Optimizing Anti-EGFR Therapy in Colorectal Cancer

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Treatment with anti-EGFR monoclonal antibodies has been successfully integrated in the continuum of care for metastatic colorectal cancer. The major challenge is the identification of patients who would benefit from treatment.

In this issue of Clinical Cancer Research, Peeters and colleagues report on clinical efficacy in a randomized phase III study of FOLFIRI plus panitumumab versus FOLFIRI as second-line treatment for metastatic colorectal cancer (1). Treatment of metastatic colorectal cancer has greatly improved in the past decade with the introduction of more effective antineoplastic drugs and with the development of a therapeutic strategy that includes several lines of non-cross-resistant drugs and the wider use of potentially curative surgery for liver and, in selected cases, for lung metastases. In this context, introduction of antiangiogenic drugs, including bevacizumab, aflibercept, ramucirumab, and regorafenib, and of anti-EGFR monoclonal antibodies, such as cetuximab and panitumumab, has given a relevant contribution to improve metastatic colorectal cancer patient prognosis (2).

Given the complex molecular heterogeneity of colorectal cancer, a major challenge is to identify valuable and reliable predictive biomarkers for appropriate patient selection to optimize treatment with molecular-targeted drugs. Hypothesis-generating predictive biomarkers are best developed prospectively as companion diagnostics in the drug development process, but they can also be developed retrospectively from prospectively randomized clinical trials data (prospective-retrospective analysis), if they follow a sound methodologic path. Mutations in oncogenes and tumor-suppressor genes can carry sensitivity (positive prediction of response) or resistance (negative prediction of response) depending on the gene and on the target. A subgroup of metastatic colorectal cancers is highly dependent on EGFR signaling, and the use of EGFR inhibitors has been demonstrated effective in early lines of treatment as well as in heavily pretreated chemotherapy-refractory colorectal cancer patients. In this latter case, approximately 10% of unselected patients respond to treatment with either cetuximab or panitumumab. The identification of activating KRAS exon 2 (codons 12 and 13) gene mutations has been the first clinically relevant step to identify those patients in which the RAS pathway is constitutively active to signal cell proliferation and survival in cancer cells and, therefore, EGFR inhibition is not effective (3). These mutations account for approximately 85% to 90% of RAS mutations in colorectal cancers. Subsequently, less frequent activating mutations in KRAS exons 3 and 4 and in NRAS exons 2, 3, and 4, which are present in approximately 15% to 20% of KRAS exon 2 wild-type tumors, have been identified as other biomarkers of intrinsic cancer cell resistance to cetuximab or to panitumumab, as it was for the first time found in the randomized phase III study of FOLFOX plus panitumumab versus FOLFOX alone (4). As a result, the European Medicines Agency has restricted the use of these drugs to metastatic colorectal cancer patients with KRAS and NRAS wild-type tumors, as recommended by all major international clinical guidelines.

Peeters and colleagues were able to retrospectively analyze 85% of tumor samples for extended KRAS and NRAS mutations. These mutations were found in approximately 18% of the original KRAS exon 2 wild-type patient population in agreement with previous reports of panitumumab or cetuximab with both FOLFIRI or FOLFOX combinations in first-line trials (4, 5). The results of the present study confirm the lack of efficacy of panitumumab plus FOLFIRI in patients with any RAS mutations and clearly show that an extended molecular selection is translated in a better clinical efficacy for patients whose tumors are RAS wild type. Therefore, this is another important experimental proof that the best tool we have for selecting patients to be treated with anti-EGFR monoclonal antibodies is to exclude from treatment patients with RAS mutations.

However, not all patients with RAS wild-type tumors will respond to treatment. In fact, is conceivable that only 50% to 65% of these patients have an EGFR-dependent cancer. How to better select patients in order to identify those that most likely will benefit from anti-EGFR therapy? First, other genes that could be responsible for resistance to cetuximab or panitumumab have been identified, although it is not clear if they are negative prognostic factors rather than true predictive biomarkers. This is the case of BRAF and of PIK3CA mutations. In the present study, there is no evidence of a predictive role of BRAF mutations, whereas PIK3CA mutations were too few for any analysis. The results of a large
References


