Liver cancer has moved up the ranks from the third most common cause of cancer-related death to the second, with 0.8 million new patients annually and a 9.1% death rate worldwide, according to the recently released World Cancer Report 2014 (1). In North America, liver cancer has also shown increasing prevalence (2). Primary liver cancer includes hepatocellular carcinoma (HCC) and intrahepatic cholangiocarcinoma (ICC), with HCC responsible for 85% of cases worldwide, making it the major type of primary liver cancer (3). HCC treatment implementations vary and depend on cancer stages. For early-stage HCCs, surgical resection is the best choice with an overall survival rate as high as 90% with well-selected patients. However, for advanced-stage disease, options in hand are extremely limited, with sorafenib the only systemic medicine available.

Sorafenib, a small molecule, targets multiple kinases, including VEGFR, PDGFRβ, RAF1, and BRAF. Both in vivo and in vitro experiments have demonstrated its abilities to inhibit tumor-cell proliferation and tumor angiogenesis and to promote apoptosis (4). In 2005, the FDA approved sorafenib for treatment of advanced renal cell carcinoma, and 2 years later, it was approved for treatment of advanced-stage HCC. Unfortunately, sorafenib’s therapeutic effects fell short of expectations. Compared with the placebo group, the experimental group exhibited only 2.8 months longer median overall survival. In addition, severe side effects, including weight loss, hypophosphatemia, diarrhea, and hand-foot skin reaction, appeared more frequently in the sorafenib group (5). One possible reason for the mild effect of sorafenib is that some patients were not sensitive to sorafenib treatment, which implies that a more stringent patient selection procedure is urgently needed to benefit treatment. Indeed, some investigations have already been performed to this end. Although lowbaseline hepatocyte growth factor (HGF) and high-baseline soluble c-KIT concentration separately showed a favorable tendency to sorafenib treatment, neither of them approached statistical significance (6). Because sorafenib is used worldwide as standard care for patients with advanced-stage HCC and is the only systemic medicine to show beneficial effect, more effort is warranted to optimize patient selection. In this issue of Cancer Discovery, a collaborative report from the laboratories of Ben-Neriah and Pikarsky (7) identified a subtype of HCCs bearing VEGFA genomic amplification that was particularly sensitive to VEGFA inhibition. Moreover, patients with HCC with similar amplification respond favorably to sorafenib treatment.

Inflammation and microenvironmental changes are hallmarks of liver cancer. In HCCs, some factors affecting these two hallmarks may be amplified or deleted. To search for these factors, the authors applied array comparative genomic hybridization (aCGH) to HCC samples isolated from Mdr2−/− mice, an inflammation-driven HCC mouse model. They found that Chr17qB3 is present among these amplified regions. VEGFA, encoding an important cytokine regulating the microenvironment, is located in this region. More importantly, Horwitz and colleagues (7) found that VEGFA amplifications also occurred in 11% of human HCC samples. Unsurprisingly, elevated VEGFA protein levels were detected in both tumor extracts and serum samples. Subsequent experiments established that HCCs harboring genomic VEGFA amplification were indeed different from those without the amplification. These tumors exhibited higher proliferation index, vessel density, and macrophage content but a lower incidence of fibrosis. All these data indicated that the microenvironment of these tumors indeed changed in correlation with VEGFA amplification.

Because VEGFA cannot directly activate hepatocytes efficiently (8), the authors proposed a very interesting macrophage–tumor cell cross-talk model. In this model, VEGFA, secreted by tumor cells, stimulates macrophages to produce more HGF, which acts back on tumor cells and stimulates their proliferation. The data they presented strongly supported this hypothesis. They observed that tumor cells are the major cell type expressing VEGFA, whereas HGF is mainly...
expressed by macrophages. Aligning with these findings, they found that the expression levels of VEGFRs and coreceptors were higher in macrophages, whereas more HGF receptors were expressed in hepatocytes. Interestingly, VEGFA can increase cellular proliferation in vivo but not in vitro, which further proved that VEGFA was not directly affecting tumor cells but rather communication with macrophages.

As VEGFR is one of the targets of sorafenib, the authors tested whether this drug had a selective advantage in mouse tumors with VEGFA genomic amplification. Although they administered sorafenib to mice only for a short period of time, the results were inspiring. Only HCC with VEGFA genomic amplification responded to sorafenib treatment and showed decreased proliferation. This conclusion was confirmed by a Hep3B xenograft experiment. Moreover, the authors extended their investigation to human HCC patient samples. A retrospective study of a human cohort showed that a dramatic improvement was observed in the samples. A Hep3B xenograft experiment further proved that VEGFA was not directly affecting tumor cells but rather communication with macrophages.

At the end of 2013, sorafenib was approved by the FDA for advanced thyroid cancer, in addition to kidney cancer in 2005 and HCC in 2007. The NCI website shows that clinical trials of sorafenib for other cancers, including lung cancer, melanoma, and prostate cancer, are on the way. One can expect that the list of cancers that sorafenib can target will be extended in the future. However, considering the pain caused by its side effects and the economic burden of its cost, the selection of patients who are suitable for sorafenib therapy is becoming an even bigger challenge. Taken together, the identification of specific biomarkers that predict response to sorafenib treatment for advanced-stage cancers, as done by Horwitz and colleagues (7) in this study, is worthy of more resources and efforts. Finally, the surprising anti-oncogenic roles of pro-oncogenic molecules recently identified in animal HCC models call for the design of therapeutic strategies for patients with HCC by targeting secondary pathways activated in response to blockade of the primary oncogenic events (10).

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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VEGFA Genomic Amplification Tailors Treatment of HCCs with Sorafenib

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