Germline Pathogenic Variants in Cancer Predisposition Genes Among Women With Invasive Lobular Carcinoma of the Breast

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PURPOSE To determine the contribution of germline pathogenic variants (PVs) in hereditary cancer testing panel genes to invasive lobular carcinoma (ILC) of the breast.

MATERIALS AND METHODS The study included 2,999 women with ILC from a population-based cohort and 3,796 women with ILC undergoing clinical multigene panel testing (clinical cohort). Frequencies of germline PVs in breast cancer predisposition genes (ATM, BARD1, BRCA1, BRCA2, cdh1, chek2, palb2, PTEN, RAD51C, RAD51D, and TP53) were compared between women with ILC and unaffected female controls and between women with ILC and infiltrating ductal carcinoma (IDC).

RESULTS The frequency of PVs in breast cancer predisposition genes among women with ILC was 6.5% in the clinical cohort and 5.2% in the population-based cohort. In case-control analysis, CDH1 and BRCA2 PVs were associated with high risks of ILC (odds ratio [OR] > 4) and CHEK2, ATM, and PALB2 PVs were associated with moderate (OR = 2–4) risks. BRCA1 PVs and CHEK2 p.Ile157Thr were not associated with clinically relevant risks (OR < 2) of ILC. Compared with IDC, CDH1 PVs were > 10-fold enriched, whereas PVs in BRCA1 were substantially reduced in ILC.

CONCLUSION The study establishes that PVs in ATM, BRCA2, CDH1, CHEK2, and PALB2 are associated with an increased risk of ILC, whereas BRCA1 PVs are not. The similar overall PV frequencies for ILC and IDC suggest that cancer histology should not influence the decision to proceed with genetic testing. Similar to IDC, multigene panel testing may be appropriate for women with ILC, but CDH1 should be specifically discussed because of low prevalence and gastric cancer risk.

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INTRODUCTION Invasive lobular carcinoma (ILC) of the breast accounts for approximately 10%-15% of all invasive breast carcinomas.1 ILC is a distinct subtype of breast cancer with unique biologic characteristics and clinical outcomes.2 Although several predisposition genes for breast cancer have been well-established, these studies primarily evaluated women with infiltrating ductal carcinoma (IDC) and there are very few studies specifically focused on genetic predisposition to ILC.3 Germline pathogenic variants (PVs) in CDH1 have been associated with hereditary diffuse gastric cancer and ILC.4 However, the magnitude of ILC risk related to PVs in CDH1 varies substantially between studies because of small numbers of carriers. In addition, the risk of ILC among carriers of PVs in other genes from multigene hereditary cancer testing panels has not been adequately defined. Some studies have reported that PVs in BRCA1 and TP53 do not predispose to ILC,5,6 whereas PVs in BRCA27 and the CHEK2 I157T missense variant have been associated with ILC.8,10 Furthermore, previous studies have primarily evaluated the frequency of germline PVs in CDH1 and other genes among high-risk women with family history of breast cancer or young age at diagnosis. Thus, the frequency of germline PVs and the associated risk for ILC in the high-risk and general populations are not currently established. Therefore, in one of the largest studies of ILC involving population-based and clinical testing cohorts, we describe the frequency of germline PVs in cancer predisposition genes in women with ILC and estimate the magnitude of risk of ILC in PV carriers.
Germline Genetic Testing in Invasive Lobular Carcinoma of Breast

CONTEXT

Key Objective
Women diagnosed with invasive lobular carcinoma (ILC) of the breast rarely benefit from hereditary cancer testing because the involvement of pathogenic variants (PVs) from cancer predisposition genes in ILC is not well-defined. In this study, population-based and clinical high-risk ILC cohorts were used to assess the risks of ILC conferred by inherited PVs.

Knowledge Generated
The frequency of PVs in breast cancer predisposition genes was 6.5% in the clinical cohort and 5.2% in the population-based cohort. PVs in CDH1, BRCA2, CHEK2, ATM, and PALB2 were associated with increased risk of ILC, whereas PVs in BRCA1 were not.

Relevance
Multigene panel testing is appropriate for women with ILC and to identify women at risk of ILC because PVs in several genes predispose to this form of breast cancer. Predisposing PVs may also inform the selection of therapy for women with ILC.

MATERIALS AND METHODS

Study Populations
The data set from the CAnceR RIsk Estimates Related to Susceptibility (CARRIERS) consortium included 3,437 women with ILC, 25,807 women with IDC, and 35,365 unaffected women from seven breast cancer case-control studies nested within prospective cohorts, two case-cohort studies, and three breast cancer case-control studies, along with five breast cancer case-control and case-cohort studies enriched for young onset disease or family history of breast cancer. A brief description of the contributing studies and the characteristics of the entire cohort is provided in the Data Supplement (online only). For the primary analysis, contributing studies enriched for young age or family history of breast cancer were excluded. Therefore, the primary analysis of this population-based cohort included 2,999 women with ILC, 20,323 women with IDC, and 32,544 unaffected female controls.

The clinical cohort data set included a nationwide sample of 3,796 adult women with ILC and 37,405 with IDC referred to Ambry Genetics, between March 2012 and December 2016, by genetic counselors or clinical care providers across the United States for clinically indicated germline genetic testing because of personal or family history of cancer. Data on patient characteristics were collected from test requisition forms and also from clinical notes and pedigrees provided by ordering clinicians. Women who had previously undergone testing for BRCA1, BRCA2, or Lynch syndrome genes before undergoing multigene panel testing were excluded from the analysis. The majority (> 85%) of women in this cohort met National Comprehensive Cancer Network (NCCN) guidelines for BRCA1 or BRCA2 testing on the basis of personal or family history of cancer.

The study was restricted to adult women with IDC or ILC. Women with mixed ILC and IDC, unknown, or other tumor histology were excluded. The Mayo Clinic institutional review board approved the research study. The analysis of the clinical testing cohort was considered exempt from review by the Western Institutional Review Board.

Genetic Testing and Classification of Variants
For the population-based cohort, germline DNA samples were subjected to multiplex amplicon–based analysis of 746 target regions covering all coding regions and consensus splice sites from 37 cancer predisposition genes using a QIAsert custom panel (Data Supplement). For the clinical testing cohort, testing of 5-49 genes, depending on the multigene panel ordered, was performed by targeted custom capture and sequencing of all coding domains and flanking 5′ and 3′ ends of all the introns and untranslated regions as described previously. For both tested cohorts, the results for 12 breast cancer predisposition genes (ATM, BARD1, BRCA1, BRCA2, BRIPI, CDH1, CHEK2, PALB2, PTEN, RAD51C, RAD51D, and TP53) and nine other cancer predisposition genes (CDKN2A, MLH1, MRE11A, MSH2, MSH6, NBN, NFI, PMS2, and RAD50) were evaluated. In the clinical cohort, PV frequency in each gene was estimated restricting to women who underwent testing for that gene on the basis of the multigene panel ordered. The pooled frequency across breast cancer predisposition genes was then estimated as the sum of frequencies of PVs in the included genes. A five-tier system was used to classify variants using a framework consistent with the guidelines published by American College of Medical Genetics. PVs and likely PVs were analyzed together. All missense and low-penetrance variants in CHEK2 (eg, c.1111C>T, c.1169A>C, c.1283C>T, c.1427C>T, c.349A>G, c.433C>T, c.499G>A, and c.917G>C) were excluded from the analysis. The CHEK2 c.470T>C (p.Ile157Thr) variant was analyzed separately because of a previous association with ILC.

Statistical Analysis
The frequency of PVs in each gene was assessed for women with ILC and IDC in the clinical testing and population-based cohorts, for subsets of women with ILC on the basis of estrogen receptor (ER) status of tumors and...
age at diagnosis (> 65 v ≤ 65 years), and for unaffected female controls in the population-based cohort and in gnomAD.19,20 gnomAD controls used in this analysis included > 90,000 alleles from unrelated women without a cancer diagnosis in the v2.1.1 data set (GRCh37/hg19). Copy number variations in all genes and gnomAD filter non-PASS variants were excluded from both cases and controls for analyses of the clinical cohort, as described previously.21 Case-control association testing for the clinical testing cohort compared frequencies of PVs in cases with gnomAD reference controls using logistic regression and with the gnomAD controls weighted so that the relative frequencies of race and ethnicity subgroups were the same between cases and controls, as described previously.22 Case-control association testing for PVs in each gene in the population-based cohort was conducted with logistic regression models adjusting for age at diagnosis, race or ethnicity, and study. Enrichment analysis comparing PVs in ILC and IDC in both clinical testing and population-based cohorts was conducted using logistic regression. Sensitivity analyses including all studies within the CARRIERS consortium and restricting to ER-positive cases were also performed. All tests were two-sided, and a P value < .05 was considered statistically significant. All analyses were performed using R version 3.4.

RESULTS

Patient Characteristics

The characteristics of women with ILC or IDC from the clinical testing and population-based cohorts included in this study are detailed in Table 1. The median age at diagnosis of ILC was approximately 54 years in the clinical testing cohort and 64 years in the population-based cohort. In both cohorts, > 95% of ILCs with available hormone receptor status were ER-positive and > 92% were human epidermal growth factor receptor 2–negative (Table 1).

| Table 1. Characteristics of Patients With ILC and IDC |
|----------|-----------------|-----------------|-----------------|
| Characteristic | Clinical Testing Cohort | Population-Based Cohort |
| | IDC (n = 37,405) | ILC (n = 3,796) | Total (n = 41,201) | IDC (n = 20,323) | ILC (n = 2,999) | Total (n = 23,322) |
| Age at diagnosis, years | | | | | | |
| Mean (SD) | 49.8 (11.6) | 53.8 (10.6) | 50.2 (11.6) | 62.5 (11.3) | 63.8 (10.7) | 62.6 (11.2) |
| Range | 15-90 | 19-90 | 15-90 | 22-94 | 29-91 | 22-94 |
| Race or ethnicity, No. (%) | | | | | | |
| White or non-Hispanic White | 25,247 (67.5) | 2,838 (74.8) | 28,085 (68.2) | 15,615 (76.8) | 2,546 (84.9) | 18,161 (77.9) |
| Black or African American | 3,240 (8.7) | 221 (5.8) | 3,461 (8.4) | 2,474 (12.2) | 242 (8.1) | 2,716 (11.6) |
| Asian | 1,908 (5.1) | 108 (2.8) | 2,016 (4.9) | 1,027 (5.1) | 87 (2.9) | 1,114 (4.8) |
| Hispanic | 2,350 (6.3) | 190 (5.0) | 2,540 (6.2) | 698 (3.4) | 70 (2.3) | 768 (3.3) |
| Others or unknown | 4,660 (12.5) | 439 (11.6) | 5,099 (12.4) | 509 (2.5) | 54 (1.8) | 563 (2.4) |
| Family history of breast cancer, No. (%) | 21,540 (60.8) | 2,475 (68.0) | 24,015 (61.4) | 3,888 (19.7) | 615 (21.2) | 4,503 (19.9) |
| ER status, No. (%) | | | | | | |
| Negative | 8,496 (27.4) | 108 (3.6) | 8,604 (25.3) | 2,879 (18.8) | 88 (4.3) | 2,967 (17.1) |
| Positive | 22,566 (72.6) | 2,867 (96.4) | 25,433 (74.7) | 12,446 (81.2) | 1,956 (95.7) | 14,402 (82.9) |
| Unknown | 6,343 | 821 | 7,164 | 4,998 | 955 | 5,953 |
| Progesterone receptor status, No. (%) | | | | | | |
| Negative | 10,404 (35.1) | 339 (11.9) | 10,743 (33.1) | 4,481 (30.0) | 399 (20.1) | 4,880 (28.8) |
| Positive | 19,238 (64.9) | 2,515 (88.1) | 21,753 (66.9) | 10,474 (70.0) | 1,588 (79.9) | 12,062 (71.2) |
| Unknown | 7,763 | 942 | 8,705 | 5,368 | 1,012 | 6,380 |
| HER2 status, No. (%) | | | | | | |
| Negative | 20,838 (79.4) | 2,339 (92.6) | 23,177 (80.6) | 8,030 (82.9) | 1,232 (93.1) | 9,262 (84.1) |
| Positive | 5,404 (20.6) | 187 (7.4) | 5,591 (19.4) | 1,660 (17.1) | 91 (6.9) | 1,751 (15.9) |
| Unknown | 11,163 | 1,270 | 12,433 | 10,633 | 1,676 | 12,309 |

Abbreviations: ER, estrogen receptor; HER2, human epidermal growth factor receptor 2; IDC, infiltrating ductal carcinoma; ILC, invasive lobular carcinoma; SD, standard deviation.

*Ashkenazi-Jewish population was included under non-Hispanic Whites.

Family history of breast cancer in first-, second-, or third-degree relatives was included for clinical testing cohort, whereas family history of breast cancer in first-degree relatives was only included in the population-based cohort.
### Gene-Specific PV Prevalence in ILC

The cumulative frequency of PVs in 12 known breast cancer predisposition genes among women with ILC was 6.5% in the clinical testing cohort and 5.2% in the population-based cohort (Table 2). PVs in CHEK2, BRCA2, and ATM were observed in > 1% of ILCs in the clinical testing cohort, whereas only CHEK2 and BRCA2 PVs were found in > 1% of ILCs in the population-based cohort. The recurrent c.1100delC CHEK2 PV was observed in 20 (0.8%) and 23 (0.8%) women with ILC in the clinical testing and population-based cohorts, respectively. CDH1 PVs were observed in 20 (0.5%) ILCs from the clinical testing cohort and 7 (0.2%) ILCs from the population-based cohort. Of the 20 women with CDH1 PVs in the clinical testing cohort, 50% had either a personal (1 of 20) or family history (9 of 20) of gastric cancer. Among women older than 65 years in the population-based cohort, PVs in breast cancer predisposition genes were detected in 2.5% with ILC (Data Supplement).

### Genes Associated With Increased Risk of ILC

In case-control association testing, PVs in BRCA2, CDH1, and CHEK2 were significantly enriched in ILC cases compared with controls in both the clinical testing and the population-based cohorts (Fig 1 and Data Supplement). The risk of ILC was highest among CDH1 PV carriers (odds ratio [OR]: 15.74; 95% CI, 5.08 to 50.22) followed by BRCA2 (OR: 4.94; 95% CI, 3.22 to 7.41) and CHEK2 (OR: 2.56; 95% CI, 1.71 to 3.73) in the population-based cohort. By contrast, the CHEK2 p.Ile157Thr variant was only associated with a mildly increased risk of ILC in the population-based cohort (OR: 1.76; 95% CI, 1.18 to 2.54; P = .004) and was not associated with increased risk in the clinical testing cohort (OR: 1.29; 95% CI, 0.79 to 1.97; P = .27). PVs in ATM and NBN were associated with moderate risk (OR > 2) of ILC in the clinical testing cohort only (Fig 1), whereas PVs in PALB2 were only significantly associated with increased risk of ILC in the population-based cohort (OR: 3.47; 95% CI, 1.72 to 6.55; P < .001). Importantly, PVs in BRCA1 were not associated with an increased risk of ILC in either cohort. Sensitivity analysis restricting to ER-positive cases demonstrated that PVs in ATM, BRCA2, CDH1, and CHEK2 were associated with increased risk of ER-positive ILC in both cohorts (Data Supplement). Further sensitivity analysis using the entire CARRIERS cohort including the family history–enriched CARRIERS studies demonstrated results similar to those from the primary analysis (Data Supplement).

### Comparison of Gene-Specific PV Frequencies in ILC and IDC

The overall frequency of PVs among ILCs was similar to that in women with IDC in the clinical (6.5% vs 9.2%) and population-based cohorts (5.2% vs 5.2%).

### Table 2. Comparison of Frequencies of Germline PVs Between ILC and IDC

| Gene         | IDC (%) | ILC (%) | OR (95% CI)* | P     | IDC (%) | ILC (%) | OR (95% CI)* | P     |
|--------------|---------|---------|--------------|-------|---------|---------|--------------|-------|
| ATM          | 314 (1.11) | 29 (1.03) | 0.71 (0.43 to 1.10) | .144  | 150 (0.74) | 20 (0.67) | 1.17 (0.66 to 1.95) | .557  |
| BARD1        | 79 (0.30)  | 5 (0.19)  | 1.52 (0.52 to 3.57) | .390  | 31 (0.15)  | 1 (0.03)  | ND            | ND    |
| BRCA1        | 844 (2.27) | 12 (0.32) | 0.37 (0.19 to 0.66) | .002  | 204 (1.00) | 5 (0.17)  | 0.36 (0.09 to 0.96) | .083  |
| BRCA2        | 877 (2.36) | 81 (2.15) | 1.17 (0.89 to 1.50) | .246  | 276 (1.36) | 34 (1.13) | 1.01 (0.63 to 1.55) | .959  |
| BRIP1        | 85 (0.32)  | 9 (0.34)  | 1.07 (0.44 to 2.22) | .863  | 45 (0.22)  | 6 (0.20)  | 1.31 (0.66 to 3.14) | .585  |
| CHEK2        | 347 (1.22) | 35 (1.25) | 0.86 (0.57 to 1.25) | .448  | 203 (1.00) | 33 (1.10) | 0.70 (0.40 to 1.15) | .187  |
| CHEK2_I157T  | 159 (0.56) | 22 (0.78) | 0.91 (1.00 to 2.13) | .005  | 125 (0.62) | 33 (1.10) | 1.47 (0.85 to 3.07) | .145  |
| PALB2        | 317 (1.05) | 11 (0.37) | 0.36 (0.16 to 0.68) | .005  | 107 (0.53) | 12 (0.40) | 0.97 (0.43 to 1.92) | .935  |
| PTEN         | 20 (0.05)  | 4 (0.11)  | ND            | ND    | 5 (0.02)  | 2 (0.07)  | ND            | ND    |
| RAD51C       | 57 (0.21)  | 5 (0.19)  | 1.46 (0.49 to 3.50) | .435  | 27 (0.13)  | 1 (0.03)  | ND            | ND    |
| RAD51D       | 26 (0.10)  | 1 (0.04)  | ND            | ND    | 18 (0.09)  | 1 (0.03)  | ND            | ND    |
| TP53         | 69 (0.18)  | 0 (0.00)  | ND            | ND    | 14 (0.07)  | 0 (0.00)  | ND            | ND    |
| Total        | 9.2       | 6.5       | 5.9           | 5.2    |

*ORs adjusted for age at diagnosis, race or ethnicity, and ER status.
*ORs adjusted for age at diagnosis, race or ethnicity, and ER status.
*Missense and low-penetrance variants in CHEK2 were excluded, and the CHEK2_I157T variant was analyzed separately.
population-based (5.2% vs 5.9%) cohorts (Table 2). However, CDH1 PVs were more than 10-fold enriched in ILCs compared with IDCs in both cohorts (Table 2). By contrast, PVs in BRCA1 were significantly reduced in ILCs relative to IDCs in the clinical cohort ($P = .002$) and were less frequent in ILCs in the population-based cohort, although the difference was not significant (OR = 0.36; $P = .08$). The frequency of PALB2 PVs was also significantly lower among ILCs compared with IDCs in the clinical testing cohort (OR = 0.36; $P = .005$), but not in the population-based cohort (Table 2). No other genes yielded a significant difference in the frequency of PVs among IDCs and ILCs in either cohort. Further analysis restricted to ER-positive ILCs and IDCs identified differences in the frequencies of PVs in BRCA1, CDH1, and PALB2 between women with ILC and IDC, similar to the primary results (Table 3).

**DISCUSSION**

We present the results from the largest study of germline PVs in cancer predisposition genes among women with ILC from a clinical testing cohort and a population-based cohort, both of which included large numbers of racially and ethnically diverse women from the United States. The study identifies the breast cancer predisposition genes with PVs associated with ILC and enumerates differences in gene-specific frequencies of PVs in women with IDC and ILC. The confirmation of the findings in two cohorts with distinct ascertainment is a significant strength of the study. Overall, the results of this study have clinical implications for germline testing, counseling of PV carriers for ILC risk, and personalized management of ILC risk among carriers.

The finding that the overall frequency of PVs in established breast cancer predisposition genes is similar between women with ILC and IDC suggests that breast cancer histology should not affect the decision to proceed with genetic testing. However, gene-specific differences in the frequencies of BRCA1 and CDH1 were observed between ILC and IDC. In particular, the frequency of BRCA1 PVs was noted to be significantly lower among women with ILC compared with IDC and BRCA1 was ruled out as an ILC predisposition gene. In addition, approximately two thirds of PVs in breast cancer predisposition genes among women with ILCs were observed in genes other than BRCA1 or BRCA2; with similar frequency of PVs in ATM, CHEK2, and PALB2 between IDC and ILC. These findings support the use of multigene panels for genetic testing of women with ILC, similar to the genetic testing approach commonly used in women with IDC. In addition, the estimates of the overall
Abbreviations: ER, estrogen receptor; IDC, infiltrating ductal carcinoma; ILC, invasive lobular carcinoma; ND, not determined because of insufficient number (< 5) of mutations; OR, odds ratio; PV, pathogenic variant.

*ORs adjusted for age at diagnosis and race or ethnicity.

*ORs adjusted for age at diagnosis, race or ethnicity, and study.

**Missense and low-penetrance variants in CHEK2 were excluded, and CHEK2_I57T variant was analyzed separately.

One of the primary benefits of detecting high-penetrance gene PVs such as BRCA1 or BRCA2 in women diagnosed with breast cancer is prevention of ovarian cancer and contralateral breast cancer through risk-reducing surgeries. Cost-effectiveness analysis of expanding genetic testing to all women with breast cancer has often taken this downstream effect of secondary cancer prevention into consideration.25,26 In this context, several guidelines and studies have advocated for an expansion of the current NCCN guidelines on germline genetic testing24 to include all women with breast cancer.23,27-29 However, these cost-benefit ratio analyses may not apply to women with ILC because of the significantly lower frequency of BRCA1 PVs. Therefore, the differences in genetic testing results between ILC and IDC should be accounted for in studies evaluating cost-effectiveness of expanding genetic testing to all women with breast cancer.

PVs in CDH1 have been associated with an increased risk of ILC and hereditary diffuse gastric cancer.30,31 However, some studies have reported CDH1 PVs among patients with ILC without a family history of hereditary diffuse gastric cancer.32-34 Furthermore, previous studies of associations between CDH1 PVs and breast cancer have primarily evaluated the risk of ILC among women who underwent testing on the basis of personal or family history of breast cancer.35 To our knowledge, the current study is the first to provide a population-based frequency of CDH1 PVs in ILC and confirms that PVs in CDH1 are associated with a high risk (OR > 15) of ILC even among women with no personal or family history of gastric cancer. Although CDH1 PVs are associated with a high penetrance of ILC, the frequency of CDH1 PVs, even in ILC, is low (0.2% in the population-based cohort and 0.5% in the clinical testing cohort). NCCN guidelines currently recommend increased breast cancer surveillance for women with PVs in CDH1 and cite insufficient evidence for risk-reducing mastectomy. The high risk of ILC among CDH1 carriers in the general population observed...
in this study may justify risk-reducing mastectomy in carriers even in the absence of a family history of breast cancer. However, such decisions need to be made on the basis of an individual’s personal preference. Furthermore, clinical management of a CDH1 PV carrier in the absence of a family history of gastric cancer, as noted in approximately 50% of CDH1 PV carriers in the clinical cohort involved in this study, can be very challenging as the management guidelines are not well-defined.37

Significant associations (OR > 2) between PVs in BRCA2 or CHEK2 and ILC were observed, as in previous studies.38,39 Since mammography and breast ultrasound are known to have lower sensitivity for detection of ILC compared with IDC,40-42 carriers of genes predisposing to ILC may benefit from magnetic resonance imaging screening. Importantly, current guidelines already support surveillance breast magnetic resonance imaging for carriers of PVs in CHEK2 or BRCA2 on the basis of > 20% lifetime risks of breast cancer.36 The association between CHEK2 and an increased risk of ILC appears to be primarily driven by the c.1100delC variant in this study. Interestingly, the p.Ile157Thr CHEK2 variant has been previously associated with a low risk of breast cancer overall (OR = 1.4).43 but an increased risk of ILC.8,9,44,45 In this study, the variant was only associated with a mildly increased risk of ILC in the population-based cohort and was not significantly associated with increased risk in the clinical testing cohort. This is consistent with a recent study that did not observe association between CHEK2 p.Ile157Thr variant and ILC. Thus, p.Ile157Thr should not be considered clinically relevant (OR < 2) for either ILC or breast cancer overall and perhaps should not influence surveillance for breast cancer.

In this study, significant associations between PVs in ATM, NBN, or PALB2 and ILC were observed in either the clinical testing or population-based cohort, but not both. Importantly, NBN has previously been excluded as a breast cancer predisposition gene.15 Thus, the current association with ILC needs to be investigated further. The association between PVs in PALB2 and ILC in the population-based cohort but not in the clinical testing cohort is interesting because the frequency of PVs in PALB2 in both sets of ILC cases was similar. This suggests that the absence of a significant association in the clinical cohort may be related to the quality of PALB2 variant calling in gnomAD controls. The association between ATM PVs and ER-positive ILC in both cohorts may most accurately reflect the known predisposition of ATM PVs to ER-positive breast cancer.18

Although this is the largest study on multigene panel testing of women with ILC, the major limitation of the present study is still the sample size, which resulted in wide confidence intervals for some associations. For the clinical testing cohort, limitations include inclusion of women from different clinical sites with potential differences in ascertainment, enrollment of women at high risk for PVs in breast cancer predisposition genes, and the procurement of clinical data through test requisition forms rather than the medical records.

In conclusion, the largest study involving multigene panel testing of women with ILC, we describe the frequency of germline PVs in ILC and the differences in gene-specific frequencies between ILC and IDC. This study establishes BRCA2, CDH1, and CHEK2 and suggests ATM and PALB2 as genes associated with increased risk of ILC, but rules out BRCA1 as an ILC predisposition gene. Similar to IDC, multigene panel testing may be appropriate for women with ILC, but CDH1 should be specifically discussed in the context of its low prevalence and attendant gastric cancer risk.

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REFERENCES

1. Li CI, Anderson BO, Daling JR, et al: Trends in incidence rates of invasive lobular and ductal breast carcinoma. JAMA 289:1421-1424, 2003
2. Rakha EA, Ellis IO: Lobular breast carcinoma and its variants. Semin Diagn Pathol 27:49-61, 2010
3. Yadav S, Couch FJ: Germline genetic testing for breast cancer risk: The past, present, and future. Am Soc Clin Oncol Ed Book: 39:61-74, 2019
4. Figureiro J, Melo S, Carneiro P, et al: Clinical spectrum and pleiotropic nature of CDH1 germline mutations. J Med Genet 56:199-208, 2019
5. Masciari S, Dillon DA, Rath M, et al: Breast cancer phenotype in women with TP53 germline mutations: A Li-Fraumeni syndrome consortium effort. Breast Cancer Res Treat 133:1125-1130, 2012
6. Ditchi Y, Broudin C, El Dakdouki Y, et al: Low risk of invasive lobular carcinoma of the breast in carriers of BRCA1 (hereditary breast and ovarian cancer) and TP53 (Li-Fraumeni syndrome) germline mutations. Breast 25:16-19, 2019
7. Mavaddat N, Barrowdale D, Andrusis IL, et al: Pathology of breast and ovarian cancers among BRCA1 and BRCA2 mutation carriers: Results from the Consortium of Investigators of Modifiers of BRCA1/2 (CIBA). Cancer Epidemiol Biomarkers Prev 21:134-147, 2012
8. Huzarski T, Cybulski C, Domagala W, et al: Pathology of breast cancer in women with constitutional CHEK2 mutations. Breast Cancer Res Treat 90:187-189, 2005
9. Muranen TA, Blomqvist C, Dork T, et al: Patient survival and tumor characteristics associated with CHEK2:p.I157T to mutation findings from the Breast Cancer Association Consortium. Breast Cancer Res 18:98, 2016
10. Lu C, Wang Y, Wang QS, et al: The CHEK2:1157T variant and breast cancer susceptibility: A systematic review and meta-analysis. Asian Pac J Cancer Prev 13:1355-1360, 2012
11. Hu C, Hart SN, Gnanagonalv R, et al: A population-based study of genes previously implicated in breast cancer. N Engl J Med 384:440-451, 2021
12. Yadav S, Hart SN, Hu C, et al: Contribution of inherited DNA-repair genes mutation to hormone-sensitive and castrate-resistant metastatic prostate cancer and implications for clinical outcome. JCO Precis Oncol 3:1-12, 2019
13. Palmier JR, Polley EC, Hu C, et al: Contribution of germline predisposition gene mutations to breast cancer risk in African American women. J Natl Cancer Inst 121:1213-1221, 2020
14. Shimelis H, LaDuca H, Hu C, et al: Triple-negative breast cancer risk genes identified by multigene hereditary cancer panel testing. J Natl Cancer Inst 110:855-862, 2018
15. Couch FJ, Shimelis H, Hu C, et al: Associations between cancer predisposition testing panel genes and breast cancer. JAMA Oncol 3:1190-1196, 2017
16. Yadav S, LaDuca H, Polley EC, et al: Racial and ethnic differences in multigene hereditary cancer panel test results for women with breast cancer. J Natl Cancer Inst 113:1429-1433, 2021
17. Richards S, Aziz N, Bale S, et al: Standards and guidelines for the interpretation of sequence variants: A joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. Genet Med 17:409-424, 2015
18. Ho C, Polley EC, Yadav S, et al: The contribution of germline predisposition gene mutations to clinical subtypes of invasive breast cancer from a clinical genetic testing cohort. J Natl Cancer Inst 112:1231-1241, 2020
19. Lek M, Karczewski KJ, Minikel EV, et al: Analysis of protein-coding genetic variation in 60,706 humans. Nature 536:285-291, 2016
20. gnomAD: http://gnomad.broadinstitute.org/
21. Hu C, LaDuca H, Shimelis H, et al: Multigene hereditary cancer panels reveal high-risk pancreatic cancer susceptibility genes. JCO Precis Oncol 2:1-28, 2018

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22. Hu C, Hart SN, Polley EC, et al: Association between inherited germline mutations in cancer predisposition genes and risk of pancreatic cancer. JAMA 319: 2401-2409, 2018

23. Manahan ER, Kuerer HM, Sebastian M, et al: Consensus guidelines on genetic testing for hereditary breast cancer from the American Society of Breast Surgeons. Ann Surg Oncol 26:3025-3031, 2019

24. National Comprehensive Cancer Network: NCCN Clinical Practice Guidelines in Oncology: Genetic/Familial High-Risk Assessment: Breast, Ovarian and Pancreatic Version 1.2020. National Comprehensive Cancer Network, 2020

25. Sun L, Brentnall A, Patel S, et al: A cost-effectiveness analysis of multigene testing for all patients with breast cancer. JAMA Oncol 5:1718-1730, 2019

26. Pal T, Agnese D, Daly M, et al: Points to consider: Is there evidence to support BRCA1/2 and other inherited breast cancer genetic testing for all breast cancer patients? A statement of the American College of Medical Genetics and Genomics (ACMG). Genet Med 22:681-685, 2020

27. Yadav S, Hu C, Hart SN, et al: Evaluation of germline genetic testing criteria in a hospital-based series of women with breast cancer. J Clin Oncol 38:1409-1418, 2020

28. Beitsch PD, Whitworth PW, Hughes K, et al: Underdiagnosis of hereditary breast cancer: Are genetic testing guidelines a tool or an obstacle? J Clin Oncol 37: 453-460, 2019

29. Desai NV, Yadav S, Batalini F, et al: Germline genetic testing in breast cancer: Rationale for the testing of all women diagnosed by the age of 60 years and for risk-based testing of those older than 60 years. Cancer 127:828-833, 2021

30. Hansford S, Kaurah P, Li-Chang H, et al: Hereditary diffuse gastric cancer syndrome: CDH1 mutations and beyond. JAMA Oncol 1:23-32, 2015

31. Kaurah P, MacMillan A, Boyd N, et al: Founder and recurrent CDH1 mutations in families with hereditary diffuse gastric cancer. JAMA 297:2360-2372, 2007

32. Masciari S, Larsson N, Senz J, et al: Germline E-cadherin mutations in familial lobular breast cancer. J Med Genet 44:726-731, 2007

33. Xie ZM, Li LS, Laquet C, et al: Germline mutations of the E-cadherin gene in families with inherited invasive lobular breast carcinoma but no diffuse gastric cancer. Cancer 117:3112-3117, 2011

34. Nicola RM, Li S, Rodriguez N, et al: Clinical features and cancer risk in families with pathogenic CDH1 variants irrespective of clinical criteria. J Med Genet 56: 838-843, 2019

35. Roberts ME, Ranola JMO, Marshall ML, et al: Comparison of CDH1 penetrance estimates in clinically ascertained families vs families ascertained for multiple gastric cancers. JAMA Oncol 5:1325-1331, 2019

36. Greville-Heygate SL, Maishman T, Tapper WJ, et al: Pathogenic variants in CHEK2 are associated with an adverse prognosis in symptomatic early-onset breast cancer. JCO Precis Oncol 4:472-485, 2020

37. Katona BW, Clark DF, Domchek SM: CDH1 on multigene panel testing: Look before you leap. J Natl Cancer Inst 112:330-334, 2020

38. Petridis C, Arora I, Shah V, et al: Frequency of pathogenic germline variants in CDH1, BRCA2, CHEK2, PALB2, BRCA1, and TP53 in sporadic lobular breast cancer. Cancer Epidemiol Biomarkers Prev 28:1162-1168, 2019

39. Dossus L, Benusiglio PR: Lobular breast cancer: Incidence and genetic and non-genetic risk factors. Breast Cancer Res 17:37, 2015

40. Johnson K, Sarma D, Hwang ES: Lobular breast cancer series: Imaging. Breast Cancer Res 17:94, 2015

41. Selvi V, Mori J, Meattini I, et al: Role of magnetic resonance imaging in the preoperative staging and work-up of patients affected by invasive lobular carcinoma or invasive ductallobular carcinoma. Biomed Res Int 2018:7, 2018

42. Oliveira TM, Elias J Jr, Melo AF, et al: Evolving concepts in breast lobular neoplasia and invasive lobular carcinoma, and their impact on imaging methods. Insights Imaging 5:183-194, 2014

43. Kilpivaara O, Vahteristo P, Falck J, et al: CHEK2 variant I157T may be associated with increased breast cancer risk. Int J Cancer 111:543-547, 2004

44. Domagala P, Wokolorczyk D, Cybulski C, et al: Different CHEK2 germline mutations are associated with distinct immunophenotypic molecular subtypes of breast cancer. Breast Cancer Res Treat 132:937-945, 2012

45. Cybulski C, Wokolorczyk D, Jakubowska A, et al: Risk of breast cancer in women with a CHEK2 mutation with and without a family history of breast cancer. J Clin Oncol 29:3747-3752, 2011
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