Predictive Biomarkers and Personalized Medicine

Prognostic and Predictive Value of Tumor Vascular Endothelial Growth Factor Gene Amplification in Metastatic Breast Cancer Treated with Paclitaxel with and without Bevacizumab; Results from ECOG 2100 Trial

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Abstract

Purpose: Clinically validated biomarkers for anti-angiogenesis agents are not available. We have previously reported associations between candidate VEGFA single-nucleotide polymorphisms (SNP) and overall survival (OS) in E2100. The associations between tumor VEGFA amplification and outcome are evaluated here.

Experimental Design: E2100 was a phase III trial comparing paclitaxel with or without bevacizumab for patients with metastatic breast cancer. FISH to assess gene amplification status for VEGFA was conducted on paraffin-embedded tumors from 363 patients in E2100. Evaluation for association between amplification status and outcomes was conducted.

Results: Estrogen receptor (ER)+ or progesterone receptor (PR)+ tumors were less likely to have VEGFA amplification than ER/PR− tumors (P = 0.020). VEGFA amplification was associated with worse OS (20.2 vs. 25.3 months; P = 0.013) in univariate analysis with a trend for worse OS in multivariate analysis (P = 0.08). There was a significant interaction between VEGFA amplification, hormone receptor status, and study arm. Patients with VEGFA amplification and triple-negative breast cancers (TNBC) or HER2 amplification had inferior OS (P = 0.047); amplification did not affect OS for those who were ER+ or PR+ and HER2−. Those who received bevacizumab with VEGFA amplification had inferior progression-free survival (PFS; P = 0.010) and OS (P = 0.042); no association was seen in the control arm. Test for interaction between study arm and VEGFA amplification with OS was not significant.

Conclusion: VEGFA amplification in univariate analysis was associated with poor outcomes; this was particularly prominent in HER2+ or TNBCs. Additional studies are necessary to confirm the trend for poor OS seen on multivariate analysis for patients treated with bevacizumab. Clin Cancer Res; 19(5); 1281–9. ©2012 AACR.

Introduction

E2100 was a randomized, phase III trial in the first-line setting for patients with metastatic breast cancer (1). This trial showed a significant improvement in progression-free survival (PFS) for the addition of bevacizumab to paclitaxel when compared with paclitaxel alone. These data led to the accelerated approval by the U.S. Food and Drug Administration (FDA) for bevacizumab in this setting. Although subsequent first-line trials such as AVADO and RIBBON-1 also met their primary endpoints for showing significantly improved PFS, the absolute improvements in median PFS were much more modest than in the original E2100 trial, and none of the trials showed an improvement in overall survival (OS; refs. 2, 3). On the basis of these more modest benefits in combination with a unique toxicity profile, the U.S. FDA subsequently recommended rescinding approval for bevacizumab in this setting (4).
One major drawback for the clinical use of bevacizumab (as well as other anti-angiogenic therapies) is the lack of a validated biomarker to predict which patients might be expected to gain the most benefit (5, 6). Our group previously reported single-nucleotide polymorphisms (SNP) that predicted a genetic subgroup that derived substantial benefit in OS for those who received bevacizumab in E2100 (7). These SNPs have been tested in other settings and have been validated in some but not all studies (8–10). Somatic aberrancy also has great potential to serve as a prognostic or predictive marker (i.e., HER2 and trastuzumab). In this study, we set out to evaluate the role of VEGFA amplification as a biomarker for bevacizumab in E2100.

**Patients and Methods**

**Samples**

In the E2100 parent trial, there were 671 eligible patients with 641 disease progression events and 344 deaths as of May 1, 2009 (1). Patients were randomized to paclitaxel with bevacizumab (arm A) or paclitaxel alone (arm B). The results from the parent trial have previously been reported. Paraffin-embedded tumor blocks were available from 367 patients (1.80–2.20 for amplification and 0.70–0.90 for deletion) or a total of 60 nuclei were scored in samples at or near the cutoff (1.80–2.20 for amplification and 0.70–0.90 for deletion) or near the 1.5 ratio for borderline amplification. Reproducibility was tested in 17 samples with interobserver concordance 88.2%; these were re-scored by a second evaluator who counted nuclei from 3 more tumor areas until 60 red signals were counted. These nuclei were preferably scored in 3 distinct tumor areas and totaled. The signals were scored in nonoverlapping nuclei where bright and point-shaped signals of balanced size could be identified. Nuclei were scored until 60 red VEGFA signals were reached and then the green signals were scored in the same nuclei (22). A minimum of 6 nuclei were scored and a total of 60 nuclei were scored in samples at or near the cutoff (1.80–2.20 for amplification and 0.70–0.90 for deletion) or near the 1.5 ratio for borderline amplification. Reproducibility was tested in 17 samples with interobserver concordance 88.2%; these were re-scored by a second evaluator who counted nuclei from 3 more tumor areas until 60 red

**VEGFA FISH**

A VEGFA/centromere enumeration-6 (CEN-6) probe set was previously created and validated (20). The validation included a test of the DNA clones by restriction enzyme fragment measurements. The final product contained a bacterial artificial chromosome (BAC) probe, RP11-710-L16, covering 183 kb including the VEGFA gene and flanking regions with a start position of 43,633,251 and an end position of 43,817,196 according to UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly. Upstream the probe overlaps the entire MRPS18 gene (human mitochondrial ribosomal protein S18-2) and 20% of the RSPH9 gene; downstream there is overlap with approximately 67% of the AK097853 gene. The CEN-6 probe was labeled with fluorescein isothiocyanate (FITC)-labeled peptide nucleic acid (PNA) oligonucleotides and the VEGFA probe labeled with Texas Red. Both the VEGFA and CEN-6 probes were tested on metaphase spreads to localize the signals to chromosome 6 and exclude cross-hybridization to other chromosomes. The concentrations of Texas Red VEGFA and FITC CEN-6 were fine-tuned to give well-balanced red and green signals when hybridized on human breast cancer tissue. A tissue microarray with 93 human primary breast tumor core specimens was then evaluated by FISH for the presence of VEGFA gene amplification and deletion on formalin-fixed, paraffin-embedded tumors using a protocol similar to the manufacturer’s protocol for TOP2A FISH pharmDx Kit (21). Results were interpreted using a fluorescence microscope equipped with appropriate filters for the fluorophors.

Cancer cells were located and then scored for total number of VEGFA/CEN-6 signals. A ratio was calculated from the average number of signals for each probe. Normal cells in the analyzed tissue section served as an internal positive control of pretreatment and hybridization efficiency. On the basis of this validation array, a ratio <0.8 was considered deleted; a ratio ≥ 1.5 but <2 was considered borderline-amplified; and a ratio ≥ 2 was considered amplified.

All samples were scored by an experienced technologist using the TOP2A FISH scoring guidelines (21). The signals were preferably scored in 3 distinct tumor areas and totaled. The signals were scored in nonoverlapping nuclei where bright and point-shaped signals of balanced size could be identified. Nuclei were scored until 60 red VEGFA signals were reached and then the green signals were scored in the same nuclei (22). A minimum of 6 nuclei were scored and a total of 60 nuclei were scored in samples at or near the cutoff (1.80–2.20 for amplification and 0.70–0.90 for deletion) or near the 1.5 ratio for borderline amplification. Reproducibility was tested in 17 samples with interobserver concordance 88.2%; these were re-scored by a second evaluator who counted nuclei from 3 more tumor areas until 60 red
signals were reached. The final ratio for each specimen was based on all scoring.

Statistical design

Comparison of VEGFA amplification with PFS and OS. To optimize power, we combined those patients who had a tumor that was amplified and borderline-amplified (this group will be referred to as amp/BA). Those with amp/BA status were compared with all other groups (normal + deleted). We evaluated the PFS and OS for those with amp/BA status compared with those who did not in univariate analysis. Univariate analysis was conducted using log-rank test. We also conducted multivariate analysis with Cox proportional hazard model using significant covariates from backward elimination stepwise regression. VEGFA amplification tests were formally evaluated using Kaplan–Meier curves. These were also conducted on subgroups based on estrogen receptor/progesterone receptor (ER/PR) status and arm of study. A formal test for interaction between arm of study and amplification status was also conducted using the Cox regression model. Cox regression analyses and Kaplan–Meier curves were conducted in R. P < 5% was considered statistically significant.

Results

Performance and frequency of VEGFA gene amplification in E2100

Of the 367 cases available for assessment of amplification for VEGFA by FISH, 324 had successful hybridization (success rate: 88.3%). Twenty-one cases showed VEGFA amplification in E2100 comprising a total of 52 patients (16%) had amp/BA status. Amp/BA status was well-balanced across arms in E2100 comprising 15.3% and 16.8% in arms A and B, respectively. There was less amplification in those who had ER- and/or PR-positive tumors (12.4%, n = 26 of 210) than in those who were ER/PR-negative (23.0%, n = 23 of 100; P = 0.020 by Fisher exact test). E2100 was predominately designed for HER2-negative patients, and thus only 6 patients in this correlative study had HER2 amplification; however 50.0% (n = 3 of 6) of these patients showed VEGFA amp/BA.

Association of VEGFA amplification with efficacy

On univariate analysis in the entire study population including both treatment arms, patients with tumor VEGFA amp/BA had significantly worse median PFS (7.8 vs. 8.3 months; P = 0.040) and median OS (20.2 vs. 25.3 months; P = 0.013) than those whose tumors did not exhibit amplification (Fig. 1). Multivariate analysis was conducted and included covariates that significantly impacted PFS (arm of study, ER/PR status, use of hormonal therapy) and OS (ER/PR status and use of hormonal therapy). On multivariate analysis, amp/BA status had no statistically significant impact on PFS (P = 0.178) or OS (P = 0.08). Because hormonal sensitivity and the arm of study nullified the significant results seen on univariate analysis, further evaluation was conducted to see whether there was an interaction between arm of study, ER/PR status, and amplification status.

In addition to having a lower likelihood of having VEGFA amp/BA, those with ER- or PR-positive tumors did not experience inferior outcome (PFS; P = 0.418 and OS; P = 0.321) whether amplified or not (Fig. 2). Patients with HER2-positive tumors were not analyzed separately for association with outcome due to insufficient numbers but were combined with those with triple-negative breast cancers (TNBC) as prior data have shown higher expression of VEGFA in both subtypes than in those who have hormone receptor–positive tumors. When combining the subtypes that displayed a higher frequency of VEGFA amp/BA (HER2-positive and triple-negative populations), those with amp/BA had a trend for inferior PFS with the curves separating late (P = 0.092) and a statistically significantly inferior OS (P = 0.047; Fig. 2). The improvement in OS was no longer statistically significant when excluding those patients with HER2+ tumors (P = 0.143).

When considering treatment arm, patients in arm A (bevacizumab and paclitaxel) of E2100 had a statistically

### Table 1. Amplification by arm of trial and ER/PR/HER2 status

<table>
<thead>
<tr>
<th>Subgroup</th>
<th>n</th>
<th>Amplified + borderline-amplified, n (%)</th>
<th>Amplified (ratio &gt; 2)</th>
<th>Borderline-amplified (ratio 1.5 but &lt; 2)</th>
<th>Normal</th>
<th>Deleted (ratio &lt; 0.8)</th>
</tr>
</thead>
<tbody>
<tr>
<td>All patients</td>
<td>324</td>
<td>52 (16.0)</td>
<td>21</td>
<td>31</td>
<td>251</td>
<td>21</td>
</tr>
<tr>
<td>Arm A</td>
<td>157</td>
<td>24 (15.3)</td>
<td>6</td>
<td>18</td>
<td>120</td>
<td>13</td>
</tr>
<tr>
<td>Arm B</td>
<td>167</td>
<td>28 (16.8)</td>
<td>15</td>
<td>13</td>
<td>131</td>
<td>8</td>
</tr>
<tr>
<td>ER+ or PR+/HER2−</td>
<td>210</td>
<td>26 (12.4)</td>
<td>6</td>
<td>20</td>
<td>172</td>
<td>12</td>
</tr>
<tr>
<td>TNBC</td>
<td>100</td>
<td>23 (23.0)</td>
<td>13</td>
<td>10</td>
<td>69</td>
<td>8</td>
</tr>
<tr>
<td>HER2+</td>
<td>6</td>
<td>3 (50.0)</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>1</td>
</tr>
</tbody>
</table>

NOTE: Ratio = VEGFA/CEN-6 signal ratio; arm A = paclitaxel with bevacizumab; arm B = paclitaxel alone; TNBC = triple negative breast cancer.
significant inferior median PFS for those with amp/BA status (10.5 months) compared with those who do not (11.3 months; \( P = 0.010 \); Fig. 3). These patients also had inferior median OS for those with amp/BA status (21.0 months) than those without (25.6 months; \( P = 0.042 \)). Those in arm B (paclitaxel alone) did not have differential PFS (\( P = 0.676 \)) or OS (\( P = 0.123 \)) based on amplification status (Fig. 3). All patients in arm B, however, fared worse than those on arm A with a median PFS of 5.6 months and a median OS of 23.7 months.

As stated above, patients with amp/BA status do worse than those who do not have amp/BA status. When specifically considering those patients in this poor prognosis group (amp/BA), there is no difference in median PFS
(10.5 vs. 5.7 months; \(P = 0.438\)) or median OS (21.0 vs. 16.9 months; \(P = 0.973\)) for those receiving bevacizumab (arm A) compared with placebo (arm B) suggesting bevacizumab has no effect in this subgroup (Fig. 4). For those patients who are not amplified, however, there is a significant improvement in median PFS for those who received bevacizumab (arm A) compared with those who did not in arm B (11.3 vs. 5.5 months; \(P = 6.29 \times 10^{-5}\)). This improvement in PFS did not translate into an improvement in median OS (25.6 vs. 24.8 months; \(P = 0.472\)). When considering both the arm of study and amplification status simultaneously, those patients who did not have amp/BA status and who received bevacizumab had the best PFS (\(P = 8.55 \times 10^{-6}\); Fig. 5). There was no corresponding OS improvement, however, seen for those who were not amp/BA and received bevacizumab and paclitaxel (\(P = 0.136\)). A formal test for interaction between amplification and arm of the trial was not significant for PFS (\(P = 0.220\)) or OS (\(P = 0.690\)).

### Discussion

In E2100, paclitaxel and bevacizumab showed an improvement over paclitaxel alone in measurement of PFS but not median OS (21.0 vs. 16.9 months; \(P = 0.973\)) for those receiving bevacizumab (arm A) compared with placebo (arm B) suggesting bevacizumab has no effect in this subgroup (Fig. 4). For those patients who are not amplified, however, there is a significant improvement in median PFS for those who received bevacizumab (arm A) compared with those who did not in arm B (11.3 vs. 5.5 months; \(P = 6.29 \times 10^{-5}\)). This improvement in PFS did not translate into an improvement in median OS (25.6 vs. 24.8 months; \(P = 0.472\)). When considering both the arm of study and amplification status simultaneously, those patients who did not have amp/BA status and who received bevacizumab had the best PFS (\(P = 8.55 \times 10^{-6}\); Fig. 5). There was no corresponding OS improvement, however, seen for those who were not amp/BA and received bevacizumab and paclitaxel (\(P = 0.136\)). A formal test for interaction between amplification and arm of the trial was not significant for PFS (\(P = 0.220\)) or OS (\(P = 0.690\)).

Amplification of HER2 is a well-studied prognostic and predictive biomarker for patients with breast cancer and represents one of the gold standards of clinical applicability (12). Here, we tested for amplification of the target gene for bevacizumab, VEGFA, using FISH. The samples from E2100 were derived from paraffin-embedded tissue from the primary tumor. In this study, we show that testing archived
tumor blocks for VEGFA amplification by FISH is feasible. Previously, we showed that VEGF expression (determined by immunohistochemistry) did not correlate with outcome in E2100 (7). From a technical standpoint, amplification is easier to quantify than expression (7, 33). From a biologic standpoint, it is likely that genomic amplification is less dynamic over time in response to changes in the microenvironment than protein expression. For example, VEGFA expression is highly variable in response to hypoxia and thus may represent a less reliable surrogate to describe the potential range of VEGFA influence at various time points in the life of a metastatic tumor (34, 35). However, it is critical to remember that bevacizumab targets the VEGFA protein. The variable nature of protein expression is a problem
exacerbated in a metastatic trial (like E2100) where the primary tumor being assessed is often far removed in time from the initiation of treatment in the metastatic setting. This issue may also be relevant to the VEGFA gene but data are not available.

While the majority of tumors have similar HER2 amplification status when comparing the primary tumor with a metachronous metastasis, several studies have shown that a clinically relevant fraction (as high as 15%) does change (36–38). As all samples evaluated in this correlative study included the primary tumor, any biologic change that took place at the time of metastasis cannot be accounted for here. Another inherent limitation of this correlative study, like many others, is that samples are not available from all cases of the parent trial. This limits statistical power and can also introduce an unintended confounder if the subgroup evaluated does not reflect the characteristics of the population and outcome in the parent trial. This latter concern is somewhat dampened as this subgroup closely mirrors the parent trial in terms of important characteristics and outcome.

Amplification of the VEGFA gene has previously been shown to serve as a poor prognostic marker in patients with colorectal cancer and osteosarcoma (39, 40). As far as we are aware, the use for VEGFA amplification as a predictive biomarker for anti-VEGF therapy has not been previously reported in a phase III trial. In this correlative study from E2100, we show those patients with VEGFA amplification and borderline amplification (together as a group) do worse than those without amplification in univariate analysis and thus this may represent a prognostic marker as seen in other tumor types. The significant inferiority seen in those with amplification was no longer significant in multivariate analysis which included ER positivity as a significant variable. There appears, then, to be an important biologic interaction with VEGFA amplification and ER expression. Tumors that were hormone-sensitive were almost 2 times less likely than those who were ER-negative to have VEGFA amplification. ER-positive patients also had lower frequency of VEGFA amplification than HER2-positive patients, but the number in the latter subgroup was too small to formally compare. Higher VEGFA expression has previously been seen in HER2-positive and TNBCs than ER-positive tumors; further validating this biologic correlation (41–45).

In addition to lower frequency of VEGFA amplification, the implication of this amplification in the ER-positive subgroup appears to be different as well. In the ER-positive population, prognosis does not appear to be adversely impacted by amplification. Those with TNBCs or HER2 positivity, however, do appear to have outcome adversely impacted by amplification. While the effect of VEGFA amplification on HER2-positive tumors (as a unique group) was not evaluated here due to small numbers, the biology would suggest it to be a provocative area of future investigation.

In this study, those patients who had VEGFA amplification did worse in univariate analysis and appeared to have no incremental benefit from bevacizumab. While the pathophysiology is not elucidated, this may simply represent a scenario where the amplification “overwhelms” the ability to successfully block VEGFA. Conversely, a significant benefit for bevacizumab in PFS was maintained in those who did not have amplification. Similar to the results of the parent trial, this effect did not carry over to a benefit in OS. The test for interaction between treatment arm and amplification was not statistically significant and thus VEGFA amplification cannot be formally considered a predictive marker for bevacizumab based on these data. However, the difference in PFS was statistically and clinically substantial when comparing those who did not have amplification but did receive bevacizumab against those who were either amplified or did not receive the anti-VEGFA blockade. It does beg the question as to whether the PFS could have been more robust in other data sets (e.g., AVADO and RIBBON-1) if the subgroups with VEGFA amplification were excluded. Furthermore, would the enrichment of this population also translate into improved OS with greater numbers and more statistical power (e.g., the first-line meta-analysis) or does the biology of this drug dictate that an improvement in OS is simply not possible for this disease type and setting?

We have previously shown that host-derived genetic variation (i.e., SNPs) correlated with improved OS for patients who received bevacizumab in E2100 (7). In that study, 2 genotypes (VEGFA -2578AA and -1544A) had superior OS in the bevacizumab-containing arm. Combining germ line (SNPs) and somatic (tumor-specific) variability to create a predictive signature is a potentially complex approach but may be necessary to uncover the most accurate biomarker. Specifically, is there a genetic subgroup (based on SNPs) that is able to overcome the poor prognostic effect seen in those with VEGFA amplified tumors while receiving bevacizumab? Alternatively, are those who do not have tumor VEGFA amplification and who have the good SNP profile destined to experience a meaningful improvement in OS? Recently, a prospective trial has begun enrolment (the MERIDIAN trial) with the goal of prospectively evaluating outcome using a biomarker-guided approach with baseline plasma VEGFA levels. The result from this study may further inform biomarker-driven trials such as MERIDIAN. Furthermore, the interaction between the host (i.e., SNPs) and the tumor represents the entire picture of variability and this interaction warrants further evaluation in larger data sets.

Disclosure of Potential Conflicts of Interest

Authors' Contributions

Conception and design: B.P. Schneider, M. Radovich, G. Vance, L. Li, E.A. Perez, K.V. Nielsen, A. Thor, G.W. Sledge Jr, N.E. Davidson, S.S. Badve

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