Predictive Biomarkers to Anti-VEGF Therapy: Progress toward an Elusive Goal

Rekha Gyanchandani1 and Seungwon Kim1,2

The search for reliable biomarkers predictive of response to anti-VEGF therapy has been elusive. VEGF-A, the therapeutic target of bevacizumab, is an intuitive candidate as a predictive biomarker to bevacizumab-based anticancer therapy. However, there remains much controversy in the use of VEGF-A as a predictor of response to bevacizumab. Clin Cancer Res; 19(4); 755–7. ©2012 AACR.

In this issue of Clinical Cancer Research, Hegde and colleagues report the results of their study that sought to determine the predictive use of circulating VEGF-A in bevacizumab-containing therapy (1). The authors analyzed the plasma levels in more than 1,800 patients, who were enrolled in multiple phase III clinical trials of bevacizumab-containing regimens in patients with various cancer types, which were then correlated with clinical outcomes.

Angiogenesis is an essential component of carcinogenesis that is driven by multiple proangiogenic cytokines with the best-characterized proangiogenic cytokine being VEGF-A. Although multiple therapeutic approaches have been developed to inhibit VEGF-driven angiogenesis including small-molecule inhibitor of VEGF receptor (VEGFR) tyrosine kinases and therapeutic antibodies against the ligand-binding portions of VEGFR, bevacizumab (a monoclonal antibody to VEGF-A) has shown greatest success in clinical development (Fig. 1). Bevacizumab has been approved by the U.S. Food and Drug Administration (FDA) for use in non–small cell lung carcinoma (NSCLC), colorectal cancer (CRC), and renal cell carcinoma (RCC; refs. 2–4). However, the excitement that surrounded the early development of bevacizumab is unclear as bevacizumab binds both VEGF 165 and 185, and the mechanism behind the association between lower VEGF 165 and improved response to bevacizumab was incorporated into the standard chemotherapy regimen (5). However, PFS obtained in subsequent trials were less than that observed in the trials prior the FDA approval (6, 7). Moreover, significant rates of adverse effects were reported in these trials including a 1% mortality rate directly attributable to bevacizumab (6, 7). These factors led the FDA to ultimately rescind its approval of bevacizumab for use in breast cancer. Finally, the use of bevacizumab has resulted in increased PFS in many clinical trials but increases in overall survival (OS) have been difficult to obtain.

While it is true that the limitations of anti-VEGF therapy are becoming more evident as our experience with these agents increases, it is also undeniable that a subset of cancer patients treated with bevacizumab do show objective clinical responses and improved survival. However, we have yet to identify predictive biomarkers that have been validated in multiple, independent studies and can reliably distinguish patients who are likely to respond from those who will not. The identification of such biomarkers will be critical in harnessing the full potential of anti-VEGF therapy and in minimizing the rates of adverse side effects. The design and implementation of clinical trials based on proven, predictive biomarkers should allow for the enrichment of proper patient cohorts and facilitate the understanding of therapeutic mechanisms behind anti-VEGF therapy.

Several cytokines have been proposed in the literature as a possible predictive biomarker for anti-VEGF therapy. However, VEGF-A, the target of bevacizumab, is the most intuitive candidate as a predictive biomarker in the case of bevacizumab therapy. The correlation between pretreatment levels of VEGF-A and response to bevacizumab therapy has been examined previously in multiple studies (8–11). One study with a positive finding between circulating cytokine and response to bevacizumab was reported by Bates and colleagues (11). In this study, the authors found higher survival in patients with tumoral VEGF165/VEGFtotal ratio below the mean compared with patients with the ratio above the mean. VEGF165c, a C-terminal splice variant of VEGF, has been shown to have antiangiogenic properties in animal models. It binds VEGFR2 with equal affinity as VEGF165 but does not activate downstream signaling proteins. The mechanism behind the association between lower VEGF165, and improved response to bevacizumab is unclear as bevacizumab binds both VEGF165 and 185.
and VEGF165b with similar affinity. In contrast to the study by Bates and colleagues, most studies reported in the literature failed to show a correlation between either the tumor or plasma levels of VEGF-A and clinical outcomes. These studies were also not powered with enough sample size to allow for a robust biomarker analysis. Finally, the heterogeneity in methods used for measuring plasma and tumor VEGF-A levels also prevents meaningful comparison of the results from these studies.

In this issue of Clinical Cancer Research, Hegde and colleagues strive to overcome these limitations by analyzing, with uniform methods, the blood and tissue specimens from more than 1,800 patients with CRC, NSCLC, or RCC who were enrolled in 4 independent phase III trials of bevacizumab-containing regimens. Although the plasma samples were available for this study from only a subset of patients in each trial, the demographic, clinical, and pathologic characteristics of the sampled patient group did not differ significantly from the patient group without plasma availability. The plasma levels of VEGF-A were measured using ELISA, which recognized all major isoforms of VEGF-A including VEGF121, VEGF165, and VEGF110 with equivalent sensitivity. Consistent with multiple studies in the literature, the plasma levels of VEGF-A were found to be prognostic and correlated with OS, regardless of whether bevacizumab was part of the treatments, in all but one clinical trial. More importantly, the authors’ analysis did not reveal any statistically significant correlation between plasma VEGF-A levels and clinical response to bevacizumab including PFS and OS in any of the trials. Although this study is not without limitations, the data presented by the authors lends strong support to the hypothesis that VEGF-A does not have predictive values in patients undergoing bevacizumab treatment, at least for metastatic CRC, NSCLC, or RCC. One possible explanation for this lack of correlation is that bevacizumab may be able to efficiently sequester plasma VEGF-A after administration regardless of the pretreatment levels. We have previously examined the plasma levels of VEGF in patients with recurrent or metastatic head and neck cancer before and after administration of bevacizumab and have found more than 90% decrease in plasma VEGF-A in all patients regardless of the pretreatment levels (12). An interesting finding by Hegde and colleagues that lends another level of complexity is the lack of correlation between the tumor expression of VEGF-A as measured by immunohistochemistry and the plasma levels of VEGF-A as measured by ELISA. Clinical investigators often take it for granted that the tumor and plasma levels of a given cytokine will correlate with each other. However, the data according to Hegde and colleagues suggest that both the tumor and plasma levels of a given cytokine should be measured in order for biomarker analysis unless it is known which of the two types of expression reflects the true biologic potential of that cytokine.

It is clear that antiangiogenic therapy has become an important element in our armamentarium against cancer. Our next challenge is to refine the indications for antiangiogenic therapy by defining the necessary biomarkers for pretreatment patient selection, and the study by Hegde and colleagues is a step in the right direction. Finally, it should be kept in mind that the angiogenic potential of a given cytokine is not determined by a single cytokine but by the sum-effects of many pro- and antiangiogenic cytokines.

Therefore, it may be too simplistic to expect that a single cytokine will be predictive of response to bevacizumab therapy. It remains to be determined whether the response to bevacizumab can be predicted on the basis of a single cytokine or by the collective effects of several cytokines.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

Authors' Contribution
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References


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