Telomeric Allelic Imbalance Indicates Defective DNA Repair and Sensitivity to DNA-Damaging Agents

Nicolai J. Birkbak1,2, Zhigang C. Wang2,3, Ji-Young Kim3,6, Aron C. Eklund1, Qiyuan Li1,2, Ruiyang Tian2, Christian Bowman-Colin2, Yang Li2, April Greene-Colozzi2, J. Dirk Iglehart2,3, Nadine Tung4, Paula D. Ryan7, Judy E. Garber2, Daniel P. Silver2,3, Zoltan Szallasi1,5, Andrea L. Richardson2,3
ABSTRACT

DNA repair competency is one determinant of sensitivity to certain chemotherapy drugs, such as cisplatin. Cancer cells with intact DNA repair can avoid the accumulation of genome damage during growth and also can repair platinum-induced DNA damage. We sought genomic signatures indicative of defective DNA repair in cell lines and tumors and correlated these signatures to platinum sensitivity. The number of subchromosomal regions with allelic imbalance extending to the telomere (N_{tel}) predicted cisplatin sensitivity in vitro and pathologic response to preoperative cisplatin treatment in patients with triple-negative breast cancer (TNBC). In serous ovarian cancer treated with platinum-based chemotherapy, higher levels of N_{tel} forecast a better initial response. We found an inverse relationship between BRCA1 expression and N_{tel} in sporadic TNBC and serous ovarian cancers without BRCA1 or BRCA2 mutation. Thus, accumulation of telomeric allelic imbalance is a marker of platinum sensitivity and suggests impaired DNA repair.

SIGNIFICANCE: Mutations in BRCA genes cause defects in DNA repair that predict sensitivity to DNA damaging agents, including platinum; however, some patients without BRCA mutations also benefit from these agents. N_{tel}, a genomic measure of unfaithfully repaired DNA, may identify cancer patients likely to benefit from treatments targeting defective DNA repair. Cancer Discov; 2(4): 0F1–0F10. ©2012 AACR.

INTRODUCTION

Cell lines carrying BRCA1 or BRCA2 mutations are more sensitive to killing by the platinum salts cisplatin and carboplatin than are wild-type cells (1, 2). Breast and ovarian cancers in patients carrying BRCA1 or BRCA2 mutations are likewise sensitive to platinum-based chemotherapy (3, 4). The majority of breast cancers arising in women with a germline BRCA1 mutation lack expression of estrogen and progesterone receptors or amplification of the HER2-neu gene (“triple-negative”). BRCA1-related breast cancers share a number of phenotypic characteristics with sporadic triple-negative breast cancer [TNBC (5–7)]. Both tumor types share a common pattern of genomic abnormalities and have high global levels of chromosomal aberrations, including allelic imbalance (AI), the unequal contribution of maternal and paternal DNA sequences with or without changes in overall DNA copy number (8–10). Because they have in common genomic aberrations suggesting a shared lesion in genomic integrity control, it is reasonable to posit that sporadic TNBC that has accumulated high levels of AI might share the sensitivity to platinum-based chemotherapy that characterizes BRCA1-associated cancer.

These observations prompted a clinical trial, Cisplatin-1, in which 28 patients with operable TNBC were treated preoperatively with cisplatin monotherapy. Preoperative treatment in the Cisplatin-1 trial resulted in greater than 90% tumor reduction in 10 of 28 (36%) patients, including pathologic complete response (pCR) in 6 women, 2 of whom had BRCA1-associated cancers (11). A second trial, Cisplatin-2, accrued 51 patients with TNBC who received the same preoperative cisplatin regimen as those in Cisplatin-1, but in combination with the angiogenesis inhibitor bevacizumab (12).

The response rate in Cisplatin-2 was similar to that in Cisplatin-1. In the second trial, a greater than 90% tumor reduction was observed in 17 of 44 women (39%) completing treatment. In Cisplatin-2, 8 patients carried a germline BRCA1 or BRCA2 mutation, of which 4 patients achieved a pCR or near pCR to the cisplatin–bevacizumab regimen. In both trials, all patients had research sequencing to determine their germline BRCA1 and BRCA2 status. We compared the number of various chromosomal abnormalities including AI present in tumor biopsies obtained before therapy to pathologically determined tumor response to cisplatin, alone or in combination with bevacizumab, assessed by examination of the posttreatment surgical specimen.

Chromosomal abnormalities such as regions of AI, other than those resulting from whole chromosome gain or loss, might result from improper repair of DNA double-strand breaks during tumor development. If so, then a genome-wide count of abnormal chromosomal regions in tumors may indicate the degree of DNA repair incompetence, independent of knowledge of any specific causative DNA repair defect. We hypothesized that the number of chromosomal regions of...
AI in tumors would predict sensitivity to drugs that induce DNA cross-links such as cisplatin.

We first sought associations between various measures of subchromosomal abnormalities and sensitivity to cisplatin in breast cancer cell lines and found the most accurate predictor to be AI extending to the telomeric end of the chromosome ($N_{\text{tAI}}$). Finally, we tested whether $N_{\text{tAI}}$ was associated with treatment response in patient tumor samples in the Cisplatin-1 and Cisplatin-2 TNBC trials and in The Cancer Genome Atlas (TCGA) public data set of serous ovarian cancer, a cancer routinely treated with platinum-based therapy. In an effort to understand more about the processes leading to telomeric AIs, we mapped the location of their breakpoints and observed a striking association of these breakpoints with regions of the genome that are difficult to replicate—common copy number variants (CNV). Furthermore, a subset of high $N_{\text{tAI}}$ tumors displays low BRCA1 mRNA levels. These observations begin to suggest models of how telomeric AI may occur.

**RESULTS**

**Cisplatin Sensitivity Correlates with Burden of Telomeric AI in Breast Cancer Cell Lines**

We obtained single-nucleotide polymorphism (SNP) genotype array data from the Wellcome Trust Sanger Institute for a set of established *BRCA1* wild-type breast cancer cell lines for which we had determined cisplatin sensitivity [Fig. 1A (13)]. Allele copy number was determined from the SNP array data and AI detected by the use of allele-specific copy number analysis of tumors, or ASCAT [Supplementary Fig. S1 (10)]. We tested for an association between the $IC_{50}$ values for cisplatin and each of 3 summary measures of chromosome alteration: the number of chromosome regions with AI ($N_{\text{cl}}$; Supplementary Fig. S2A), the number of regions with copy number gains ($N_{\text{gAI}}$; Supplementary Fig. S2B), and the number of regions with copy number loss ($N_{\text{lAI}}$; Supplementary Fig. S2C). None of these measures was correlated with cisplatin sensitivity in the cell lines.

**Tumors Sensitive to Cisplatin-Based Chemotherapy Have Greater Levels of Telomeric AI**

We then investigated whether the association between $N_{\text{tAI}}$ in clinical tumor samples and cisplatin sensitivity was
present in the Cisplatin-1 trial. Sensitivity was measured by pathologic response determined after preoperative treatment (11). Molecular inversion probe SNP genotype data from pretreatment tumor samples (n = 27) were evaluated by ASCAT to determine N\textsubscript{tAI}. We compared tumors with a reduction of at least 90% in the content of malignant cells (cisplatin-sensitive) to tumors with limited or no response to cisplatin (cisplatin-resistant, defined by tumor reduction of <90%). Cisplatin-sensitive tumors had significantly higher levels of N\textsubscript{tAI} (median 24 vs. 17.5, P = 0.047, Fig. 2A). We tested the ability of N\textsubscript{tAI} to predict cisplatin response by calculating the area under the receiver operating characteristic (ROC) curve (AUC). ROC analysis showed that higher levels of N\textsubscript{tAI} were associated with cisplatin sensitivity [AUC = 0.74, 95% confidence interval (CI) 0.50–0.90; Fig. 2B].

In the Cisplatin-2 trial, cisplatin-sensitive tumors (n = 9) had significantly greater N\textsubscript{tAI} than -resistant tumors (n = 17, median 27 vs. 20, P = 0.019; Fig. 2C). N\textsubscript{tAI} was also associated with response to cisplatin and bevacizumab by ROC analysis (AUC = 0.79, 95% CI 0.55–0.93; Fig. 2D). The association between N\textsubscript{tAI} and cisplatin sensitivity remained significant when cases with BRCA1 or BRCA2 mutation were excluded and only BRCA normal cases were analyzed (P = 0.030 and P = 0.023 in Cisplatin-1 and Cisplatin-2, respectively). Therefore, in 2 separate preoperative trials in breast cancer, in which treatment sensitivity was assessed by a quantitative measure of pathologic response, N\textsubscript{tAI} reliably forecast the response to cisplatin-based treatment.

To test whether the N\textsubscript{tAI} metric indicates platinum sensitivity in cancers other than breast, we determined the association between N\textsubscript{tAI} and initial treatment response in a TCGA cohort of serous ovarian cancer patients who had received adjuvant platinum and taxane chemotherapy (19). Among the ovarian cancers without mutation in BRCA1 or BRCA2 (wtBRCA), the platinum-sensitive tumors had significantly higher levels of N\textsubscript{tAI} than did the platinum-resistant cancers (median 22 vs. 20, P = 0.036; Fig. 3) and N\textsubscript{tAI} was predictive of treatment response by ROC analysis (AUC = 0.63, 95% CI 0.50–0.76, Supplementary Fig. S4). The ovarian cancers with somatic or germline mutation in BRCA1 or BRCA2 that were sensitive to platinum therapy had even higher levels of N\textsubscript{tAI} (median 26, P = 0.0017 and median 23.5, P = 0.037 vs. resistant wtBRCA, respectively, Fig. 3). All of the BRCA2-mutated cancers were platinum sensitive; however, 5 BRCA1-mutated tumors were resistant to platinum therapy yet appeared to have relatively high levels of N\textsubscript{tAI}. Thus, high N\textsubscript{tAI} is characteristic of serous ovarian cancer with known mutation in either BRCA1 or BRCA2; high N\textsubscript{tAI} is also found in a subset of sporadic cancers without BRCA mutations, where it is predictive of platinum sensitivity.

**Locations of N\textsubscript{tAI}-Associated Chromosomal Breaks Are Not Random**

To develop a better understanding of the processes leading to telomeric Al, we mapped the location of the chromosome breakpoints defining the boundary of the telomeric Al regions. We observed that many breakpoints were located in very close proximity to each other (Supplementary Fig. S5), suggesting a nonrandom distribution of DNA breaks causing telomeric Al. Recurrent chromosomal translocation breakpoints may be associated with regions of repeated
DNA sequence that may cause stalled replication forks, an increased frequency of DNA breaks, and subsequent rearrangement by nonallelic homologous recombination or other similar mechanisms (20, 21). CNVs are highly homologous DNA sequences for which germline copy number varies between healthy individuals (22, 23). CNVs have been proposed to facilitate the generation of chromosomal alterations, similar to fragile sites (21, 24, 25).

We compared the number of observed breaks within 25 kB of a CNV to the frequency expected by chance alone on the basis of permuted data. In the Cisplatin-1 cohort, of 517 N_tAI breakpoints, 255 (49%) were associated with overlapping CNVs. Similarly, in the cisplatin-2 cohort, of 599 N_tAI breakpoints, 340 (57%) were associated with CNVs. In both trials, the observed number of N_tAI breaks associated with CNVs was significantly greater than expected by chance (Fig. 4A and B). Thus, many of the breakpoints leading to telomeric AI in TNBC occur near CNVs, suggesting that stalled replication forks, replication stress, or other CNV-associated mechanisms may be involved in the genesis of telomeric AI.

**Low BRCA1 mRNA Is Associated with High N_tAI and Sensitivity to Cisplatin**

In our previous report of the Cisplatin-1 trial, we found an association between low BRCA1 transcript levels and better response to cisplatin (11). In the more recent trial, Cisplatin-2, BRCA1 transcript levels measured by quantitative real-time PCR (qRT-PCR) are also associated with cisplatin response (P = 0.015; Fig. 5A). In a combined analysis of data from both trials, lower BRCA1 transcript levels are associated with methylation of the BRCA1 promoter (P = 0.027; Fig. 5B), although BRCA1 promoter methylation itself is not significantly associated with cisplatin response (P = 0.25; Fisher exact test). BRCA1 mRNA levels are inversely associated with N_tAI in the 2 cisplatin trials (r = −0.50, P = 0.0053; Fig. 5C). This finding suggests that dysfunction of a BRCA1-dependent process or other abnormality causing low BRCA1 mRNA may be responsible for the high level of telomeric AI and also cisplatin sensitivity in many of these TNBCs.

ROC analysis of the combined TNBC trials suggests that BRCA1 expression level or N_tAI may provide a similar predictive accuracy for cisplatin sensitivity (Supplementary Fig. S6A). When high N_tAI and low BRCA1 expression are combined in a predictive model, the positive predictive value and specificity of prediction improved considerably, but the sensitivity was decreased relative to N_tAI alone (Supplementary Fig. S6B), suggesting that low BRCA1 expression does not account for all cisplatin-sensitive tumors.

In the TNBC trials, we noted a few cisplatin-sensitive tumors with high levels of N_tAI but high BRCA1 mRNA, suggesting that alternative mechanisms may drive the generation of tAI in some tumors. Analysis of TCGA data of ER/HER2 breast cancer and wtBRCA serous ovarian cancer reveals an inverse correlation between N_tAI and BRCA1 expression. Yet, in both cohorts, there was a considerable subset of tumors with high N_tAI and high BRCA1 expression (Supplementary Fig. S7A and B). Unlike N_tAI, BRCA1 expression was not apparently different between sensitive and resistant wtBRCA serous ovarian cancers (Supplementary Fig. S7C). These findings suggest a model whereby high N_tAI may represent a readout of DNA repair deficiency resulting from either low BRCA1 expression or from other known or unknown mechanisms (Fig. 6).

**DISCUSSION**

Our study analyzed 2 preoperative clinical trials in women with TNBC treated with cisplatin, in which pathologic response at the time of surgery provided an experimental endpoint. Sporadic TNBCs are heterogeneous in their responses to platinum salts, which are chemotherapeutic agents that depend in part on DNA repair defects for their cytotoxic activity (26, 27). Lesions in DNA repair caused by BRCA1 or BRCA2 dysfunction lead to platinum sensitivity; we reasoned that the types of chromosomal aberrations arising in the context of BRCA dysfunction might also be associated with platinum sensitivity in wtBRCA cancers.

On the basis of results in cell lines, we chose to enumerate one such chromosomal abnormality, telomeric AI, in pre-treatment tumor genomes and to relate this to pathologic response after cisplatin therapy. N_tAI was associated with response to platinum treatment in our TNBC cisplatin trials and in platinum-treated serous ovarian cancer, and these findings suggest that the burden of this genomic abnormality exposes an underlying deficiency of DNA repair in the...
platinum-sensitive subset of these cancers. AI propagated from a given chromosomal location to the telomere suggests the operation of error-prone processes giving rise to abnormal cross-over or template switching events, rather than error-free DNA repair.

We found that the breakpoints of telomeric AI regions are nonrandom and enriched for CNVs. This pattern also suggests defective DNA repair. CNVs are associated with other repeat sequences, such as Alu repeats, are concentrated in pericentromeric and subtelomeric regions, and are associated also with common fragile sites (28, 29). These repeat elements are thought to result in replication "slow zones," which are prone to replication stalling and formation of DNA double-strand breaks (30, 31). Furthermore, downregulation of Rad51 or inhibition of BRCA1 increases the fragility at such sites when cells are under replication stress (32, 33). The observed association of low BRCA1 expression levels in many tumors with high NtAI suggests defective DNA repair. CNVs are associated with error-prone repair, other explanations should be considered. Both BRCA1 and AI in a majority of samples despite low tumor cell content. NtAI may prove useful in predicting response to a variety of drug resistance, and other as-yet unappreciated factors may determine NtAI are feasible via the use of formalin-fixed paraffin-embedded tumor material, and recent algorithms such as ASCAT permit the accurate determination of copy number and AI in a majority of samples despite low tumor cell content. NtAI may prove useful in predicting response to a variety of therapeutic strategies exploiting defective DNA repair.

Reversion has also been seen in a cell line with a BRCA2 mutation selected for PARP inhibitor resistance (27). Reversion mutations and in cis compensating mutations were observed in patients with Fanconi anemia, resulting in improvement in their bone marrow function (35). Inactivation of TP53BP1 restores the balance between homologous recombination and nonhomologous end joining in BRCA1-mutated cells and renders them resistant to PARP inhibitors (36, 37). Finally, drug transporters may prevent accumulation of platinum agents in tumor cells (38). Therefore, reversion of or compensation for a preexisting DNA repair defect may generate a tumor with high NtAI but resistance to platinum treatment; other platinum resistance mechanisms unrelated to DNA repair would have the same effect.

Our analysis begins to suggest an outline of the molecular taxonomy of TNBC and ovarian cancer with respect to DNA repair and drug sensitivity. Most platinum-resistant breast or ovarian cancers are tumors with repair proficiency and low NtAI. Two subsets of wtBRCA tumors possess high NtAI and are sensitive to platinum-containing drugs. In one of these subsets, repair deficiency may be the consequence of low BRCA1 expression and, in the other subset, repair may be crippled by mechanisms that do not depend upon BRCA1 expression. These observations will no doubt be further refined; inclusion of reversion mutations, compensations by other events in DNA repair pathways, other mechanisms of drug resistance, and other as-yet unappreciated factors may help to enhance our prediction of drug sensitivity in the future.

In conclusion, a summary measure of telomeric chromosome aberrations in the tumor genome, NtAI, predicts sensitivity to platinum treatment. Our findings implicate NtAI as a marker of impaired DNA double-strand break repair. Assays to determine NtAI are feasible via the use of formalin-fixed paraffin-embedded tumor material, and recent algorithms such as ASCAT permit the accurate determination of copy number and AI in a majority of samples despite low tumor cell content. NtAI may prove useful in predicting response to a variety of therapeutic strategies exploiting defective DNA repair.
instructions (Promega). Drug sensitivity was quantified as the dose number was quantified by the use of CellTiter 96 AQueous One
lished article (13).

Patient progressed on therapy and 44 patients completed 4 cycles of cisplatin therapy (11). Cisplatin-2 consisted of 51 TNBC pa-
monotherapy, of whom 4 progressed on therapy and 24 completed 4
gical samples after therapy (40). The Cisplatin-1 trial consisted of 28
ement, which estimates the percentage of reduction in invasive tumor
was available from the pretreatment biopsy. Therapeutic response

HCC1143, MDA-MB-231, MDA-MB-468, HCC38, MDA-MB-453
microarray core laboratory in September 2011. Drug sensitivity
Promega PowerPlex 1.2 short tandem repeat profiling at the DF/HCC
Type Culture Collection and were most recently authenticated by

Cell Lines and Drug Sensitivity Assays

Breast cancer cell lines were originally obtained from American
Type Culture Collection and were most recently authenticated by
Promega PowerPlex 1.2 short tandem repeat profiling at the DF/HCC
microarray core laboratory in September 2011. Drug sensitivity
measurements in breast cancer cell lines BT20, BTS49, HCC1187,
HCC1143, MDA-MB-231, MDA-MB-468, HCC38, MDA-MB-453
(triple-negative), CAMA-1, MCF7, T47D (ER+), BT474, HCC1954,
and MDA-MB-361 (HER2) were originally generated for a separate
study in which it was reported as “data not shown” in a recently pub-
lished article (13).

To summarize in brief, cells were exposed to a series of concentra-
tions of various chemotherapeutic agents for 48 hours. Viable cell
number was quantified by the use of CellTiter 96 AQueous One
Solution Cell Proliferation Assay according to the manufacturer’s
instructions (Promega). Drug sensitivity was quantified as the dose
of drug resulting in a 50% reduction of growth (IC50). We found
MCF7 to be highly resistant to all of the chemotherapeutic agents
tested, consistent with its reported caspase-3 deficiency and resis-
tance to drug-induced apoptosis (39). In our analyses with measures
of genomic aberration, MCF7 was the only clear outlier, and for these
reasons, was excluded from our analyses.

Breast Cancer Cohorts and Assessment of
Therapeutic Response

For this study, subjects were included for analysis of response to
cisplatin if they progressed on therapy or if they received at least 3 of
the planned cisplatin therapy, had received no other non-
protocol therapy before surgery, and if an adequate amount of tumor
was available from the pretreatment biopsy. Therapeutic response
was measured with the semiquantitative Miller–Payne grading sys-
tem, which estimates the percentage of reduction in invasive tumor
volume and cellularity on the basis of pathologic assessment of sur-
gical samples after therapy (40). The Cisplatin-1 trial consisted of 28
mainly sporadic TNBC patients treated with preoperative cisplatin
monotherapy, of whom 4 progressed on therapy and 24 completed 4
cycles of cisplatin therapy (11). Cisplatin-2 consisted of 51 TNBC pa-
tients treated with preoperative cisplatin and bevacizumab, of which
1 patient progressed on therapy and 44 patients completed 4 cycles
of cisplatin therapy before surgery (12). Two patients included in
this study were taken to surgery after completing 3 cycles of cisplatin
therapy because of the development of toxicity; in both cases there
was no appreciable pathologic response in the excised tumor after 3
cycles of cisplatin.

Preparation of Breast Cancer Samples

For both trials, core biopsies of tumor were obtained before
initiation of treatment. Adequate tumor for analysis was present
for 27 of 28 subjects in Cisplatin-1 and 37 of 51 subjects
in Cisplatin-2. Hematoxylin and eosin–stained tissue sections of
pretreatment core-needle biopsies were examined microscopically;
for all biopsies for which enrichment was deemed feasible, sec-
tions were manually microdissected with the use of an 18-gauge
needle. DNA was extracted by protease K and RNase A diges-
tions, phenol/chloroform extraction, and ethanol precipitation.
Paired normal DNA from patients was obtained from peripheral
blood lymphocytes for all cases in Cisplatin-1 and from 10 cases in
Cisplatin-2.

TCGA Ovarian and Breast Cancer Cohorts

Public SNP array data, expression data, and clinical annotation
data were obtained for the TCGA ovarian (19) and breast cancer
cohorts from the TCGA web site (41). BRCA1 and BRCA2 mutation
status for the ovarian cancers was obtained from cBio data portal
(42). In the ovarian cohort, we identified 218 samples with SNP
data that passed ASCAT (see the section entitled “Genotyping and
Copy Number Analysis”), BRCA mutation status, and interpretable
clinical annotations for treatment and outcomes indicating initial
initial treatment with adjuvant platinum-based chemotherapy, predomi-
nantly the combination of carboplatin and docetaxel. We classified
“treatment sensitive” patients as those annotated as having shown
a partial or complete response to initial treatment and no progres-
sion or recurrence within 6 months of initial treatment (n = 187);
the term “treatment resistant” was applied to those annotated as
having stable or progressive disease on initial therapy or disease
recurrence or progression within 6 months (n = 31). In the breast
cohort, we identified 78 samples with matched gene expression and
SNP data that passed ASCAT, which were classified as ER+/HER2+
on the basis of clustering of the ESR1 and ERBB2 transcripts (see
Supplementary Methods).
Telomeric Al Reflects Sensitivity to DNA-Damaging Agents

Figure 6. A model relating DNA repair to accumulation of telomeric Al and response to platinum agents. α, in DNA repair-competent cells, DNA breaks are repaired by the use of error-free homologous recombination employing the identical sister chromatid as a template, resulting in no AI. B, and C, compromised DNA repair favors the use of error-prone repair pathways, resulting in chromosome rearrangements and aberrant radial chromosome formation. After mitotic division, daughter cells will have imbalance in the parental contribution of telomeric segments of chromosomes (telomeric Al). B, nonhomologous end joining is one error-prone mechanism that joins a broken chromatid of one chromosome (dark blue) to the chromatid of another, usually nonhomologous, chromosome (white). Mitotic segregation results in cells with telomeric Al as the result of monoallelic change in DNA copy number of the affected telomeric region. C, mitotic recombination may result in rearrangements between homologous chromosomes (dark blue and light blue). Mitotic segregation results in cells with copy neutral loss of heterozygosity. D, the same compromise in DNA repair that causes telomeric Al may also result in the inability of the tumor cell to repair drug-induced DNA damage, leading to tumor sensitivity to drugs such as platinum salts.

Genotyping and Copy Number Analysis

DNA was sent to Affymetrix, Inc. for determination of genotypes via use of the molecular inversion probe-based genotyping system, OncoScan FFPE Express (43). The commercial assay, which determines genotype of 330,000 SNPs, was used for analysis of the Cisplatin-2 trial. An early version of the OncoScan assay, which genotypes 42,000 SNPs, was used for the Cisplatin-1 trial. Allele signal intensity and genotypes from the OncoScan genotyping assay were processed and provided to us by Affymetrix. The OncoScan SNP genotype data for the cisplatin therapy trials were submitted to the National Center for Biotechnology Information Gene Expression Omnibus database under accession number GSE28330. Public SNP array raw data for the breast cancer cell lines were obtained from the Sanger Institute Catalogue Of Somatic Mutations In Cancer website (44, 45), public SNP array data from an independent breast cancer cell line study conducted by Heiser and colleagues (18), and public SNP array data from the TCGA ovarian (19) and breast cancer cohorts were preprocessed by the AROMAv2 and CalMaTe algorithms (46) and, when a paired normal sample was available, TumorBoost (47).

Processed genotype data from OncoScan genotyping and public SNP array data were analyzed for allele-specific copy numbers and tumor cell content by the aforementioned algorithm, ASCAT (10). ASCAT is designed to correct for normal cell contamination and tumor cell ploidy but occasionally fails to fit a model to a given sample. In this study, ASCAT failed to process 3 of 14 cell lines from Sanger, 15 of 42 cell lines from Heiser and colleagues (18), and 5 of 37 samples from the Cisplatin-2 trial. Al was defined as any time the copy number of the 2 alleles was not equal, and at least one allele was present (Supplementary Fig. S1). To ensure that all trial cases were comparable, we eliminated cases estimated by ASCAT to have less than 36% tumor cell content, the highest level of normal cell admixture in the Cisplatin-1 trial, which was the trial with an overall greater tumor purity. Thus, we included all 27 samples with SNP array data from the Cisplatin-1 trial and 26 of 32 samples with SNP array data that passed ASCAT from the Cisplatin-2 trial. A minimum number of consecutive probes showing an aberration was required to call regions of AI and copy number change with confidence. To ensure similar aberration detection across the 3 platforms that were used, the minimum number of probes required to define a region of aberration was set to be proportional to the overall SNP density of the platform. The probe densities of the platforms were 42,000/genome OncoScan (prototype), 330,000/genome OncoScan FFPE Express, and 900,000/genome SNP6.0 for an approximate ratio of 1:8:20. Minimum probe requirements of 25 probes for 42-k OncoScan prototype, 200 probes for 330-k OncoScan FFPE Express, and 500 probes for SNP6.0 platform were chosen on the basis of...
optimizing for correlation of aberration measurement in a subset of samples with replicate data generated on both versions of the OncoScan platform (see also Supplementary Methods).

Telomeric AI and telomeric copy number change were defined as regions that extend to one of the subtelomeres but do not cross the centromere. Copy number of telomeric AI regions was defined as the mean copy number of the probes mapping to the region. Copy loss was defined as a mean of less than 1.5 copies, and copy gain was defined as a mean of greater than 2.5 copies. Association between NAI and response to cisplatin was measured by the AUC of the ROC curve for binary response. Correlation was determined by the Spearman rank correlation coefficient. Statistical significance was assessed by the Wilcoxon rank sum test. All P values are 2-sided.

**Enrichment of CNVs at site of DNA Breakpoints**

The genomic location of common CNVs was acquired from the Database of Genomic Variants (48). Mapping for HG17 and HG18 was acquired to match the SNP probe mapping of the 42-k prototype and 330-k commercial OncoScan platforms, respectively. CNVs were considered associated with a breakpoint if they overlapped within a 25-kb window on either side of the breakpoint. To test for enrichment, we performed 1,000 permutations for each cohort, where we randomly shuffled the location of the DNA breakpoints based on the location of the SNP probes, and determined how many were associated with CNVs.

**BRCA1 Transcript Quantitation and Promoter Methylation Analysis**

BRCA1 exon 16/17 and RPLP0 (control) qRT-PCR assay was performed as previously described (11) by the use of amplified tumor cDNA generated with the Ovation RNA Amplification System V2 kit (NuGen Technologies, Inc.). BRCA1 promoter methylation assay was performed as previously described (11). To combine the qRT-PCR transcript data from the Cisplatin-1 and Cisplatin-2 trials, the data were z-transformed within each cohort by centering it and dividing by the standard deviation.

**BRCA1 mRNA Expression in Public TCGA Cohorts**

Public normalized and summarized Agilent-based gene expression data were acquired from the TCGA for all breast cancer samples (level 3). Raw Affymetrix CEL files were obtained for ovarian cancer samples (level 1). Expression data for all TCGA ovarian cancer samples were normalized and summarized by the use of robust multiarray average, and the probe set “204531_s_at” was identified as the optimum probe set for measuring BRCA1 expression with the R package “JetSet” (49).

**Disclosure of Potential Conflicts of Interest**

A.L. Richardson, Z. Szallasi, Z.C. Wang, D.P. Silver, A.C. Ecklund, and N.J. Birkbak are inventors on a pending patent application based on this work.

**Acknowledgments**

The authors thank Affymetrix scientists Malek Faham, Yuker Wang, and Victoria Carlson, who performed the tumor genotype analysis of Cisplatin-1 by using an early version of OncoScan FFPE Express under a research agreement with Affymetrix, Inc.

**Grant Support**

This work is partly supported by the Dana-Farber/Harvard SPORF in Breast Cancer, grant number CA089393, by an Avon supplement to 5 P30 CA06516 Dana-Farber/Harvard Cancer Center Support Grant, and by the V Foundation for Cancer Research. J.E. Garber, N. Tung, Z.C. Wang, J.D. Iglehart, Z. Szallasi, and A.L. Richardson are supported by the Breast Cancer Research Foundation. N.J. Birkbak, A.C. Ecklund, Q. Li, and Z. Szallassi are supported by The Danish Council for Independent Research Medical Sciences (FSS). D.P. Silver gratefully acknowledges support of the Cogan Family Foundation.

Received August 22, 2011; revised February 14, 2012; accepted February 14, 2012; published OnlineFirst March 22, 2012.

**REFERENCES**

Telomeric AI Reflects Sensitivity to DNA-Damaging Agents


Correction: Telomeric Allelic Imbalance Indicates Defective DNA Repair and Sensitivity to DNA-Damaging Agents

In this article (Cancer Discov 2012;2:366–75), which was published in the April 2012 issue of Cancer Discovery (1), the following text was inadvertently omitted: “The results published here are in whole or part based upon data generated by The Cancer Genome Atlas (TCGA) pilot project established by the NCI and NHGRI (Accession number: phs000178.v1.p1). Information about TCGA and the investigators and institutions who constitute the TCGA research network can be found at http://cancergenome.nih.gov/.” The authors regret this omission.

REFERENCE


Published online August 8, 2013.
doi: 10.1158/2159-8290.CD-13-0326
©2013 American Association for Cancer Research.
Telomeric Allelic Imbalance Indicates Defective DNA Repair and Sensitivity to DNA-Damaging Agents

Nicolai J. Birkbak, Zhigang C. Wang, Ji-Young Kim, et al.

Cancer Discovery  Published OnlineFirst March 22, 2012.

Updated version: Access the most recent version of this article at: doi:10.1158/2159-8290.CD-11-0206

Supplementary Material: Access the most recent supplemental material at: http://cancerdiscovery.aacrjournals.org/content/suppl/2012/02/15/2159-8290.CD-11-0206.DC2

E-mail alerts: Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions: To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions: To request permission to re-use all or part of this article, use this link http://cancerdiscovery.aacrjournals.org/content/early/2012/03/15/2159-8290.CD-11-0206. Click on "Request Permissions" which will take you to the Copyright Clearance Center's (CCC) Rightslink site.