Tumor Mutation Burden Forecasts Outcome in Ovarian Cancer with BRCA1 or BRCA2 Mutations

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Abstract

Background: Increased number of single nucleotide substitutions is seen in breast and ovarian cancer genomes carrying disease-associated mutations in BRCA1 or BRCA2. The significance of these genome-wide mutations is unknown. We hypothesize genome-wide mutation burden mirrors deficiencies in DNA repair and is associated with treatment outcome in ovarian cancer.

Methods and Results: The total number of synonymous and non-synonymous exome mutations (Nmut), and the presence of germline or somatic mutation in BRCA1 or BRCA2 (mBRCA) were extracted from whole-exome sequences of high-grade serous ovarian cancers from The Cancer Genome Atlas (TCGA). Cox regression and Kaplan-Meier methods were used to correlate Nmut with chemotherapy response and outcome. Higher Nmut correlated with a better response to chemotherapy after surgery. In patients with mBRCA-associated cancer, low Nmut was associated with shorter progression-free survival (PFS) and overall survival (OS), independent of other prognostic factors in multivariate analysis. Patients with mBRCA-associated cancers and a high Nmut had remarkably favorable PFS and OS. The association with survival was similar in cancers with either BRCA1 or BRCA2 mutations. In cancers with wild-type BRCA, tumor Nmut was associated with treatment response in patients with no residual disease after surgery.

Conclusions: Tumor Nmut was associated with treatment response and with both PFS and OS in patients with high-grade serous ovarian cancer carrying BRCA1 or BRCA2 mutations. In the TCGA cohort, low Nmut predicted resistance to chemotherapy, and for shorter PFS and OS, while high Nmut forecasts a remarkably favorable outcome in mBRCA-associated ovarian cancer. Our observations suggest that the total mutation burden coupled with BRCA1 or BRCA2 mutations in ovarian cancer is a genomic marker of prognosis and predictor of treatment response. This marker may reflect the degree of deficiency in BRCA-mediated pathways, or the extent of compensation for the deficiency by alternative mechanisms.


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Introduction

Reliable biomarkers predicting resistance or sensitivity to anti-cancer therapy facilitate selection of proper therapeutic drugs in individual cancer patients. In breast cancer, the estrogen receptor and HER2 (erbB-2/neu) are used clinically to make therapeutic decisions about endocrine therapy and HER2-targeted drugs, respectively [1,2]. Both the estrogen receptor and HER2 participate in pathways that promote cancer growth. Likewise, BRCA1 and BRCA2 participate in error-free repair of double-strand DNA breaks by homologous recombination (HR) and inherited mutations in these genes predispose to breast and ovarian cancers [3]. Ovarian cancers carrying BRCA1 and BRCA2 mutations (mBRCA) display...
massive chromosomal alterations [4,5], and are more sensitive to DNA cross-linking agents containing platinum, and to PARP inhibitors [6,7]. Patients with high-grade serous ovarian cancer who carry germline mBRCA experience a longer progression-free survival (PFS) and better overall survival (OS) than non-carriers [6,8,9]. Therefore, BRCA1 and BRCA2 may be considered biomarkers that predict response to platinum-containing chemotherapy and to PARP inhibitors. However, in previous studies 15-18 % of BRCA-associated ovarian cancers responded poorly to platinum-based chemotherapy regimens, and either recurred or progressed shortly after initial surgery and chemotherapy [6,9].

Most sporadic high-grade serous ovarian cancer and triple-negative breast cancer do not have mutations in BRCA genes, but a subset of these tumors do exhibit massive chromosomal aberrations and responsiveness to DNA damaging chemotherapy [9-11]. An appealing hypothesis posits chromosomal aberrations are a gauge of the degree of impairment in HR. Proposed surrogates for HR defects include measures of chromosomal aberrations including whole genome loss of heterozygosity (LOH) and telomeric allelic imbalance [11,12]. Lack of Rad51 foci after DNA damage may also mark cells with impaired HR [13].

Recently, a significantly higher mutation burden was detected by whole genome or exome sequencing in breast and ovarian cancer with mBRCA, compared with their counterparts carrying the wild-type BRCA1 and BRCA2 (wtBRCA) genes [14,15]. Whole exome sequencing of high-grade serous ovarian cancers was reported by The Cancer Genome Atlas (TCGA) consortium[9]. The DNA sequence of ovarian cancers was compared to germline DNA sequence from the same subject to make somatic mutation calls. Identified mutations included base substitutions, insertions or deletions [9,15]. The vast majority of mutations were single base substitutions [9]. Accumulation of genome-wide mutations may be the consequence of unique mutational processes associated with DNA repair deficiency in tumors carrying BRCA1 or BRCA2 mutations.

Since ovarian cancers with mutations in BRCA1 or BRCA2 are more sensitive to platinum-containing chemotherapy, we asked whether the total number of somatic mutations in ovarian cancer predicts sensitivity to chemotherapy and clinical outcome. We used whole exome sequencing data from TCGA to enumerate somatic mutations and compared this to chemotherapy sensitivity, progression free survival (PFS) and overall survival (OS). A significant association between the total number of somatic exome mutations per genome (Nmut) and patient outcomes was observed in patients whose ovarian cancers possessed mutations in BRCA1 or BRCA2.

Results

Association of mutation burden with chemotherapy sensitivity and outcome

Using data from TCGA, we found that 95% of mutations in exomes of ovarian cancer are single base substitutions. Across the TCGA cohort of 316 tumors, the number of exome mutations in individual cancers (Nmut) varies widely, from 9 to 210 (median 54.5, Table S1). To determine whether Nmut is associated with chemotherapy resistance after initial surgery, we separated patients into Nmut high and low groups based on the median Nmut of the whole cohort. A higher rate of resistance to initial chemotherapy was observed in Nmut low compared to the Nmut high group (40.2 vs. 23.9 %, Figure 1A). Nmut was lower in treatment-resistant patients than sensitive patients (median 46 vs. 59, Figure 1B). Cox regression showed a correlation between Nmut and progression-free survival (PFS) or overall survival (OS) (P = 0.013 and 0.0014, respectively, Table 1). Kaplan-Meier analysis showed a significantly longer PFS and OS in the Nmut high group compared to the Nmut low group (Figure 1C and 1D).

Effect of BRCA1 and BRCA2 on mutation burden and outcome

Seventy patients either carried a germline BRCA1 or BRCA2 mutation or possessed tumors bearing somatic BRCA1 or BRCA2 mutations (mBRCA). We found no differences in tumor Nmut, PFS or OS between patients with germline and tumor somatic mutations in BRCA1 and BRCA2 (Figure S1). However, mBRCA-associated tumors possessed a higher Nmut than tumors without BRCA mutations (wtBRCA; median 67.5 vs. 49.5, Figure S2A). When we investigated all patients with tumors containing mBRCA, we found a significantly higher tumor Nmut in the treatment-sensitive group versus the treatment-resistant group (median 74 vs. 44, Figure 2A). In patients with wtBRCA tumors, there were no significant differences in Nmut between the treatment sensitive and resistant groups (median 52 vs. 47, Figure 2B). Cox regression showed a significant correlation between tumor Nmut and PFS and OS in patients with mBRCA-associated tumors (HR = 0.02, 0.002 and HR = 0.83, 0.011, respectively), but not in patients with wtBRCA tumors (Table 1). When patients with mBRCA-associated tumors were stratified by the median Nmut of the whole cohort, patients with high tumor Nmut showed a significantly longer PFS and OS (Figure 2C and 2D). PFS and OS in patients with wtBRCA and low tumor Nmut were shorter, similar to patients with wtBRCA tumors (Figure 2C to 2F). In patients with wtBRCA tumors, there was no significant relationship between Nmut and PFS or OS (Figure 2E and 2F). Therefore, the effect of tumor Nmut on treatment response and outcome was chiefly confined to those tumors with either germline or somatic mutations in BRCA1 or BRCA2.

In univariate and multivariate analysis, stage at presentation, size of residual tumors after debulking surgery, patient age and Nmut were associated with either PFS or OS in all patients with clinical follow-up (Table 1). Strikingly, for the patients with mBRCA-associated ovarian cancer, only Nmut was significantly associated with treatment outcome in both univariate and multivariate analysis. In multivariate analysis of
Cancers with wtBRCA, residual disease left after initial surgery was significantly associated with both PFS and OS. Nmut and age were significantly associated with OS, but not PFS in patients with wtBRCA (Table 1). These results show Nmut is significantly associated with clinical outcome and is independent of other prognostic factors in patients with mBRCA-associated tumors.

All 51 germline mutations in BRCA1 and BRCA2 were truncating mutations. Of the 21 somatic mutations in the two genes, 4 were missense and the others truncating. We examined location of the mutations in BRCA1 and BRCA2 genes for association with Nmut in tumors (Figures S3A and S3B). We separated BRCA mutations into ring, middle and BRCT domains of BRCA1 and N-terminal, RAD51 binding and C-terminal regions of BRCA2. Differences in Nmut among

Figure 1. Total number of exome mutations (Nmut) and clinical outcome in high-grade serous ovarian cancer. All patients received platinum and most received taxanes in combination. A) Tumors were separated into Nmut high and low groups defined by the median Nmut across the whole cohort and compared to the rate of chemotherapy resistance. The significance of the differences was determined by Fisher’s exact test. B) The number of mutations (Nmut) for each tumor was compared in chemotherapy resistant and sensitive patients and is shown by dot plots. Median and 25-75 percentiles are indicated by horizontal lines. P-value is derived from the Wilcoxon rank-sum test. C) Kaplan-Meier analysis compared the progression-free survival (PFS) and D) overall survival (OS) between patients with high and low tumor Nmut. Patients that were progression-free or still alive at the time of last follow-up were censored (+). Numbers of patients at risk at each interval are given below the graphs. P-values are obtained by Log-rank test.

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Mutation and Outcome in Ovarian Cancer Patients

Table 1. Univariate and Multivariate analysis of Nmut and other clinical variables with PFS and OS.

<table>
<thead>
<tr>
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<th>Univariate</th>
<th>Multivariate</th>
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<tr>
<td></td>
<td>HR</td>
<td>95% CI</td>
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<tr>
<td>All cases</td>
<td></td>
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<tr>
<td>Nmuta</td>
<td>0.944</td>
<td>(0.990-0.999)</td>
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<tr>
<td>Stage</td>
<td>0.926</td>
<td>(0.988-0.997)</td>
</tr>
<tr>
<td>Residualb</td>
<td>1.466</td>
<td>(1.072-2.005)</td>
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<td>Age (yrs)</td>
<td>1.325</td>
<td>(0.960-1.828)</td>
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<tr>
<td></td>
<td>1.183</td>
<td>(1.026-1.365)</td>
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<tr>
<td></td>
<td>1.267</td>
<td>(1.091-1.470)</td>
</tr>
<tr>
<td>Age (yrs)</td>
<td>0.995</td>
<td>(0.982-1.009)</td>
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<td>1.019</td>
<td>(1.005-1.033)</td>
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<tr>
<td>Mbrca</td>
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<tr>
<td>Nmut</td>
<td>0.817</td>
<td>(0.968-0.993)</td>
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<tr>
<td>Stage</td>
<td>0.828</td>
<td>(0.967-0.996)</td>
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<tr>
<td>Residual</td>
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<td>Age (yrs)</td>
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<td>(0.539-3.154)</td>
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<td>0.999</td>
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<td></td>
<td>1.362</td>
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<td>(0.960-1.016)</td>
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<td></td>
<td>1.017</td>
<td>(0.985-1.049)</td>
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<tr>
<td>wtBRCA</td>
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<tr>
<td>Nmut</td>
<td>0.987</td>
<td>(0.994-1.003)</td>
</tr>
<tr>
<td>Stage</td>
<td>0.966</td>
<td>(0.992-1.001)</td>
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<tr>
<td>Residual</td>
<td>1.369</td>
<td>(0.980-1.913)</td>
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<td>Age (yrs)</td>
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<td>(0.871-1.719)</td>
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<td></td>
<td>1.231</td>
<td>(1.048-1.447)</td>
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<td></td>
<td>1.195</td>
<td>(1.011-1.414)</td>
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<tr>
<td>Age (yrs)</td>
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<td>(0.979-1.010)</td>
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<td>1.017</td>
<td>(1.001-1.033)</td>
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a. Hazard ratio  
 b. 95% confidence interval  
 c. P-value from Cox proportional hazard regression  
 d. HR for Nmut is expressed the ratio per 10 mutations  
 e. Residual disease left after initial surgery  

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Figure 2. Total number of exome mutations (Nmut) and clinical outcome in high-grade serous ovarian cancer with germline or somatic mutations in BRCA1 or BRCA2 (mBRCA) or with wild-type BRCA1 and BRCA2 (wtBRCA). A) Nmut in tumors with mBRCA. Chemotherapy resistant and sensitive ovarian cancers are shown by dot plots. P-value is derived from the Wilcoxon rank-sum test. B) Nmut in tumors with wtBRCA. Chemotherapy resistant and sensitive tumors are shown with dot plots of each tumor as in Figure 1. Median and 25-75 percentiles are indicated by horizontal lines. P-value is derived from Wilcoxon rank-sum test. C) Kaplan-Meier analysis compared PFS and D) OS between patients with high and low Nmut in their mBRCA-associated tumors. E) Kaplan-Meier analysis compared PFS and F) OS in patients with high and low Nmut in their wtBRCA tumors. The median for Nmut was computed from the whole cohort of 316 tumors. In Kaplan-Meier analyses, patients that were progression-free or still alive at the time of last follow-up were censored (+). Numbers of patients at risk at each interval are given below the graphs. P-values are obtained from Log-rank test.

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Figure 3. Tumor Nmut and clinical treatment outcome in ovarian cancer patients carrying BRCA germline mutations with LOH at the BRCA loci in tumors. A) Kaplan-Meier analysis compared PFS and B) OS between Nmut high and low ovarian cancers, all of which carried either a BRCA1 or BRCA2 germline mutation with LOH at the corresponding BRCA locus. C - F) Analysis in individual BRCA1 and BRCA2 mutation carrier groups. C) Kaplan-Meier analysis in patients with BRCA1-associated tumors comparing PFS, and D) OS. E) Kaplan-Meier analysis in patients with BRCA2-associated tumors comparing PFS, and F) OS. Nmut high and low are defined as a value above or below median Nmut of all mBRCA-associated tumors. Numbers of patients at risk at each interval are given below the graphs. P-values are calculated by log-rank test.

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cancers with $BRCA1$ mutation, but not in those cancer with $BRCA1$ epigenetic alteration.

Correlation between Nmut and age or chromosomal damage

Nmut in tumors from patients with germline $BRCA1$ or $BRCA2$ mutations (BRCA mutations) increased with patient age at diagnosis (Figure S5A). However, this relationship was lost when tumors with somatic BRCA mutations were included or those with wtBRCA were analyzed separately, (Figures S5B and S5C). These finding are consistent with a distinct pathogenic process in germline BRCA-associated cancers with haplo-insufficiency of BRCA function in premalignant tissue, and those cancers that acquire BRCA mutations later in their development. A similar correlation between accumulated mutations and age was reported in cancers that arise from tissues which normally replicate during life (e.g., colonic epithelium), but are not seen in cancers from tissue normally dormant (e.g., cells in the exocrine pancreas)[16].

Both the fraction of LOH per genome (FLOH) and the number of episodes of telomeric allelic imbalance (NtAI) reflect the extent of tumor chromosomal damage [11,12]. Using TCGA SNP6 data from the same cohort, Nmut positively correlated with FLOH and NtAI in mBRCA-associated tumors; NtAI correlated with Nmut in wtBRCA tumors (Figure S6). The association between high mutation burden and high level of chromosomal damage suggests a link between the processes that produce or fail to repair these distinct types of DNA damage.

Influence of residual disease on the association of mutation burden and outcome

Residual disease after initial surgery is a prognostic factor in ovarian cancer and was confirmed in both mBRCA- and wtBRCA-associated ovarian cancer (Figure S7). In patients with mBRCA-related cancers, those with a high tumor Nmut had better outcomes than those with a low tumor Nmut regardless of whether residual disease was present after initial surgery (Figure S8). Patients with no residual disease and a high tumor Nmut had an especially favorable outcome (5 year PFS was 58% and OS was 100%; Figure S8). In the subset of patients with wtBRCA tumors and no residual disease after surgery, high tumor Nmut predicted a longer PFS and a trend towards longer OS (Figure 4). No such differences were found in patients with wtBRCA tumors and residual disease after surgery (data not shown). Residual disease is a powerful prognostic factor, which may mask the effect of tumor Nmut in patients with wtBRCA tumors. The result suggests Nmut is potentially associated with treatment outcome in sporadic ovarian cancer with wtBRCA and no residual disease.
Discussion

High-grade serous ovarian cancer in carriers of BRCA1 or BRCA2 has a better prognosis than the same disease in non-carriers, and may be more sensitive to cisplatin-based chemotherapy or to PARP inhibitors that target DNA repair [6-8]. However, within the group of women with somatic or inherited mutations in BRCA1 or BRCA2, some patients will still have poor outcomes. There are currently no markers of treatment outcome in patients with mBRCA-associated ovarian cancer. Possible markers might include impaired apoptosis, multi-drug resistance and DNA repair proficiency. The present study sought to correlate whole-exome mutation burden in tumor tissue (Nmut) to treatment outcome in ovarian cancer patients, and to examine this relationship in patients with BRCA1 and BRCA2 mutations in their ovarian tumors.

The most remarkable association of Nmut with treatment response and outcome was seen within the subset of patients with mBRCA-associated tumors. A substantial proportion of patients with mBRCA-associated ovarian cancer but low Nmut experienced a relatively poor treatment outcome, and similar to patients with wtBRCA ovarian cancer. However, for women whose cancers were mBRCA-associated and had a high tumor Nmut, outcome was remarkably good. This was true for both BRCA1 and BRCA2 mutations, both germline and somatic mutations, and for tumors with LOH at the corresponding locus. In patients with mBRCA-associated cancers and no residual disease after initial surgery, those with high Nmut had especially good outcomes. In fact, long survival in high-grade serous ovarian cancer, when it is observed, may be attributable to mutation in either BRCA1 or BRCA2 when these genotypes are coupled with a high tumor Nmut. Nmut is a candidate genomic marker for predicting treatment outcome in patients with mBRCA-associated ovarian cancer. The association of Nmut and outcome may reflect the degree of deficiency in BRCA1- or BRCA2-mediated DNA repair pathway(s), or the result of compensation for the deficiency by alternative mechanisms. However, all of the patients in the TCGA cohort received platinum-based chemotherapy, and the beneficial effect of a BRCA1 or BRCA2 deficiency on OS may be due to improved treatment response, or due to the less lethal potential of mBRCA-associated cancers.

In our analysis of TCGA data, BRCA1 mutation-associated ovarian cancer had a better outcome when coupled with a high tumor Nmut. In addition, BRCA1 mutation-associated cancer that lost the wild-type BRCA1 allele had a better outcome than ovarian cancer with only wild-type BRCA1 (data not shown). It is unclear why BRCA1 methylation, even coupled with high Nmut, does not translate into the same survival benefit seen in ovarian cancer with BRCA1 mutations and high Nmut. BRCA1 methylation is associated with a significant decrease of BRCA1 transcript levels, higher levels of genome-wide LOH and, in this study, higher mutation burden [9,11,15]. Under selection of platinum treatment, it is possible BRCA1 methylation may be reversible, and lead to the restoration of BRCA1 expression. In breast cancer xenografts, therapy resistant triple-negative cancer lost BRCA1 promoter methylation and re-expressed the BRCA1 protein [17]. The epigenetic co-inactivation of other gene(s), for instance in pro-apoptotic pathway(s), is a possibility that could explain the worse outcome of patients with BRCA1 methylation compared to those with BRCA1 mutation. These possibilities remain open to future studies.

Next-generation DNA sequencing is widely used in research and may become a clinical tool to detect specific and targetable mutations. A by-product of the increased use of whole-genome and whole exome sequencing studies may be a simple enumeration of genome-wide mutations, which may itself represent a genomic biomarker for predicting outcomes in patients receiving optimal surgery and chemotherapy.

Our observations are consistent with the concept that BRCA1 and BRCA2 regulate error-free repair of nucleotide damage and act to minimize single nucleotide mutations. There is evidence of BRCA1 DNA repair activity in pathways other than HR. Pathania, et al demonstrated BRCA1 played a role in repair of UV radiation-damaged DNA. BRCA1 participated in DNA replication-dependent but nucleotide excision repair (NER)-independent repair processes by promoting photoprotein excision and suppression of error-prone translesion synthesis (TLS) at UV-induced stalled replication forks [18]. High activity of TLS may be induced by FANCJ activity when there is loss of BRCA1 binding to FANCJ [19]. As TLS polymerases are error-prone, an up-regulation of TLS in the setting of BRCA1 deficiency may explain a higher rate of somatic nucleotide substitutions.

Whole genome sequencing in breast cancer identified a characteristic distribution of single nucleotide mutations with an increased overall mutation burden in both BRCA1- and BRCA2-associated tumors. All possible nucleotide substitutions were seen within 96 possible trinucleotide sequence contexts without predominant patterns of particular trinucleotides, which was a characteristic signature of both BRCA1- and BRCA2-associated breast cancers [14]. This characteristic appears consistent with loss of a key mechanism(s) for error-free DNA repair in addition to HR, or activation of an error-prone DNA replication process.

Other lines of evidence show differences between BRCA1 and BRCA2 mutation-associated ovarian cancers. These differences include relatively earlier onset in BRCA1 than BRCA2 germline mutation carriers, and a relatively better survival in patients with BRCA2 than BRCA1 mutation-associated tumors in comparison to that in patients with wtBRCA-associated ovarian cancer [6,15]. Our results show the same associations between tumor Nmut and treatment outcome in both BRCA1- and BRCA2-associated ovarian cancers. This observation is consistent with similar signatures of mutational processes in breast and ovarian cancers from patients with either BRCA1 or BRCA2 germline mutations [14,20]. There are other well-recognized similarities between BRCA1- and BRCA2-associated diseases. These similarities include HR-mediated DNA repair deficiencies, sensitivity to DNA damaging agents and PARP inhibitors, and reversion mutation-associated treatment resistance [3,6,7,9,21,22].

A low mutation burden in tumors with either a homozygous BRCA1 or BRCA2 damaging mutation and LOH at the corresponding BRCA locus may be explained by activation of alternative mechanism(s) capable of bypassing the defect and
restoring error-free DNA repair. Our knowledge of bypass pathways of repair is limited. Alternative activation of HR by concomitant loss of 53BP1 in BRCA1-deficient cells may restore resistance to PARP inhibitors, but does not change the sensitivity to cisplatin [23,24]. Reversion mutation of BRCA1/2 genes in recurrent disease may result in resistance to platinum chemotherapy and PARP inhibitors, but is rarely found in the primary disease [21]. Our results are based on a relatively small set of patients carrying BRCA1 and BRCA2 mutations, and should be considered hypothesis generating until confirmed in a larger cohort. In addition, tumors may possess de novo mechanisms leading to resistance to chemotherapy and targeted treatments. Our preliminary results suggest low tumor Nmut may identify BRCA-associated primary tumors in which the original deficiency of BRCA1 and BRCA2 pathways, including impaired DNA repair, is compensated for by alternative pathways.

Materials and Methods

Datasets

We obtained exome sequencing data of 316 high-grade serous ovarian cancers and follow-up information from TCGA [9]. Any sequence alteration in the ovarian tumor exome that was not present in the germline DNA sequence was called a somatic mutation and included both non-synonymous and synonymous changes. In the exome mutation data published by the TCGA consortium, a total of 19,356 somatic mutations were identified in the cohort, and most independently validated by a second assay using whole-genome amplification of a second sample from the same tumor [9]. Mutations that were not independently validated were computationally evaluated and had a high likelihood to be true mutations as described [9]. Based on TCGA mutation calls explained above, the total number of somatic mutations in the tumor exome (Nmut) was determined for each case (Table S1). Affymetrix SNP6 genotyping data and updated clinical information were obtained from the TCGA data portal (http://tcga-data.nci.nih.gov/tcga/, dbGaP accession no. phs000178.v5.p5, acquired 2011 Oct 27). BRCA1 and BRCA2 gene mutation status, BRCA1 and RAD51C methylation status and ethnic/racial information were acquired from the cBio SU2C data portal (http://cbio.msckc.org/su2c-portal/).

Clinical assessment of therapy response

All patients underwent debulking surgery prior to platinum and taxane-based chemotherapy. The outcome of debulking surgery was the presence or absence of visible residual disease at the end of surgery; in TCGA the dimensions of residual disease were estimated. All patients received platinum-based chemotherapy after surgery. Chemotherapy resistance was defined as disease progression during first-line platinum-based chemotherapy or progression within 6 months after completion of first-line therapy [25]. Chemotherapy sensitivity was defined as progression-free survival longer than 6 months.

Bioinformatics analysis

Affymetrix SNP6 array data for tumor-normal pairs were normalized using the Aroma CRMv2 algorithm, and B-allele fraction (BAF) was adjusted using the CalMaTe and TumorBoost Aroma packages [26-28]. Processed data were analyzed for LOH, allelic imbalance, copy number changes and normal cell contamination using ASCAT [29], as described elsewhere [12,29]. Nmut was determined by counting all mutation calls for each sample reported by the TCGA consortium (Table S1). Mutations include missense, nonsense, silent, frameshift and splice variants [9]. The median value for Nmut was determined for the cohorts and high Nmut was defined as those values above the median, and low Nmut was values equal to or below the median. Correlation was determined by the Spearman rank correlation coefficient. Statistical significance was assessed by the Wilcoxon rank-sum test for two-group comparison or by Kruskal-Wallis test for multiple-group comparison. Survival analysis was performed using Kaplan-Meier analysis and Cox regression. For Kaplan-Meier analysis, Nmut was dichotomized around its median value in study cohorts. In Cox regression, Nmut is continuous, but hazard ratio (HR) is reported per 10 mutations. The variables for multivariate analysis included Nmut, age, stage (II, III, IV), and residual disease (not visible, < 1 cm, 1-2 cm, and > 2 cm). All P values are 2-sided, and all bioinformatics analysis was performed in the R 2.15.2 statistical framework.

Supporting Information

Table S1. Genomic and ethnic/race information of TCGA ovarian cancer cohort used in the present study.

Figure S1. A) Total number of exome mutations (Nmut) in high-grade serous ovarian cancer carrying wtBRCA or mutated BRCA1/2 genes(s) (mBRCA). The tumor Nmut is presented by dot plots. Median and 25-75 percentiles are indicated by horizontal lines. P-value is derived from Wilcoxon rank-sum test. B-C: Tumors were separated into Nmut high and low groups defined by the median Nmut across the whole cohort and compared to the rate of chemotherapy resistance. The significance of the differences was determined by Fisher’s exact test. OR: Odds Ratio. Confidence intervals in brackets. B) mBRCA, C) wtBRCA.

Figure S2. Nmut and survival in mBRCA cases based on germline or somatic origin of the BRCA1/2 mutation. A) Total number of exome mutations (Nmut) in high-grade serous ovarian cancer carrying mutated BRCA1/2 genes(s) of either germline or somatic origin. The tumor Nmut is presented by dot plots. Median and 25-75 percentiles are indicated by horizontal lines. P-value is derived from Wilcoxon rank-sum test. B) and C) Kaplan-Meier analysis comparing PFS (B) and OS (C) between serous ovarian cancer patients with either germline or somatic mBRCA.
Figure S3. Position of mutations in BRCA1 and BRCA2 proteins by amino acid number, and their association with Nmut. A) and B) shows BRCA1 (A) and BRCA2 (B), with the domains of BRCA1 and BRCA2 proteins illustrated with different colors on top of each panel. The Y-axis shows for each mBRCA tumor Nmut, with the corresponding position of the BRCA1/2 mutation indicated on the X-axis. Germline mutations are indicated in blue, somatic in red. Missense mutations are shown as diamonds. C) and D) shows Nmut by grouping the locations of BRCA mutations according to relevant regions in BRCA1 and BRCA2, respectively. Red dotted lines on A) and B) shows the exact grouping cut-offs. P-values comparing Nmut by location is determined by a Kruskal-Wallis test.

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Author Contributions

Conceived and designed the experiments: ZCW NJB JDI ALR ZS. Performed the experiments: NJB BK. Analyzed the data: NJB ZCW BK. Contributed reagents/materials/analysis tools: NJB JMI. Wrote the manuscript: JDI ZCW NJB ALR.

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