Clinical Cancer Research

Breast Cancers with a *BRCA1*-like DNA Copy Number Profile Recur Less Often Than Expected after High-Dose Alkylating Chemotherapy

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Abstract

Purpose: Breast cancers in carriers of inactivating mutations of the *BRCA1* gene carry a specific DNA copy-number signature ("*BRCA1*-like"). This signature is shared with cancers that inactivate *BRCA1* through other mechanisms. Because BRCA1 is important in repair of DNA double-strand breaks through error-free homologous recombination, patients with a *BRCA1*-like tumor may benefit from high-dose alkylating (HD) chemotherapy, which induces DNA double-strand breaks.

Experimental Design: We investigated a single institution cohort of high-risk patients that received tandem HD chemotherapy schedule comprising ifosfamide, epirubicin, and carboplatin or conventional chemotherapy. We classified copy-number profiles to be *BRCA1*-like or non–*BRCA1*-like and analyzed clinical associations and performed survival analysis with a treatment by biomarker interaction design.

Results: *BRCA1*-like status associated with high-grade and triple-negative breast cancers. *BRCA1*-like cases benefitted from the HD compared with a conventional regimen on disease-free survival (DFS): [hazard ratio (HR), 0.05; 95% confidence interval (CI), 0.01–0.38; $P = 0.003$]; distant DFS (DDFS): (HR, 0.06; 95% CI, 0.01–0.43; $P = 0.01$); and overall survival (OS; HR, 0.15; 95% CI, 0.03–0.83; $P = 0.03$) after correction for prognostic factors. No such benefit was observed in the non–*BRCA1*-like cases on DFS (HR, 0.74; 95% CI, 0.38–1.46; $P = 0.39$), DDFS (HR, 0.79; 95% CI, 0.41–1.52; $P = 0.47$), and OS (HR, 0.93; 95% CI, 0.52–1.64; $P = 0.79$). The *P* values for interaction were 0.01 (DFS), 0.01 (DDFS), and 0.045 (OS).

Conclusions: *BRCA1*-like tumors recurred significantly less often after HD than conventional chemotherapy. *BRCA1*-like copy-number profile classification may be a predictive marker for HD alkylating chemotherapy. *Clin Cancer Res; 21(4); 763–70. ©2014 AACR.*

Introduction

Inactivating germline mutations in the *BRCA1* gene confer a high risk of developing breast cancer. Although these germline mutations are shown to be rare in the general population (1, 2), it is thought that a considerable subgroup of breast cancers has characteristics similar to *BRCA1* germline mutated breast cancer but without harboring a *BRCA1* mutation, so called BRCAness (3). BRCA1 is important in error-free DNA double-strand break (DSB) repair through the homologous recombination pathway (4, 5). In the absence of functional homologous recombination, DNA repair is mostly performed by error-prone nonhomologous end-joining (NHEJ). This in turn leads to genomic instability (6, 7). Genomic instability can be measured with DNA copy-number (CN) profiles. It has been established that DNA CN profiles of breast cancers that developed in *BRCA1* mutation carriers have a specific signature (8, 9). To detect these tumors, classifiers have been trained that estimate the probability that a CN profile is similar to a *BRCA1* mutated breast cancer ("*BRCA1*-like"; ref. 10). In addition, this classification can also identify tumors that have a defect in *BRCA1* due to other causes than mutation, for example hypermethylation of the gene promoter (11, 12). This means that the biomarker (*BRCA1*-like signature) captures aspects of the broader concept BRCAness. Preclinical mechanistic studies indicate that deficiencies in this pathway strongly sensitize tumors to drugs inducing DNA damage through DNA DSBs, such as platinum compounds and bifunctional alkylators (3, 13–16). In general, these drugs are currently not standard therapy in breast cancer. High-dose regimens contain such agents. However, in the general population, these regimens did

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Translational Relevance

The identification of biomarker-treatment combinations that enable selection of patients is of importance to tailor treatment to the patient's tumor characteristics. The study investigated the combination of *BRCA1*-like signature with DNA double-strand break inducing chemotherapy, which in preclinical work has been identified as an effective biomarker-treatment combination. The findings can be used separately or combined: *BRCA1*-like signature selected patients with a targetable deficiency in homologous recombination DNA repair due to BRCA1 inactivation, so it can be tested to predict benefit of other drugs targeting this defect. High-dose double-strand break inducing chemotherapy may be particularly suited for patients with a BRCA1 deficiency so this treatment could be tested with other markers that identify such a defect. The combination of *BRCA1*-like signature and DNA double-strand break inducing chemotherapy is particularly translatable because preclinical and clinical observations replicated, the drugs are approved, and clinical experience is present.

not confer a sufficient large survival advantage in the adjuvant or metastatic setting that could justify its toxicity profile. In addition, no known prognostic indicators could identify a subgroup of patients that benefitted substantially from this therapy. Young patients, however, seemed to have a better recurrence-free survival (RFS) than older patients (17, 18). We therefore investigated in a randomized clinical trial whether patients that classified as *BRCA1*-like based on their DNA CN profiles form a subgroup of patients that benefit substantially from DSB inducing high dose (HD) chemotherapy (19). The HD regimen in these previous studies contained four cycles of 5-fluorouracil, epirubicin, and cyclophosphamide (FEC, 500/90/500 mg/m^2) followed by one cycle of carboplatin (1,600 mg/m^2), thiotepa (480 mg/m^2), and cyclophosphamide (6 g/m^2). Patients in the control arm received five cycles of FEC (500/90/500 mg/m^2) only. We found that patients with a *BRCA1*-like profile had an approximately 6-fold lower hazard for an event for disease-free survival (DFS), RFS, and overall survival (OS; refs. 20, 21).

In this study we investigated in an independent single institution cohort whether *BRCA1*-like patients also benefitted from a *tandem* HD regimen (22).

Materials and Methods

Patients

The patients in this study consist of a cohort of patients that has been treated with adjuvant HD therapy or conventional chemotherapy. High-risk breast cancer patients in the HD cohort were enrolled in a single-arm study that was conducted between 1992 and 1997 that evaluated safety and efficacy of the regimen. High risk was defined as stage II or III primary breast cancer with more than 10 tumor-positive lymph nodes, premenopausal patients with three to nine tumor-positive lymph nodes, or hormone receptor–negative disease. Conventionally treated patients from the same time period were identified by the cancer registry of the University of Heidelberg Gynecology and Obstetrics department. Conventionally treated patients were matched for nodal ratio, tumor size, and hormone receptor and HER2 status (22). We collected all available archival tissue from the archives of the Institute of Pathology Heidelberg. The HD regimen consisted of two cycles induction chemotherapy (total dose, 7,500 mg/m^2 ifosfamide, 120 mg/m^2 epirubicin every 3 weeks), followed by two cycles of 12 g/m^2 ifosfamide, 900 mg/m^2 carboplatin, and 180 mg/m^2 epirubicin every 4 to 6 weeks, with autologous stem-cell transplantation. Following chemotherapy, hormone receptor–positive premenopausal patients received gosereline as adjuvant endocrine therapy for 2 years and hormone receptor–positive postmenopausal patients received tamoxifen for 5 years. The conventional regimen consisted of 500 mg/m^2 cyclophosphamide, 40 mg/m^2 methotrexate, 600 mg/m^2 5-fluorouracil (CMF) or 60/90 mg/m^2 epirubicin, 600 mg/m^2 cyclophosphamide (EC) or 600 mg/m^2 5-fluorouracil, 60 mg/m^2 epirubicin, 600 mg/m^2 cyclophosphamide (FEC) chemotherapy. The Ethical Committee of the University of Heidelberg approved this study. Patients enrolled in the trials supplied written informed consent.

DNA isolation and array CGH

We collected archival FFPE tissue and selected tumor blocks that contained a region with 60% tumor cells. Tumor DNA isolation and Array Comparative Genomic Hybridization was performed as previously reported (23). One microgram of DNA was labeled using the Enzo Genomic Labeling Kit (Enzo Life Sciences) according to the manufacturer's instruction. The labeled DNA was then hybridized to a Nimblegen 135k whole-genome array containing 134,937 *in situ* synthesized oligonucleotides (Roche NimbleGen) according to the manufacturer's protocol. Slides of the arrays were scanned using a G2505C microarray scanner (Agilent Technologies). Images were analyzed using Nimblescan version 2.5.26 feature extraction software (Roche Nimblegen). Oligonucleotides were mapped according to the human genome build NCBI36.

BRCA1-like CN aberration classification

Raw image files were processed using Nimblescan software and the DNAcopy algorithm. Unaveraged DNAcopy files were used as input for the *BRCA1*-like classifier as previously described (i.e., no training was performed, just application as described; ref. 24). The *BRCA1*-like classifier is a nearest shrunken centroids classifier (25) that was trained to distinguish CN profiles of *BRCA1*-mutated tumors from tumors without a *BRCA1* mutation. Visualization of characteristic regions of CN alteration (10), and the actual locations and centroids of the classifier have been described before (20). This classifier assigns a class label to a CN profile, either *BRCA1*-like or non–*BRCA1*-like, based on the posterior probability of being non–*BRCA1*-like (probability, 0) or being *BRCA1*-like (probability, 1). The cutoff for optimal chemotherapy prediction was 0.63, as determined on a training cohort (metastatic breast cancer series), and validated on a randomized trial of high-dose chemotherapy versus conventional chemotherapy (20). We used these settings to investigate the current cohort. The data discussed in this publication have been deposited in NCBI's Gene Expression Omnibus (GEO; ref. 26) and are accessible through GEO Series accession number GSE50407 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE50407).

Statistical analysis

Calculations were performed in R v3.0.1 (27). Categorical clinical characteristics were compared with Fisher exact (2×2 Tables) or χ^2 tests (larger than 2×2 Tables). Survival was

evaluated according to *BRCA1*-like status by Kaplan–Meier curves and log-rank statistics. Hazard ratios were estimated with a Cox Proportional Hazards model adjusting for relevant prognostic factors. To assess whether *BRCA1*-like status is a predictive marker, a test for interaction with chemotherapy regimen was performed (28). A description of this study according to the REporting recommendations for tumor MARKer prognostic studies (REMARK) guidelines is provided in Supplementary Table S1. Survival was calculated from start date of chemotherapy until date of event or date of last follow-up. Events were defined as any relapse or death (DFS), any relapse other than in the ipsi-lateral breast, chest wall, axillary or supraclavicular lymph nodes or death (DDFS) or death (OS). We assessed both DFS and DDFS to investigate whether a treatment benefit would be due to decreased systemic disease events, i.e., the adjuvant treatment is successful in its aim to kill occult micrometastases.

Results

We collected the archival material for 82% of the patients that were treated at the University of Heidelberg. A flow diagram of patients included is shown in Fig. 1.

We generated CN profiles for 117 of these patients. The clinical characteristics for these patients are shown in Table 1. The treatment cohorts were not significantly different, except that patients treated with HD chemotherapy were more likely to have higher lymph node stage (non–*BRCA1*-like $P < 0.001$; *BRCA1*-like $P = 0.05$). *BRCA1*-like tumors have a higher N stage ($P = 0.01$), higher grade ($P = 0.03$), and are more often estrogen receptor (ER)–negative ($P = 0.01$) and triple negative ($P < 0.001$). A trend for fewer events in the conventionally treated non–*BRCA1*-like patients compared with high dose–treated non–*BRCA1*-like patients is present for DFS ($P = 0.05$) and DDFS ($P = 0.07$). Concluding, *BRCA1*-like patients treated with HD chemotherapy have more unfavorable prognostic factors than the other patients in this study.

The median follow-up for DFS and DDFS were 2.4 and 2.5 years, respectively. The median follow-up for OS was 8.5 years. Kaplan–Meier curves for non–*BRCA1*-like patients and *BRCA1*-like patients comparing the outcome of conventional and HD chemotherapy on DFS, distant DFS (DDFS), and OS are shown in Fig. 2.

When adjusted for the potential confounding factors, ER status, HER2 status, size, number of tumor-positive lymph nodes and grade, *BRCA1*-like patients had a better DFS (HR, 0.05; 95% CI, 0.01–0.38; $P = 0.003$); DDFS (HR, 0.06; 95% CI, 0.01–0.43; $P = 0.01$), and OS (HR, 0.15; 95% CI, 0.03–0.83; $P = 0.03$) with adjuvant HD chemotherapy than with conventional chemotherapy. No such benefit was observed in the non–*BRCA1*-like cases for DFS (HR, 0.74; 95% CI, 0.38–1.46; $P = 0.39$), DDFS (HR, 0.79; 95% CI, 0.41–1.52; $P = 0.47$), and OS (HR, 0.93; 95% CI, 0.52–1.64; $P = 0.79$), The P values for interaction were 0.01 (DFS), 0.01 (DDFS), and 0.045 (OS; Table 2). No evidence against proportionality of treatment-specific hazards was observed among *BRCA1*-like and non–*BRCA1*-like patients.

Discussion

We investigated a single institution cohort treated with high-dose and conventional chemotherapy to assess whether *BRCA1*-

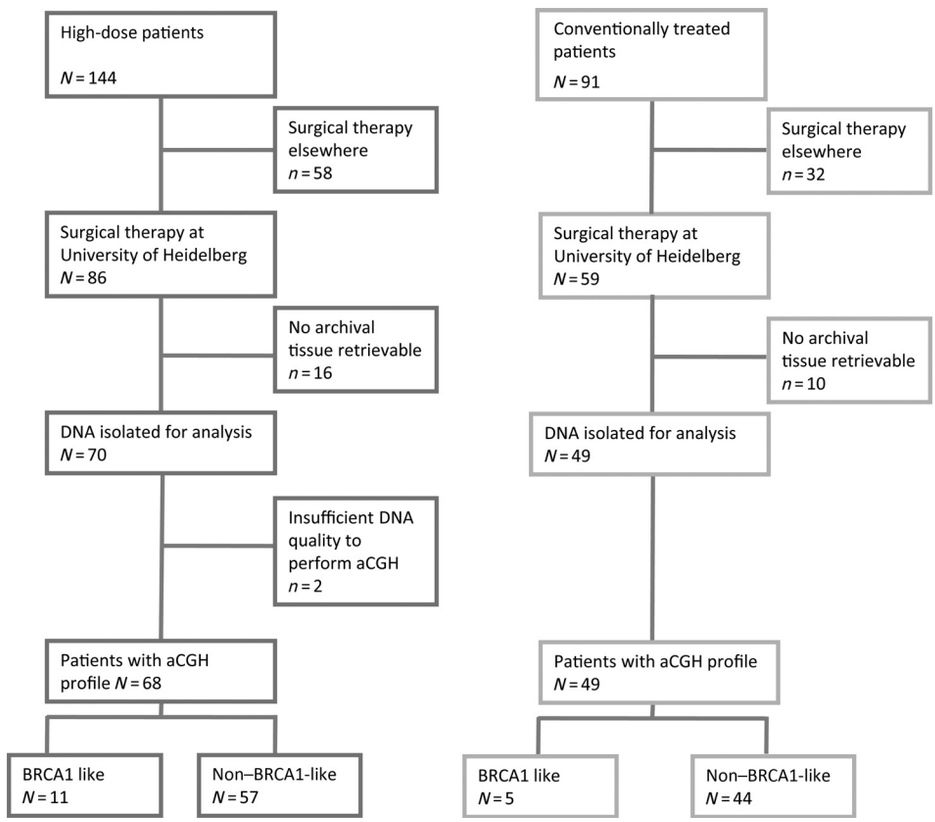

Figure 1.
Flow diagram of patients in this study.

Table 1. Clinical characteristics of the cohort

	Conv non-BRCA1 (%) (*N* = 44)	HD non-BRCA1 (%) (*N* = 57)	*P*	Conv BRCA1 (%) (*N* = 5)	HD BRCA1 (%) (*N* = 11)	*P*	*P* non-BRCA1 [a] vs. BRCA1
Pathologic T stage							
1	6 (13.6)	13 (22.8)		1 (20.0)	2 (18.2)		
2	27 (61.4)	25 (43.9)		4 (80.0)	5 (45.5)		
3	7 (15.9)	12 (21.1)		0 (0.0)	4 (36.4)		
4	2 (4.5)	6 (10.5)	0.26	0 (0.0)	0 (0.0)	0.28	0.67
Missing	2 (4.5)	1 (1.8)		0 (0.0)	0 (0.0)		
Pathologic N stage							
1	0 (0.0)	1 (1.8)		1 (20.0)	1 (9.1)		
2	23 (52.3)	8 (14.0)		2 (40.0)	0 (0.0)		
3	21 (47.7)	48 (84.2)	0.00	2 (40.0)	10 (90.9)	0.05	0.01
Missing	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		
Grade							
1	2 (4.5)	0 (0.0)		0 (0.0)	0 (0.0)		
2	17 (38.6)	29 (50.9)		1 (20.0)	1 (9.1)		
3	25 (56.8)	28 (49.1)	0.16	4 (80.0)	10 (90.9)	1.00	0.03
Missing	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		
ER							
Neg	19 (43.2)	25 (43.9)		4 (80.0)	9 (81.8)		
Pos	25 (56.8)	32 (56.1)	1.00	1 (20.0)	2 (18.2)	1.00	0.01
Missing	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		
PR							
Neg	20 (45.5)	35 (61.4)		4 (80.0)	8 (72.7)		
Pos	24 (54.5)	22 (38.6)	0.16	1 (20.0)	3 (27.3)	1.00	0.17
Missing	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		
HER2							
Neg	26 (59.1)	32 (56.1)		3 (60.0)	7 (63.6)		
Pos	13 (29.5)	19 (33.3)	0.82	2 (40.0)	2 (18.2)	0.58	0.77
Missing	5 (11.4)	6 (10.5)		0 (0.0)	2 (18.2)		
Triple negative							
No	37 (84.1)	48 (84.2)		2 (40.0)	5 (45.5)		
Yes	5 (11.4)	9 (15.8)	0.77	3 (60.0)	6 (54.5)	1.00	0.00
Missing	2 (4.5)	0 (0.0)		0 (0.0)	0 (0.0)		
Histology							
Ductal	36 (81.8)	46 (80.7)		5 (100.0)	8 (72.7)		
Lobular	8 (18.2)	7 (12.3)	0.58	0 (0.0)	1 (9.1)	1.00	0.69
Missing	0 (0.0)	4 (7.0)		0 (0.0)	2 (18.2)		
DFS event							
No	29 (65.9)	26 (45.6)		3 (60.0)	8 (72.7)		
Yes	15 (34.1)	31 (54.4)	0.05	2 (40.0)	3 (27.3)	1.00	0.42
Missing	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		
DDFS							
No	31 (70.5)	29 (50.9)		3 (60.0)	8 (72.7)		
Yes	13 (29.5)	28 (49.1)	0.07	2 (40.0)	3 (27.3)	1.00	0.59
Missing	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		
OS event							
No	19 (43.2)	19 (33.3)		2 (40.0)	8 (72.7)		
Yes	25 (56.8)	38 (66.7)	0.41	3 (60.0)	3 (27.3)	0.30	0.10
Missing	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		

NOTE: *P* values were calculated with χ^2 test (>2 × 2 Tables) for trend or Fisher Exact tests (2 × 2 Tables).

Abbreviation: PR, progesterone receptor.

[a]*P* values for comparing all non–BRCA1-like patients and all BRCA1 like patients with χ^2 tests (>2 × 2 Tables) for trend or Fisher Exact tests (2 × 2 tables).

like patients benefit from a tandem HD alkylating chemotherapy regimen (20). Patients with a *BRCA1*-like breast cancer significantly recurred less after the tandem HD alkylating chemotherapy regimen. *BRCA1*-like status may therefore serve as a predictive marker for tandem HD chemotherapy with iphosphamide, epirubicin, and carboplatin.

High-dose alkylating regimens in breast cancer are not used anymore after it has been shown that this regimen does not confer a survival benefit (17, 18). However, these regimens contain potent inducers of DNA DSBs, which are predicted beneficial in patients with tumors that do not have a functional homologous recombination, due to a defect in BRCA1 (4, 14–16, 29). To identify these patients, we used a *BRCA1*-like classifier, which assigns patients that share specific DNA CN aberrations with *BRCA1*-mutated tumors to the *BRCA1*-like class (8–10). The tumors assigned to be *BRCA1*-like comprise *BRCA1*-mutated and *BRCA1*–wild-type tumors that have another mechanism to inactivate BRCA1 function, for example *BRCA1* promoter hypermethylation (11, 12, 20). Previously, we investigated this classifier in patients that were randomized to receive either five cycles of conventional adjuvant 5-FU, epirubicin, and cyclophosphamide (FEC) or four cycles of conventional FEC followed by one cycle

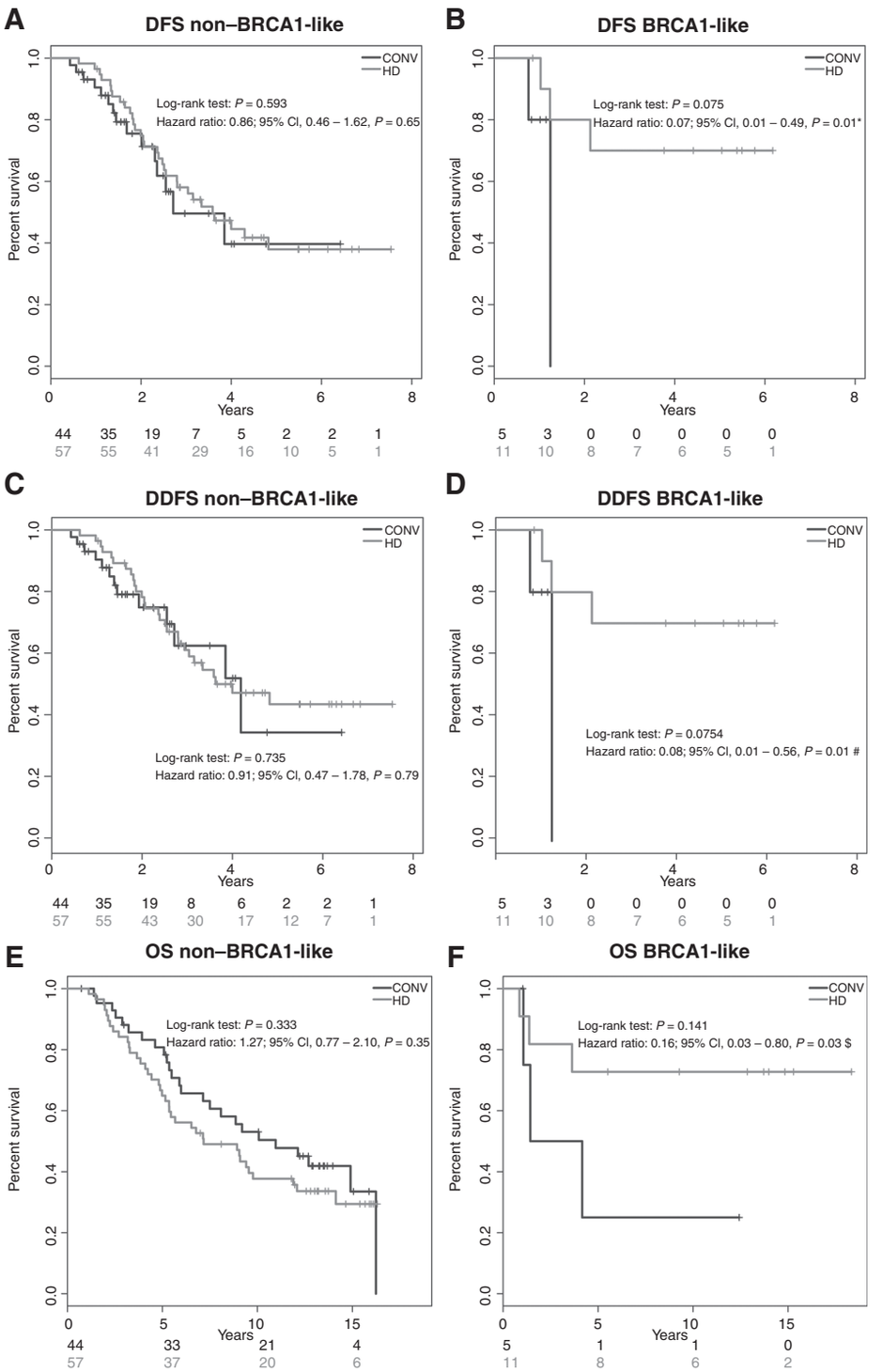

Figure 2
A, Kaplan–Meier curves of DFS of non–*BRCA1*-like patients treated with high-dose (HD) or conventional chemotherapy. B, Kaplan–Meier curves of DFS of *BRCA1*-like patients treated with HD or conventional chemotherapy (CONV). C, Kaplan–Meier curves of DDFS of non–*BRCA1*-like patients treated with high-dose or conventional chemotherapy. D, Kaplan–Meier curves of DDFS of *BRCA1*-like patients treated with HD or conventional chemotherapy. E, Kaplan–Meier curves of OS of non–*BRCA1*-like patients treated with HD or conventional chemotherapy. F, Kaplan–Meier curves of overall survival of *BRCA1*-like patients treated with HD or conventional chemotherapy. The *P* values for interaction, i.e., for a difference between the HRs by *BRCA1*-like status without adjustment for prognostic factors were *, $P = 0.01$; #, $P = 0.02$; and $, $P = 0.02$.

of the HD regimen carboplatin (1,600 mg/m^2), thiothepa (480 mg/m^2), and cyclophosphamide (6 g/m^2; ref. 19). In this study, patients with a *BRCA1*-like CN profile in their tumor derived a substantial benefit from another HD regimen compared with conventional chemotherapy. Patients with a non–*BRCA1*-like tumor that received HD chemotherapy did not benefit at all compared with conventional FEC. Although the HD regimen in the current study (2 cycles induction + 2 cycles of 12 g/m^2 ifosfamide, 900 mg/m^2 carboplatin, and 180 mg/m^2 epirubicin) is different from our previous study, we obtained similar results. Our data suggest that patients with a *BRCA1*-like tumor benefit from an HD alkylating regimen, whereas patients with a non–

Table 2. Cox proportional hazards models for DFS, DDFS, and OS

	DFS			DDFS			OS		
Variable	**Event/total n**	**HR (95% CI)**	***P***	**Event/total *n***	**HR (95% CI)**	***P***	**Event/total *n***	**HR (95% CI)**	***P***
ER									
Negative		1.00			1.00			1.00	
Positive		1.04 (0.542–.02)	0.90		0.97 (0.50–1.87)	0.92		1.17 (0.66–2.06)	0.59
HER2									
Negative		1.00			1.00			1.00	
Positive		1.36 (0.7–2.61)	0.36		1.20 (0.63–2.26)	0.58		1.78 (1.00–3.19)	0.05
Pathologic T stage									
Stage I/II		1.00			1.00			1.00	
Stage III/IV		1.29 (0.69–2.41)	0.42		1.35 (0.72–2.53)	0.35		1.61 (0.91–2.86)	0.10
Lymph nodes									
<10 positive		1.00			1.00			1.00	
$\geq$ 10 positive		1.97 (0.87–4.45)	0.10		1.74 (0.77–3.94)	0.18		1.68 (0.87–3.26)	0.12
Grade									
Grade 1/2		1.00			1.00			1.00	
Grade 3		1.17 (0.63–2.19)	0.62		1.11 (0.60–2.07)	0.73		0.90 (0.53–1.53)	0.70
BRCA1-like status									
Non–BRCA1-like		1.00			1.00			1.00	
BRCA1-like		7.48 (1.41–39.76)	0.02		7.46 (1.39–40.01)	0.02		2.99 (0.87–10.28)	0.08
BRCA1-like									
Conv	2/5	1.00		2/5	1.00		3/5	1.00	
High dose	3/11	0.05 (0.01–0.38)	0.00[a]	3/11	0.06 (0.01–0.43)	0.01[b]	3/11	0.15 (0.03–0.83)	0.03[c]
Non–BRCA1-like									
Conv	15/44	1.00		13/44	1.00		25/44	1.00	
High dose	31/57	0.74 (0.38–1.46)	0.39	28/57	0.79 (0.41–1.52)	0.47	38/57	0.93 (0.52–1.64)	0.79

NOTE: Cox proportional hazards model of DFS, DDFS, and OS adjusted for potentially confounding clinical factors.

Abbreviations: Conv, conventional regimen; T, tumor.

Interaction tests between *BRCA1*-like status and chemotherapy regimen adjusted for confounders: [a]$P = 0.01$; [b]$P = 0.01$; [c]$P = 0.045$.

BRCA1-like tumor do not. Given the differences in drugs and doses, it may be that *BRCA1*-like tumors, generally are more sensitive to the dose or DNA crosslinking properties, rather than a specific agent.

Our present study is limited by several factors, which are shared by other investigations of BRCA1 deficiency as a potential biomarker. In clinical studies, there is to date neither agreement on different biomarkers that can be used to identify *BRCA1* defects, nor any randomized evidence to demonstrate that selection of patients with a BRCA1 defect for a particular therapy results in improved treatment outcomes as has been reviewed extensively (3, 30–32). Clearly, our present study is limited by a small sample size and the nonrandomized design relying on a balanced patient cohort treated with several chemotherapy combinations during the same time period at the same institution. Strikingly, the patients expected to have a poor prognosis, (*BRCA1*-like patients associated with high N stage, high-grade, and ER-negative/triple-negative tumors) have a significantly better survival when treated with HD chemotherapy in comparison with conventional chemotherapy, whereas the non–*BRCA1*-like patients do not experience that HD treatment benefit.

Regarding the therapy regimens, patients in the control group received conventional chemotherapy consisting of either EC, CMF, or EC-CMF as they were treated in the pretaxane era. This allows for a unique view on biology but limits the conclusions on whether HD chemotherapy is better than a modern taxane-containing regimen. However, it has been suggested that *BRCA1*-mutated patients are relatively resistant to taxanes (33). Because we do not have an untreated control group, it is not possible to accurately model a potential prognostic effect that the *BRCA1*-like profile status may confer. Second, due to the combinations of different drugs, it is impossible to dissect whether the survival benefit could be due to a particular drug. Third, it could also be that the amount of DNA damage is greatly increased due to the higher dose, and that the cumulative dose is responsible for efficient killing of tumor cells.

Further research should therefore aim to overcome the limitations. First, by investigating other randomized trials between high-dose and conventional chemotherapy whether *BRCA1*-like patients benefit from the HD regimen. Single cohorts and especially nonrandomized cohorts do not reach the highest level of evidence and findings should therefore be confirmed in independent studies. (34, 35). These studies can strengthen the evidence while prospective, randomized evidence is being gathered in (neo-) adjuvant and metastatic breast cancer (http://clinicaltrials.gov: NCT01898117, NCT01057069, NCT01646034). Furthermore, identifying the role or contribution of specific agents, dose, and biomarker are important to determine the use of this information in the treatment of breast cancer. Specifically, the treatment burden associated with an HD chemotherapy regimen requires proper selection of patients. If possible, less toxic therapy should be investigated, for example, an intermediate dose or only the effective drug in this regimen. Furthermore, Poly(ADP)-Ribose Polymerase 1 (PARP1) inhibitors may prove effective with a more beneficial toxicity profile (36–39).

Conclusion

Concluding, in this single institution study, we observed that *BRCA1*-like CN profiles identify a group of patients that recur less often than expected after receiving HD than after conventional chemotherapy treatment. *BRCA1*-like CN profile status may therefore be a predictive biomarker for HD alkylating chemotherapy

and could then be used to guide treatment choices to improve OS among patients with a poor prognosis.

Disclosure of Potential Conflicts of Interest

S.C. Linn is an inventor on a BRCA1-like patent. No potential conflicts of interest were disclosed by the other authors.

Authors' Contributions

Conception and design: P.C. Schouten, F. Marmé, A. Schneeweiss, S.C. Linn
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