriers, 2.5%), followed by ATM (81 carriers, 1.4%) and PALB2 (68 carriers, 1.2%). The prevalence of deleterious variants in the CDH1, NBN, RAD51C, RAD51D, and TP53 genes in the overall patient sample was 0.3% or lower for each gene (Table 3). Overall, 147 distinct deleterious variants were identified in 339 patients, of which 45 were recurrent (Table). With a carrier frequency of 1.4%, the c.1100del founder variant in the CHEK2 gene was the most prevalent deleterious variant observed (Table 3).

Deleterious variants in non-BRCA1/2 genes according to personal and family history of cancer

Among the 5589 BC index patients, 629 were affected by bilateral BC. In this subgroup, 8.3% of patients (52 of 629) carried a deleterious variant in at least one of the eight selected genes. This was significantly higher than the prevalence of deleterious variants in the 4960 BC index patients affected by unilateral BC (5.8%, 289 in 4960; P = .021). On a gene-specific level, the CHEK2 c.1000del founder variant (2.5% vs. 1.3%; P = .018), deleterious variants in the PALB2 gene (2.2% vs. 1.1%; P = .020), and deleterious variants in the TP53 gene (0.79% vs. 0.24%; P = .035) were significantly associated with bilateral BC (Table 3). Of the 5589 BC index patients, 934 reported a family history of OC. The prevalence of deleterious variants was not significantly different in BC index patients with a family history of OC versus the 4655 BC index patients who had no family history of OC (data not shown).

Deleterious variants in non-BRCA1/2 genes according to age at first diagnosis of BC

In a gene-specific analysis, only patients carrying deleterious TP53 variants showed a younger mean age at first BC diagnosis (TP53: 39.7 years, range 23–71 years) compared with the overall sample (46.7 years, range 17–92 years), with differences reaching levels of significance (P = .004, Student’s t-test, Table 4). For example, 52.9% (9 of 17) of the TP53 mutation carriers showed an age at first BC diagnosis below the age of 40 years compared with 26.0% (1440 of 5540) of the BC index patients overall (P = .021, Table 4). Overall, no significant difference in age at first BC diagnosis was observed between patients carrying deleterious variants and the overall sample (Table 4).

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Deleterious variants in BC index patients according to ER/PR/HER2 status

Information regarding hormone receptor (ER/PR) and HER2 status was available for a subgroup of 3104 of the 5589 BC index cases. Within this subgroup, 482 showed a triple-negative breast cancer (TNBC) phenotype (15.5%, Table 1). The mutation prevalence in patients with ER-positive BC was significantly increased in patients with ER-negative tumors (7.3% vs. 4.7%, \( P = .014 \); Table 5).

In a gene-specific analysis, this difference was highest in the ATM (1.83% vs. 0.53%, \( P = .009 \); Table 5) and CHEK2 genes (3.2% vs. 1.9%, \( P = .060 \); Table 5). The overall prevalence of deleterious variants was not significantly different when stratified by PR or HER2 status (Table 5). On a gene-specific level, however, a particularly high CHEK2 mutation prevalence was observed in patients with HER2-positive tumors compared with patients with HER2-negative tumors (5.2% vs. 2.3%; \( P < .001 \); Table 5).
Predicts a significantly lower mutation probability in the selected genes. While deleterious mutations were present in 186 of the 2622 patients with non-TNBC (7.1%), only 20 of the 482 patients with TNBC (4.1%) carried a deleterious mutation ($P = .017$; Table 5). Both the ATM and CHEK2 genes showed significantly higher mutation rates in patients with non-TNBC versus patients with a TNBC tumor phenotype (ATM: 1.7% vs. 0.4%; $P = .026$; CHEK2: 3.3% vs. 0.8%, $P = .002$; Table 5).

### Discussion

In our sample of 5589 BC index cases, we confirmed that PTVs in the ATM, CDHI, CHEK2, PALB2, and TP53 genes increase BC risk. The ORs for the most frequently mutated genes (ATM (OR: 3.63, 95% CI 2.67–4.94), CHEK2 (OR: 2.93, 95% CI 2.29–3.75), and PALB2 (OR: 9.53, 95% CI 6.25–14.51) are compatible with published data, according to a meta-analysis focusing on PTVs [33]. In this meta-analysis, an aggregated OR of 3.20 (95% CI 2.04–5.04; analysis of 4266 cases and 5566 controls) was calculated for ATM, an aggregated OR of 3.25 (95% CI 2.55–4.13, analysis focusing on PTVs [33]. In this meta-analysis, an aggregated OR of 3.20 (95% CI 2.04–5.04; analysis of 4266 cases and 5566 controls) was calculated for ATM, an aggregated OR of 3.25 (95% CI 2.55–4.13, analysis focusing on PTVs [33].

In contrast to previous studies focusing on the c.657_661del, p.(Lys219Asnfs*16) founder mutation [24],
we could not confirm NBN as a BC predisposition gene (OR: 1.39, 95% CI 0.73–2.64; P = .363; Table 2). This is consistent with the panel gene analyses by Couch et al. (OR: 1.27, 95% CI 0.81–2.01; P = .32) and Thompson et al. (OR: 0.67, 95% CI 0.11–4.0; P = 1.00) [4, 9]. For RAD51D mutations, we demonstrated some indication of an association with BC (OR: 3.04, 95% CI 0.99–9.30; P = .0558), which is compatible with the results obtained by Couch et al. using the same control dataset (OR: 2.90, 95% CI 1.12–7.21; P = .02) [4]. However, these associations did not reach levels of significance. Thus, we suggest that larger collaborative studies are necessary to assess the role of RAD51D in BC pathogenesis. The same holds true for RAD51C mutations for which we showed an elevated prevalence in BC index patients versus hyper-normal controls but not versus ExAC data (Table 2).

We demonstrated significantly higher mutation prevalence in bilateral versus unilateral BC cases, with highest differences in CHEK2, PALB2, and TP53 (Table 3). In agreement with the data presented here, Couch et al. showed that pathogenic variants in CHEK2, PALB2, and TP53 were associated with bilateral BC [4]. A young age at BC disease onset, a personal or family history of OC, and the occurrence of the TNBC tumor phenotype predict high mutation probabilities in the BRCA1 gene and to a lesser extent in the BRCA2 gene [2]. However, these criteria do not effectively enrich for patients with mutations in non-BRCA1/2 genes. In this investigation, age at first BC diagnosis did not significantly predict mutation probabilities overall, with the exception of TP53 mutations, which is well in line with published data [34, 35]. The mutation prevalence in non-BRCA1/2 genes stratified by age likewise did not differ markedly in the studies of Thompson et al. and Buyse et al. [5, 9]. Of note, the subgroup of patients with TNBC, a tumor phenotype closely associated with a high BRCA1 mutation prevalence [35, 36], showed lower mutation probabilities in non-BRCA1/2 genes, especially for ATM and CHEK2 mutations, we identified a negative association with this subtype (Table 5). Similar results were observed by Buyse et al., demonstrating significantly lower mutation probabilities for both genes in patients with TNBC versus other subtypes [5]. Deleterious ATM and CHEK2 mutations were particularly frequent in ER-positive tumors, while CHEK2 mutations were also frequently found in HER2-positive tumors.

Our study confirmed the benefit of multi-gene testing for risk assessment in BC/OC families. Here, we identified deleterious variants in validated BC predisposition genes (ATM, CDH1, CHEK2, PALB2, and TP53) in 312 of 5589 BC index cases, enabling the offer of predictive testing and adjusted surveillance programs in these families. Of note, we identified a high prevalence of VUS which is still a major drawback of multi-gene testing in a diagnostic setting.

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**Conflict of Interest**

The authors have nothing to disclose.

**References**


Supporting Information

Additional supporting information may be found in the online version of this article:

Table S1. Inclusion criteria for germline testing.

Table S2. Class 3, 4 and 5 mutations identified in the study sample.

Table S3. Prevalence of rare missense variants.