Clinical Cancer Research

Mutations in Homologous Recombination Genes and Outcomes in Ovarian Carcinoma Patients in GOG 218: An NRG Oncology/Gynecologic Oncology Group Study

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Abstract

Purpose: We hypothesized that mutations in homologous recombination repair (HRR) genes beyond *BRCA1* and *BRCA2* improve outcomes for ovarian carcinoma patients treated with platinum therapy and would impact the relative benefit of adding prolonged bevacizumab.

Experimental Design: We sequenced DNA from blood and/or neoplasm from 1,195 women enrolled in GOG-0218, a randomized phase III trial in advanced ovarian carcinoma of bevacizumab added to carboplatin and paclitaxel. Defects in HRR were defined as damaging mutations in 16 genes. Proportional hazards models were used to estimate relative hazards for progression-free survival (PFS) and overall survival (OS).

Results: Of 1,195 women with ovarian carcinoma, HRR mutations were identified in 307 (25.7%). Adjusted hazards for progression and death compared with those without mutations were lower for women with non-*BRCA* HRR mutations [HR = 0.73; 95% confidence interval (CI), 0.57–0.94; $P = 0.01$ for PFS; HR = 0.67; 95% CI, 0.50–0.90; $P = 0.007$ for OS] and *BRCA1* mutations (HR = 0.80; 95% CI, 0.66–0.97; $P = 0.02$ for PFS; HR = 0.74; 95% CI, 0.59–0.94; $P = 0.01$ for OS) and were lowest for *BRCA2* mutations (HR = 0.52; 95% CI, 0.40–0.67; $P < 0.0001$ for PFS; HR = 0.36; 95% CI, 0.25–0.53; $P < 0.0001$ for OS). A test of interaction showed no difference in the effect of bevacizumab on PFS between cases with and without mutations.

Conclusions: HRR mutations, including non-*BRCA* genes, significantly prolong PFS and OS in ovarian carcinoma and should be stratified for in clinical trials. The benefit of adding bevacizumab was not significantly modified by mutation status. *Clin Cancer Res; 24(4); 777–83. ©2017 AACR.*

Introduction

BRCA1 and BRCA2 are key components of the BRCA–Fanconi anemia DNA repair pathway that controls DNA repair via homologous recombination (1–3). Germline and somatic mutations affecting homologous recombination repair (HRR) genes are relatively common, found in approximately one third of ovarian carcinoma patients, with the majority of mutations occurring in *BRCA1* and *BRCA2* (4, 5). Ovarian carcinoma patients with inherited mutations in *BRCA1* and *BRCA2* have longer 5-year survival, likely due to improved sensitivity to platinum chemotherapy (6–8). This may also be true for somatic and germline mutations in other HRR genes, although the number of cases with non-*BRCA* HRR mutations studied to date is small (5). In addition, *BRCA1*- and *BRCA2*-mutated ovarian carcinomas may have a lower angiogenic profile (9) and more favorable immunophenotype than those without mutations, which might also contribute to better outcomes (10, 11).

GOG-0218 was a randomized, phase III trial for patients with primary advanced ovarian, peritoneal, and fallopian tube carcinoma (ovarian carcinoma), examining the addition of the anti-angiogenesis drug bevacizumab to standard chemotherapy with carboplatin and paclitaxel. Patients in this study who received extended bevacizumab had a significant prolongation in median progression-free survival (PFS) of 3.8 months (12). In the parallel

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Translational Relevance

In the setting of a large clinical trial in primary ovarian cancer patients, we have demonstrated that damaging mutations in a selected set of genes affecting homologous recombination repair beyond *BRCA1* and *BRCA2* are associated with improved progression-free and overall survival, controlling for known prognostic features, with an outcome similar to that seen for *BRCA1* mutations. Cases with *BRCA2* mutations had even better outcomes. Given the magnitude of these effects, consideration should be given to assessing homologous recombination repair in the design and analyses of ovarian carcinoma clinical trials. We found mutations in homologous recombination repair genes, including *BRCA1* and *BRCA2*, in all histologic subtypes, with only low-grade serous having a significantly lower mutation frequency. Our data do not support restricting access to clinical trials, or to germline genetic testing, on the sole basis of histology. We did not see a differential effect of the impact of bevacizumab on progression-free survival by mutation status. Therefore, mutation status should not be used to decide who is a candidate for bevacizumab.

European ICON-7 trial, a non-prespecified subgroup analysis suggested that extended bevacizumab was of greatest benefit for patients with poor prognostic features, such as stage IV disease, or unresectable or suboptimally resected tumors, demonstrating a benefit in overall survival (OS) in these "high-risk" patients (13).

We hypothesized that ovarian carcinoma patients with inherited mutations in HRR genes, including a select set of genes beyond *BRCA1* and *BRCA2*, have longer survival and improved platinum sensitivity and may derive less benefit from extended bevacizumab. We tested this hypothesis using tissues from patients in GOG-218 who had provided consent for translational research.

Materials and Methods

GOG-0218 clinical trial details have been described previously (12). DNA from tumor and blood from patients on GOG-0218 were sequenced using BROCA, a targeted capture, massively parallel sequencing test developed at the University of Washington (Seattle, WA; ref. 14). All available germline DNA samples extracted from blood were sequenced ($n = 788$). These patients have been described previously (8). To improve detection of HRR deficiency in this group by detection of somatic mutations in HRR genes, we also sequenced DNA from neoplastic tissue from a subset of these patients with negative germline testing ($n = 324$). Finally, we sequenced DNA from neoplastic tissue from 407 additional cases that did not have available DNA from blood, detecting both germline and somatic mutations (bringing the total number of sequenced patients to 1,195). Distinguishing between germline and somatic mutations could not be done with certainty in the group with only tumor sequencing. As the effect on outcome was predicted to be similar, germline and somatic mutations were combined for analyses. All patients provided written informed consent as approved by an Institutional Review Board, in accordance with ethical guidelines as described in the U. S. Common Rule. As patients were not specifically consented for open access genomic data, complete sequencing data, such as BAM files, cannot be shared publicly.

A subset of genes predicted to impact homologous recombination repair (HRR) when mutated was selected prior to analysis based on review of the available literature and expert opinion, including *ATM*, *ATR*, *BARD1*, *BLM*, *BRCA1*, *BRCA2*, *BRIP1*, *CHEK2*, *MRE11A*, *NBN*, *PALB2*, *RAD51C*, *RAD51D*, *RBBP8*, *SLX4*, and *XRCC2*. Sequencing reads were aligned to the human reference genome (hg19). Variants were identified using GATK37 and Pindel after indel realignment and base quality calibration. Copy number variations were detected in germline samples as described previously (14–16). Missense mutations were only included if proven to be damaging in functional assays or classified as likely pathogenic on ClinVar (https://www.ncbi.nlm.nih.gov/clinvar/; ref. 17).

Clinical information was collected as per the GOG-0218 protocol (12). All pathology was centrally reviewed. PFS and OS were defined as the time between enrollment and progression or death, respectively. Proportional hazards models were used to provide estimates of the relative hazards for progression and death by genotype, adjusted by clinical characteristics. The effect of mutation status on the impact of bevacizumab on progression was assessed with a test of interaction. All *P* values are 2-sided.

Results

Study population

Of 1,873 women in GOG 218, 1,195 (63.8%) had DNA available for sequencing. Baseline characteristics of sequenced and not sequenced patients are described in Table 1. The distribution of race was significantly different between the groups, with more non-Hispanic Whites and fewer Asian/Pacific Islanders in the sequenced group ($P < 0.001$, χ^2). There were more optimally debulked stage III patients and less stage IV patients in the sequenced group ($P < 0.001$, χ^2). The distribution of histologic subtypes also differed, with fewer patients with clear cell carcinoma in the sequenced group ($P = 0.012$, χ^2). The median PFS duration for those who were not sequenced was 10.5 months compared with 13.5 months for those sequenced ($P < 0.001$) and the median overall survival for those not sequenced was 30.9 months compared with 46.2 months for those who were sequenced.

Sequencing results

In total, 307 of 1,195 (25.7%) sequenced patients had damaging mutations in one of the selected genes affecting HRR. There were 148 (12.4%) with mutations in *BRCA1*, 78 (6.5%) with mutations in *BRCA2*, and 81 (6.8%) with mutations in other HRR genes. Ten patients (0.8%) had more than one mutation. Of these 10, three were in the *BRCA1* mutation group, with additional mutations in *RBBP8* (one) and *NBN* (two), and four were in the *BRCA2* group (one with *CHEK2*, one with *RBBP8*, one with both *ATM* and *CHEK2*, and one with *BRIP1* and *CHEK2*). Of the 81 patients in the other HRR group, there were 84 mutations in the following genes: 12 in *ATM*, five in *ATR*, three in *BARD1*, five in *BLM*, 19 in *BRIP1*, two in *CHEK2*, two in *MRE11A*, three in *NBN*, six in *PALB2*, seven in *RAD51C*, seven in *RAD51D*, eight in *RBBP8*, two in *SLX4*, and three in *XRCC2*. Details of the patients with non-*BRCA* HRR mutations are provided in Supplementary Table S1.

In the subset of 324 patients with negative germline testing who had subsequent sequencing of neoplastic DNA, there were 32 (9.9%) somatic mutations in HRR genes [(17 (5.2%) in *BRCA1*, seven (2.2%) in *BRCA2*, and eight (2.5%) in other HRR

Table 1. Clinical characteristics of ovarian carcinoma patients, sequenced vs. not sequenced

Characteristics	Sequenced	Not sequenced
N	1,195	678
Age		
<40	40 (3.3%)	23 (3.4%)
40–49	176 (14.7%)	90 (13.3%)
50–59	385 (32.2%)	221 (32.6%)
60–69	374 (31.3%)	236 (34.8%)
70–79	205 (17.2%)	91 (13.4%)
≥80	15 (1.3%)	17 (2.5%)
Race/ethnicity[a]		
Non-Hispanic White	1,048 (87.7%)	518 (76.4%)
Hispanic	51 (4.3%)	23 (3.4%)
Non-Hispanic Black	46 (3.8%)	34 (5.0%)
Asian/Pacific Islander	31 (2.6%)	86 (12.7%)
Other or unknown	19 (1.6%)	17 (2.5%)
Disease site		
Ovary	998 (83.5%)	565 (83.3%)
Peritoneal	171 (14.3%)	103 (15.2%)
Fallopian tube	26 (2.2%)	10 (1.5%)
Stage[a]		
III/Optimal	465 (38.9%)	175 (25.8%)
III/Suboptimal	453 (37.9%)	299 (44.1%)
IV	277 (23.2%)	204 (30.1%)
Histology[b]		
HG Serous	971 (81.3%)	526 (77.6%)
LG Serous	46 (3.8%)	25 (3.7%)
Carcinoma, NS	84 (6.2%)	81 (14.2%)
LG Endometrioid	4 (0.3%)	2 (0.3%)
HG Endometrioid	38 (3.2%)	15 (2.2%)
Clear cell	28 (2.3%)	27 (4.0%)
Mucinous	7 (0.6%)	12 (1.8%)
Treatment		
CT + P → P	408 (34.1%)	217 (32.0%)
CT + B → P	386 (32.3%)	239 (35.3%)
CT + B → B	401 (33.6%)	222 (32.7%)

Abbreviations: HG, high-grade, grades 2 and 3; LG, low-grade, grade 1; NS, not specified; CT, chemotherapy; P, placebo; B, bevacizumab.
[a]$P < 0.001$, χ^2.
[b]$P = 0.012$, χ^2.

Table 2. Clinical characteristics and mutation category in ovarian carcinoma patients

Characteristics	*BRCA1*	*BRCA2*	Other HRR	WT
N	148	78	81	888
Disease site				
Ovary	131 (88.5%)	65 (83.3%)	68 (85.2%)	734 (82.7%)
Peritoneal	16 (10.8%)	12 (15.4%)	12 (14.8%)	131 (14.8%)
Fallopian tube	1 (0.7%)	1 (1.3%)	1 (1.2%)	23 (2.6%)
Stage				
III/Optimal	59 (39.9%)	26 (33.3%)	37 (45.7%)	343 (38.6%)
III/Suboptimal	58 (39.2%)	29 (37.2%)	25 (30.9%)	341 (38.4%)
IV	31 (20.9%)	23 (29.5%)	19 (23.5%)	204 (23.0%)
Histology				
HG Serous	127 (85.8%)	70 (89.7%)	65 (80.2%)	709 (79.8%)
LG Serous[a]	4 (2.7%)	0	1 (1.2%)	41 (4.6%)
Carcinoma, NS	12 (8.1%)	6 (7.7%)	4 (12.6%)	79 (8.9%)
Endometrioid	3 (2.0%)	1 (1.3%)	6 (7.4%)	32 (3.6%)
Clear cell	2 (1.4%)	1 (1.3%)	3 (3.7%)	22 (2.5%)
Mucinous	0	0	2 (2.5%)	5 (0.6%)
Treatment				
CT + P → P	53 (35.8%)	28 (35.9%)	27 (33.3%)	300 (33.8%)
CT + B → P	34 (23.0%)	19 (24.4%)	26 (32.1%)	307 (34.6%)
CT + B → B	61 (41.2%)	31 (38.3%)	28 (34.6%)	281 (31.6%)

NOTE: Other HRR (other homologous recombination repair) refers to those with mutations in non-*BRCA* genes, including *ATM, ATR, BARD1, BLM, BRIP1, CHEK2, MRE11A, NBN, PALB2, RAD51C, RAD51D, RBBP8, SLX4*, and *XRCC2*.
Abbreviations: HG, high-grade, grades 2 and 3; LG, low-grade, grade 1; NS, not specified; CT, chemotherapy; P, placebo; B, bevacizumab.
[a]Low-grade serous carcinoma had a significantly lower total mutation rate when compared with high-grade serous carcinoma. $P = 0.02$, Fisher exact.

genes]. In a small exploratory analysis, these 32 "definitely somatic" mutation carriers had significantly lower hazards of both progression and death when compared with 174 patients with "definitely germline" mutations (Supplementary Fig. S1). Mutation rates by the source of sequenced DNA are described in more detail in Supplementary Table S2.

Clinical characteristics by mutation status

The proportion of patients in each mutation group by clinical characteristics is shown in Table 2. Mutation status did not differ by disease stage or primary site. Mutations in HRR genes were found in all histologic subtypes. The overall mutation rate in the high-grade serous carcinomas was 27.0% (262/971), which was not significantly different from the rate in unspecified carcinoma (22/101, 21.8%, $P = 0.29$), endometrioid (10/42, 23.8%, $P = 0.73$), clear cell (6/28, 21.4%, $P = 0.67$), or mucinous carcinoma (2/7, 28.6%, $P = 1.0$). The low-grade serous carcinomas had a lower HRR mutation rate of 10.9% [5/46, 95% confidence interval (CI), 4.8–23.1; $P = 0.02$, Fisher exact] when compared with high-grade serous carcinomas.

Effect of mutation status on survival

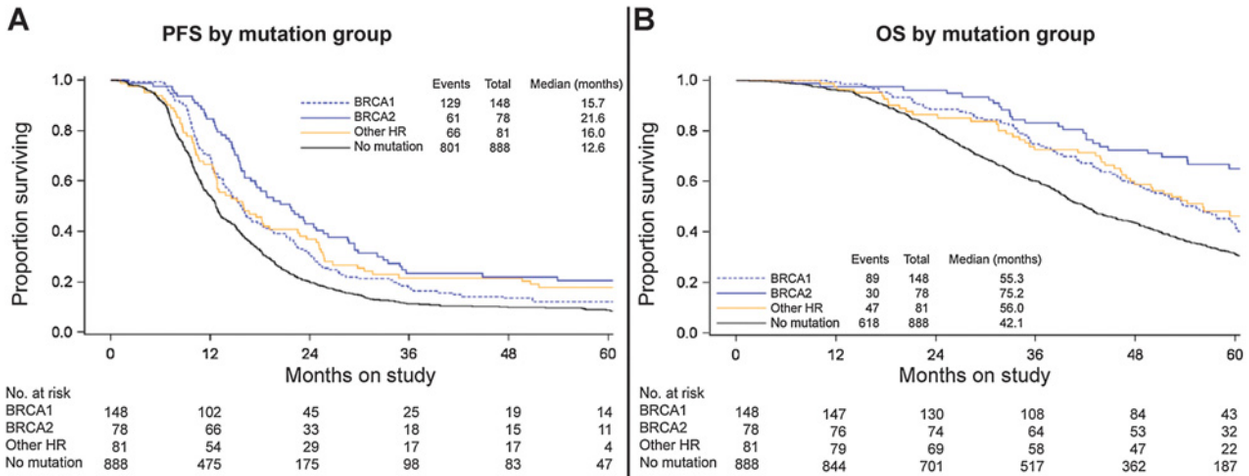
Damaging mutations in *BRCA1*, *BRCA2*, or other non-*BRCA* HRR genes were all associated with longer PFS and OS relative to cases without mutations (Fig. 1). After adjusting for study treatment, stage of disease, size of residual disease, and initial performance status, adjusted HRs for both progression and death were significantly lower in cases with HRR mutations when compared with those with no mutations (Fig. 1). This effect was strongest for *BRCA2* mutations and was similar for *BRCA1* and non-*BRCA* HRR mutations.

Interaction between mutation status and the effect of bevacizumab on progression

For this analysis, only patients from arm 1 (carboplatin/paclitaxel with placebo) and arm 3 (carboplatin/paclitaxel with bevacizumab and bevacizumab maintenance) were included ($n = 809$). In patients with no mutations ($n = 581$), extended bevacizumab significantly prolonged PFS (15.7 months vs. 10.6 months; HR = 0.71; 95% CI, 0.60–0.85; $P = 0.0001$; Fig. 2A). In those with mutations ($n = 228$), extended bevacizumab conferred a median PFS of 19.6 months versus 15.4 months (HR = 0.95; 95% CI, 0.71–1.26; Fig. 2C). Using a test of interaction, mutation status did not significantly modify the effect of extended bevacizumab on progression [(0.95/0.71) = 1.33; 95% CI, 0.95–1.85; $P = 0.10$].

Discussion

GOG-0218 was a large randomized, placebo-controlled phase III clinical trial with standardized treatment, central pathology review, and follow-up, providing a unique opportunity to assess the impact of HRR deficiency on clinical outcomes. In this trial, patients with ovarian carcinoma with defective HRR, defined by damaging somatic or germline mutations in one of 16 genes, had significantly prolonged PFS and OS when compared with those without mutations (Fig. 1). This is the first study in ovarian carcinoma large enough to separately assess the impact on



Adjusted hazards for progression by mutation category

Gene category	Total *N*	Events (%)	aHR (95% CI)	*P* value
BRCA1	148	129 (87.2)	0.80 (0.66–0.97)	0.02
BRCA2	78	61 (78.2)	0.52 (0.40–0.67)	<0.0001
Other HRR	81	66 (81.5)	0.73 (0.57–0.94)	0.01
No mutation	888	801 (90.2)	1.0 (referent)	Referent

Adjusted hazards for death by mutation category

Gene category	Total *N*	Events (%)	aHR (95% CI)	*P* value
BRCA1	148	89 (60.1)	0.74 (0.59–0.94)	0.01
BRCA2	78	30 (38.5)	0.36 (0.25–0.53)	<0.0001
Other HRR	81	47 (58.0)	0.67 (0.49–0.90)	0.007
No mutation	888	618 (69.6)	1.0 (referent)	Referent

Figure 1.

Progression-free and overall survival in ovarian carcinoma patients by mutation category. **A** and **B,** Kaplan–Meier curves for progression-free and overall survival by mutation category, with adjusted HRs for progression or death. HRs were adjusted for study treatment, stage of disease, size of residual disease, and initial performance status. The no mutation group was the referent group. Events were progression or death in 60 months. Abbreviation: aHR (adjusted HR).

outcomes of non-*BRCA* HRR mutations, which are less common than mutations in *BRCA1* and *BRCA2*, although our smaller single institution study showed a trend toward improved OS with mutations in a subset of non-*BRCA* genes (5). We carefully selected a list of 14 non-*BRCA* genes *a priori* that we thought would be most likely to impact outcomes based on *in vitro* data. Ovarian carcinomas with mutations in other HRR pathway genes such as *FANCM*, *FANCA*, and *FANCI* were not classified as HRR deficient. Interestingly, the non-*BRCA* HRR mutations were associated with PFS and OS curves that were almost identical to *BRCA1* mutations, supporting our *a priori* selection of HRR genes as meaningful.

As expected, *BRCA1* and *BRCA2* mutations were associated with longer survival, with the most profound effect seen for *BRCA2* mutations with a median survival advantage of 33 months compared with those without mutations. These patients were treated years before PARP inhibitors became available, and these outcome differences would likely be even greater with current treatments. Previous studies have also demonstrated a better outcome for *BRCA2* compared with *BRCA1* mutations (5–8), but ours is the first large study to include somatic mutations and to assess outcomes relative to mutation status for patients treated on a phase III clinical trial with standardized treatment and follow-up. Given the meaningful impact of HRR deficiency on both PFS and OS, the presence of HRR mutations, including *BRCA1* and *BRCA2*, should be carefully considered in the design and analyses of ovarian carcinoma clinical trials.

Mutations in HRR genes were found in all histologic subtypes of ovarian carcinoma, and rates were only significantly lower in low-grade serous carcinomas, 5/46 (10.9%) versus 262/971 (27%) in high-grade serous carcinomas, $P = 0.02$, (Table 2). All tumors in GOG-0218 underwent centralized review by gynecologic pathologists, minimizing pathologic misclassification. These results are similar to our recent observation that germline HRR mutations are distributed across many histologic subtypes without a clear predilection for high-grade serous carcinomas (8). Therefore, HRR status cannot be assumed by histologic type. Some clinical trials targeting HRR deficiency, such as those using PARP inhibitors, are restricted to patients with high-grade serous carcinomas (18), or to those with either high-grade serous or high-grade endometrioid histology (19). Our data do not support restricting access to these clinical trials or to germline genetic testing or tumor sequencing for HRR defects based on histologic subtype alone.

The role of antiangiogenesis-targeted therapy in ovarian carcinomas with and without HRR deficiency has not been previously defined. In the subset of patients with HRR mutations in GOG-0218, extended bevacizumab did not confer a statistically significant prolongation in PFS (Fig. 2C). However, there was insufficient evidence that bevacizumab had a different effect on PFS or OS in HRR-mutated versus nonmutated cases, using a test of interaction (Fig. 2). The power of this analysis was limited by not having translational samples from all participants in GOG-0218; therefore, the number of mutation carriers was relatively small. Sequenced patients were less likely to be stage IV and had better

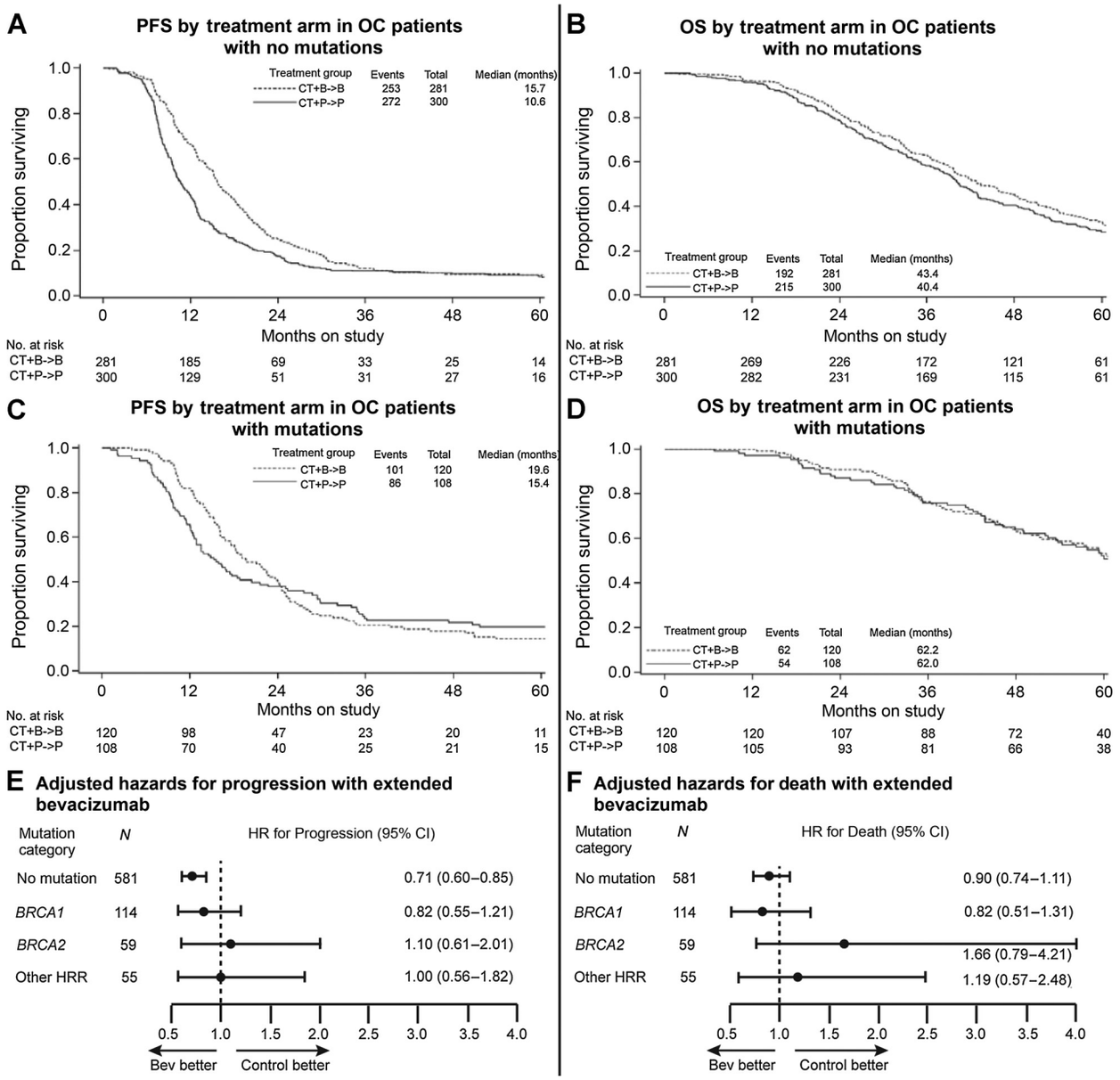


Figure 2.

Effect of extended bevacizumab on survival in ovarian carcinoma patients with and without mutations. **A–D,** Kaplan–Meier curves for progression-free and overall survival in ovarian carcinoma patients with and without mutations in genes affecting HRR. **E–F,** Adjusted HRs for progression or death by individual mutation categories. Using a test of interaction, mutation status did not significantly modify the effect of extended bevacizumab on progression [(0.95/0.71) = 1.33; 95% CI, 0.95–1.85; $P = 0.10$].

PFS and OS, which also may have reduced our ability to detect a difference. Within the similar ICON7 trial, a subset of 359 cases subjected to expression profiling, proliferative, and mesenchymal subtypes may have derived greater benefit from bevacizumab therapy; however, tests of interaction were not done to formally test that hypothesis. The mutation status of the ICON7 cancers was not determined (20). Further studies are needed to identify ovarian carcinomas best treated with bevacizumab, but our data do not currently support *BRCA* mutation status as a determinant.

This study has several limitations. Although germline sequencing data are available on all patients (by sequencing DNA from blood or tumor), around 40% of patients did not have tumor sequenced. This likely underestimated the true mutation frequency by missing some somatic mutations. In addition, as germline and somatic HRR mutations are rarely present in the same patient, utilizing a "germline negative" group ($n = 324/1{,}195$, 27.1%) for additional tumor sequencing likely overestimated the somatic mutation rate by excluding those with germline mutations who were unlikely to have somatic mutations (Supplementary Table S2).

Exome sequencing data from The Cancer Genome Atlas (TCGA) demonstrated somatic or germline mutations in DNA repair genes in around 40% of patients with high-grade serous histology ovarian carcinomas (4), compared with 27% in patients with high-grade serous carcinomas in this trial. This difference is likely due to a combination of (i) our preselected shorter HRR gene list chosen to maximize likelihood of therapeutic impact; (ii) our incomplete tumor sequencing data in 40% of cases; and (iii) our more stringent definition of damaging mutations compared with TCGA. Finally, mutations in non-BRCA "other" HRR genes were too few to allow a survival analysis by individual gene, necessitating combining these patients into one group for analysis.

In conclusion, HRR deficiency is a strong predictor of both PFS and OS in ovarian carcinoma, including mutations in 14 non-*BRCA* HRR genes (*ATM*, *ATR*, *BARD1*, *BLM*, *BRIP1*, *CHEK2*, *MRE11A*, *NBN*, *PALB2*, *RAD51C*, *RAD51D*, *RBBP8*, *SLX4*, and *XRCC2)*. Histologic subtype does not provide sufficient information to predict either inherited or somatic HRR mutations. There is insufficient evidence that HRR mutations should be a criterion, either positive or negative, in the decision to use bevacizumab maintenance therapy for advanced ovarian carcinoma.

Disclosure of Potential Conflicts of Interest

T. Walsh is a consultant/advisory board member for Color Genomic. R.A. Burger is a consultant/advisory board member for Amgen, Astra Zeneca, Clovis, Genentech, Gradalis, Invitae, Janssen, Merck, Morphotek, NuCana, Tesaro, and VBL Therapeutics. K.S. Tewari reports receiving speakers bureau honoraria from Roche and is a consultant/advisory board member for Genentech. F. Backes is a consultant/advisory board member for Tesaro. M.C. King is a consultant/advisory board member for Color Genomics. No potential conflicts of interest were disclosed by the other authors.

Disclaimer

The funders/sponsors had no role in the design and conduct of the study; collection, management, analysis, and interpretation of the data; preparation, review, or approval of the manuscript; and decision to submit the manuscript for publication.

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