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Beyond KRAS: Predictive factors of the efficacy of anti-EGFR monoclonal antibodies in the treatment of metastatic colorectal cancer

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cancer. All most recent findings are described to offer a contribution to define a correct approach to anti-epidermal growth factor receptor based treatment.

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Abstract

Systematic analysis of the epidermal growth factor receptor (EGFR) pathway revealed that biomarkers could be used to predict the response to and outcome of anti-EGFR therapies in patients affected by metastatic colorectal cancer. We have conducted a review on the most recent findings and advances on this topic. To this aim, we searched the PubMed database for articles devoted to predictive and prognostic biomarkers for patients administered cetuximab- and panitumumab-based therapies. Here we review the state of the art and the controversies about the molecular factors known to be predictors of the efficacy of anti-EGFR therapy, namely, KRAS, BRAF, NRAS, PI3KCA and PTEN, and we discuss their prognostic value in colorectal cancer patients.

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Key words: KRAS; Anti-epidermal growth factor receptor; Metastatic colorectal cancer; Biomarkers

Core tip: This is a review underlining the importance of biomarkers in the treatment of metastatic colorectal

INTRODUCTION

Thanks to the advent of targeted therapies for colorectal cancer (CRC), it is now possible to assign, more accurately than hitherto, therapy according to specific molecular profiles within a distinct tumour and subsequently to personalize treatment. Although discoveries such as *KRAS* gene mutations were a breakthrough in targeted therapy for CRC patients, various factors must be clarified to maximize the efficacy of this strategy. In particular, studies are required to identify other intracellular anomalous pathways involved in CRC so that drugs targeting them may be developed in order to have the right drug for the right patient.

Colorectal cancer is the third most common neoplastic disease worldwide^[1]. It is one of the leading causes of cancer mortality, accounting for about 10% of all cancer deaths, with approximately 40%-50% of all cases diagnosed as metastatic^[2]. Advances in the treatment of metastatic CRC (mCRC) over the last 20 years have improved overall survival (OS) from a median of 10 mo to approximately 24 mo^[1]. Although CRC is considered curable if diagnosed at an early stage, 5-year survival is less than 10% in patients with unresectable metastatic

disease^[3,4]. About 40%-50% of CRC patients develop metastases during their clinical history, and 80%-90% of them have liver secondary lesions^[5].

Approximately 50% of mCRC patients present with a synchronous primary tumour and metastatic lesions, whereas the others develop metachronous relapses. Surgery is the only potentially curative therapy for mCRC. Resection of hepatic metastases results in 5-year survival rates ranging from 35% to 55%, although the outcome depends on tumour- and treatment-related variables such as number of lesions, the maximum diameter of lesions and resection margins^[6,7]. Similarly, 5-year survival rates after resection of lung metastases from CRC range from 20% to 60%^[8]. Chemotherapy is palliative in metastatic patients; although used as pre-operative conversion treatment it can be part of "curative" treatment^[9]. In fact, in patients with initially unresectable liver metastases, conversion chemotherapy enabled liver resection in up to one-third of cases, with survival rates similar to those of patients with initially resectable liver metastases^[10-12]. Unfortunately, most mCRC patients are not eligible for surgical resection and the only treatment option to prolong survival times is palliative chemotherapy.

For several decades, the mainstay of mCRC treatment was 5-fluorouracil (5-FU)/leucovorin (LV) chemotherapy which resulted in a median survival of about 11 mo^[13]. During the last 15 years, combination regimens with oxaliplatin or irinotecan added to 5-FU/LV have led to a considerable improvement of the outcome of patients with mCRC^[14,15]. Irrespective of the first-line chemotherapy regimen, an OS exceeding 2 years is currently achieved when patients receive all available active anti-CRC cytotoxic drugs^[16]. The introduction of the so-called targeted or biological drugs (namely, bevacizumab, cetuximab, panitumumab, aflibercept and regorafenib) has further improved the survival of mCRC patients. In contrast to standard drugs that target cell proliferation, targeted agents interfere with processes that control cell growth, survival, angiogenesis and spread. Because these compounds act on selective pathways, their efficacy is limited when treatment selection is driven by particular molecular profiles.

Most of the targeted inhibitors currently under development or in clinical use are molecules with high affinity for growth factor receptors, *i.e.*, the fibroblast growth factor receptor, vascular endothelial growth factor receptor, platelet-derived growth factor receptor, mast/stem cell growth factor receptor and epidermal growth factor receptor (EGFR). The addition of monoclonal antibodies (mAbs) that bind the vascular endothelial growth factor and the EGFR to chemotherapy regimens in mCRC has been shown to be effective, thereby increasing treatment options^[17,18].

It is now generally recognized that the large individual differences in treatment response among mCRC patients are due to the fact that tumours differ at the molecular level because of the unique genetic and environmental context of each specific patient. Therefore, it is essential

to understand these different molecular properties in order to optimize treatment. Personalized treatment is one of the most challenging aspects of medicine, particularly oncology. It is defined as treatment that is based on the patient's individual genetic features, and it improves cancer OS and it reduces detrimental side effects. Several prognostic and predictive biomarkers have been identified over the past decade and they can be used to personalize treatment for patients affected by mCRC. Prognostic biomarkers identify patients with different disease outcomes regardless of treatment, and may provide details about the disease prognosis/behaviour. Predictive biomarkers help to categorize patients who are most likely to benefit from a specific treatment and can guide or support therapeutic decisions^[19]. Thus, efforts have been made to identify tumour-related predictive factors that can suggest treatment response^[20]. Patient-related aspects, such as age, gender and presence of comorbidities, are candidate prognostic factors.

This review focuses on the advances made in the personalized treatment of mCRC and discusses the potential of new markers in selecting patients. The results obtained in clinical trials are analyzed, particularly in view of how these may influence routine clinical practice

FACTORS PREDICTIVE OF THE EFFICACY OF ANTI-EGFR TREATMENT IN MCRC PATIENTS

The Erb family of cell membrane receptors includes HER1/erbB1 (EGFR), HER2/c-neu (ErbB-2), HER3 (ErbB-3), and HER4 (ErbB-4)^[21]. Since the *EGFR* gene was identified as an oncogene, it has become one of the major targets of biologic therapeutics, and prompted the development of anti-EGFR mAbs and tyrosine kinase inhibitors (TKIs). The mAbs cetuximab (anti-IgG1) and panitumumab (anti-IgG2) act by binding to the extracellular ligand site of the receptor, whereas erlotinib and gefitinib, the two major EGFR TKIs, compete with the binding of ATP to the TK domain of the receptor, thereby resulting in inhibition of EGFR autophosphorylation. Both strategies (mAb and TKI) interrupt the intracellular downstream signalling cascade.

The first clinical trials with anti-EGFR mAbs enrolled patients whose tumours expressed high levels of EGFR; however overall response rates (ORRs) were low^[22], which suggested that other unidentified factors could affect response to these agents^[23]. Lièvre *et al*^[24] were the first to identify a link between KRAS mutations and lack of response to EGFR-targeted therapy. They analysed 30 patients receiving cetuximab plus irinotecan as second- or third-line treatment. *KRAS* mutations were observed in 13 of the 30 (43%) patients. None of the responders (0/11) presented *KRAS* mutations, whereas 68.4% (13/19) of non-responders did ($P = 0.0003$). The OS was significantly higher in *KRAS*-WT patients than in patients carrying a *KRAS* mutation (median OS: 16.3 mo

vs 6.9 mo, respectively, $P = 0.016$).

The next challenges were to understand why *KRAS*-mutated tumours do not respond to anti-EGFR mAbs, and to investigate if other components of the EGFR pathway could help to predict the effect of anti-EGFR therapies. In this context, studies focused on key signalling molecules downstream of the EGFR, including mutations in the *KRAS*, *NRAS*, *BRAF*, and *PIK3CA* genes, and PTEN protein expression. *KRAS* mutations result in constitutive activation of downstream EGFR signalling pathways thereby determining an unfavourable prognosis and a poor treatment response. Mutations in the *BRAF* gene, which encodes a serine/threonine kinase that activates the RAS-MAPK pathway, have been found in 4%-15% of CRCs^[25-27]. Cell lines harbouring *RAS/BRAF* mutations are more resistant to cetuximab *in vitro* compared with wild-type cells^[28]. The *PIK3CA* gene encodes the p110 α catalytic subunit of the phosphoinositide 3-kinase (PI3K) protein, which is a component of the PI3K-Akt signalling pathway downstream of ligand-induced EGFR activation. This catalytic subunit is activated consequent to its interaction with RAS proteins. *PIK3CA* mutations occur in 10%-18% of CRCs^[25,28,29]. Cell lines with activating *PIK3CA* mutations have been found to be resistant to cetuximab as compared with wild-type cell lines^[28]. However, two studies found a lack of correlation between mutational status and cetuximab response in patients with colon cancer^[24,30]. As *PIK3CA* mutations are rare, these data were based on only five patients, which could explain the lack of association between *PIK3CA* mutations and treatment response. The phosphatase and tensin homolog (PTEN) acts as a tumour suppressor protein by inhibiting the PI3K-Akt signalling pathway. Cell lines deficient in PTEN expression are more resistant to cetuximab *in vitro* than those with normal PTEN expression^[28]. The loss of PTEN protein expression is a negative predictive factor of the efficacy of cetuximab therapy in patients with mCRC^[31]. Subsequently, Sartore-Bianchi *et al.*^[32] devised the Quadruple Index, which is based on changes in the four above-mentioned factors. They found that 70% of tumours harboured at least one molecular alteration, and that the probability of treatment response was 51% among patients with no alterations, 4% among patients with 1 alteration, and 0% for patients with ≥ 2 alterations ($P < 0.0001$). Accordingly, PFS and OS decreased in the following order: patients with tumors harboring none, 1 or ≥ 2 molecular alterations ($P < 0.001$).

KRAS AS PREDICTIVE FACTOR

Within the EGFR/RAS/RAF/MEK/ERK kinase signalling pathway, the *KRAS* protein is a GTPase normally bound to the internal part of the cell wall. It serves as a molecular switch that transmits extracellular signals from the EGFR to the nucleus, thereby regulating cell growth, proliferation, and apoptosis. The *KRAS* gene is located on the short arm of chromosome 12 and belongs to the

Erb family of oncogenes. Patients with point mutations in the *KRAS* gene generally exhibit mutations within codon 12 at exon 2 (82%-87%), codon 13 (13%-18%), codon 61 (exon 3) and 146 (exon 4)^[33]. In patients carrying a wild-type *KRAS* gene copy, the binding of anti-EGFR antibodies to the external part of receptor induces conformational changes with its internalization and a sequential direct inhibition of TK activity, and blockage of downstream RAS/RAF/MEK/ERK pathway. *KRAS* mutations prevent the mAb-induced inhibition of EGFR activity because they induce constitutive activation of the intracellular domain of the *KRAS* protein. In CRC patients the incidence of *KRAS* mutations is about 30%-45%^[34]. *KRAS* mutational status can be evaluated on samples of either the primary tumour or the metastases because *KRAS* mutations are highly concordant (approximately 95%) in the two tissue samples^[35].

The proof of principle that patients carrying *KRAS* mutations do not benefit from treatment with either of the two anti-EGFR mAbs comes from two randomized clinical trials comparing panitumumab or cetuximab with best supportive care in heavily pretreated mCRC patients^[33,36]. In the CO.17^[36] and AMGEN^[33] studies, a survival benefit over best supportive care was observed only in *KRAS*-WT patients treated with cetuximab (median OS: 9.5 mo *vs* 4.8 mo) or panitumumab (median PFS: 12.3 wk *vs* 7.3 wk), respectively. In patients with *KRAS* mutated tumours mAbs did not prolong PFS or OS as compared with best supportive care. Furthermore, the efficacy of first-^[37-39] and second-line^[40,41] chemotherapy improved when it was combined with anti-EGFR antibodies in the mCRC setting.

The cetuximab combined with irinotecan in first-line therapy for metastatic colorectal cancer phase III study evaluated 599 patients receiving FOLFIRI with cetuximab and 599 patients receiving FOLFIRI alone^[37]. Sixty-four per cent of the cases evaluated were exon 2-*KRAS*-WT, and both the risk of disease progression (HR of PFS: 0.68, 95%CI: 0.50-0.94) and death (HR of OS: 0.84, 95%CI: 0.64-1.11) were lower in cetuximab-treated patients. No difference in PFS or OS was noted when cetuximab was added to FOLFIRI in *KRAS*-MUT patients.

The fluorouracil, leucovorin, oxaliplatin with and without cetuximab in the first-line treatment of metastatic colorectal cancer study also evaluated the effect of *KRAS* mutational status on clinical outcome of patients^[42]. This was a phase II study in which 169 mCRC patients were randomized to receive FOLFOX-4 plus cetuximab, and 168 to receive FOLFOX-4 alone. Patients with *KRAS*-WT tumours treated with cetuximab had a significant increase in tumour response rate (61% *vs* 37%, OR = 2.54, $P = 0.011$) and a decrease in the risk of disease progression (HR = 0.57, $P = 0.016$) compared with patients receiving FOLFOX-4 alone. In the *KRAS* mutant population, patients treated with FOLFOX-4 plus cetuximab had a median PFS lower than patients administered FOLFOX-4 alone (8.6 mo *vs* 5.5 mo, respectively)^[42].

Similarly, the addition of panitumumab to first-line chemotherapy with FOLFOX^[39,43] and to second-line chemotherapy with FOLFIRI^[41] significantly prolonged PFS and OS only in KRAS-WT mCRC patients.

KRAS AS PROGNOSTIC FACTOR

The role of KRAS as an independent prognostic marker in CRC is largely controversial. The CO.17 study^[36] analysed the prognostic implications of KRAS status by assessing the interaction between KRAS status and survival in patients receiving best supportive care alone. There was no significant difference in median OS in patients with the KRAS-WT or KRAS-MUT (4.8 mo *vs* 4.6 mo, respectively, the HR for death in the KRAS mutant population was 1.01, $P = 0.97$).

Similarly, Kim *et al*^[44] found that the response rate, PFS and OS did not differ between KRAS-WT and KRAS-MUT mCRC patients treated with chemotherapy alone. These findings suggested that KRAS is not a prognostic marker for CRC. In contrast, the results of a multivariate analysis of 89 mCRC patients treated with cetuximab after failure of irinotecan-based chemotherapy, suggested that KRAS mutational status is an independent prognostic factor in mCRC^[45]. KRAS-MUT patients had a lower relative risk (RR) (0% *vs* 40%, $P < 0.001$), and a shorter PFS (median PFS: 10.1 wk *vs* 31.4 wk, $P = 0.0001$) and OS (median OS: 10.1 mo *vs* 14.3 mo, $P = 0.026$) than KRAS-WT patients. However, interpretation of these data should be tempered by the fact that it is difficult to differentiate the effect of KRAS mutational status on survival from the response to treatment in a patient population treated with cetuximab^[46].

The RASCAL Collaborative Group evaluated thousands of patients with any-stage colorectal cancer to study the prognostic value of mutations in codons 12 and 13 of the KRAS gene^[47,48]. They found that KRAS-MUT patients had a higher risk of disease progression and death compared with patients not carrying KRAS mutations, particularly when valine codon 12 was involved^[47]. The RASCAL-2 study concluded that the G12V mutation in the KRAS gene at codon 12 increases the risks of recurrence or death only in Dukes' C colorectal tumours^[48].

The retrospective analysis of mCRC patients enrolled in the MRC FOCUS trial^[49] showed that KRAS mutations have a modest negative prognostic impact on OS (HR = 1.24, 95%CI: 1.06-1.46, $P = 0.008$) but not on PFS (HR, 1.14, 95%CI: 0.98-1.36, $P = 0.09$).

Contrasting results also emerged when the prognostic significance of KRAS mutations was evaluated in patients with non-metastatic colorectal cancer. In fact, in the retrospective analysis of more than 1050 stage II-III colon cancer patients enrolled in the PETACC-3 trial, KRAS mutations did not have any prognostic value regarding PFS or OS^[50]. The QUASAR trial randomized stage II-III colon and rectal cancer patients to receive adjuvant 5FU-FA or nothing. Overall, KRAS mutant patients had a higher rate of recurrence (28% *vs* 21%, $P = 0.002$), but

the difference was much more pronounced in a subgroup of rectal patients (43% *vs* 22%)^[51].

TYPE OF KRAS MUTATION AND RESPONSE TO ANTI-EGFR MABS

Exon-2 KRAS mutations are highly specific negative biomarkers of the efficacy of anti-EGFR mAbs in mCRC. However, not all KRAS mutations are equal in terms of effect on cell proliferation and resistance to anti-EGFR inhibitors^[52]. Preclinical data showed that cell lines with KRAS codon 13 glycine (G)-to-aspartate (D) mutations (p.G13D) respond to treatment with cetuximab similarly to WT clones^[53]. Moreover, it has been reported that about 10% of patients carrying a KRAS mutation in tumour tissue respond to anti-EGFR mAbs^[31,54,55] and a further 15% reach long-term disease stabilization^[56]. In patients responding or showing long-term stabilization, codon 13 mutations are more frequent than in the overall KRAS-mutated tumour population.

A recent large retrospective analysis of 579 chemorefractory mCRC patients treated with cetuximab demonstrated that not all KRAS mutations are equally effective in predicting resistance to anti-EGFR mAbs^[52]. Among patients receiving any cetuximab-based treatment, OS and PFS were significantly longer in patients bearing a p.G13D-mutation ($n = 32$) (median OS = 7.6 mo; median PFS = 4 mo) than in patients with other KRAS-mutated tumours (median OS = 5.7 mo; median PFS = 1.9 mo) in both univariate and multivariate analysis adjusted for potential prognostic factors and data set. Overall response rate did not differ significantly between patients with p.G13D mutations and other KRAS mutations (6.3% *vs* 1.6%, respectively, $P = 0.15$). There was a significant interaction between type of KRAS mutation (p.G13D *vs* other KRAS mutations) and OS benefit with cetuximab treatment (HR = 0.30, 95%CI: 0.14-0.67, $P = 0.003$).

The addition of cetuximab to first-line chemotherapy in patients with KRAS p.G13D mutations seemed to be beneficial in a pooled analysis of CRYSTAL and OPUS studies in which patients were randomized to receive FOLFIRI (CRYSTAL) or FOLFOX (OPUS) with or without cetuximab as first-line treatment for mCRC^[57]. Among the 83 patients harbouring the G13D mutation, those receiving chemotherapy plus cetuximab had a better PFS and OS than did patients treated with chemotherapy alone, whereas patients with any other KRAS mutation did not benefit from combination therapy.

Peters *et al*^[58] examined the role of mutations in codons 12 or 13 of the KRAS gene in a pooled analysis of patients enrolled in three clinical trials in which panitumumab was added to FOLFOX4 in first-line treatment^[59], to FOLFIRI in second-line treatment^[41], or compared with best supportive care in heavily pre-treated mCRC patients^[22]. They did not find that G13D mutation performs differently than codon 12 mutations, and thus concluded that codon 13 KRAS-MUT tumours are unlikely to benefit from panitumumab in the same way as

codon 12 KRAS-MUT tumours.

Two studies evaluated whether KRAS codon 61 and 146 mutations were associated with clinical outcome in mCRC patients treated with cetuximab^[60,61]. Loupakis *et al*^[60] found KRAS codon 61 and 146 mutations in 7 (8%) and 1 (1%) cases, respectively, among 87 patients with WT KRAS codons 12 and 13 treated with cetuximab plus irinotecan. None of the 8 patients with mutations in KRAS responded to the treatment, while 22 of the 68 WT cases (32.3%) did. KRAS 61 and 146 mutations caused a significantly shorter PFS (median PFS, 3.8 mo *vs* 5.1 mo, $P = 0.028$) as compared with KRAS 61/146 WT, whereas no significant differences were detected in OS (median OS, 9.7 mo *vs* 14.7 mo, respectively, $P = 0.39$). In the European Consortium study^[61], 40% of patients harboured a KRAS mutation, 2.1% (16/747) in codon 61, and 2% (15/747) in codon 146. Patients with codon 61 mutations had a lower RR than WT patients.

In conclusion, assessment of KRAS codon 61/146 mutations might help to identify mCRC patients who may benefit from treatment with anti-EGFR mAbs. In fact, the recently updated guidelines on for cetuximab and panitumumab usage include the analysis of KRAS exon 3 codon 61 and exon 4 codon 146 mutations (www.emea.com).

BRAF

The BRAF protein is a cytoplasmic serine-threonine kinase that is mutated in approximately 7% of human cancers: specifically, in 8%-10% of sporadic CRCs^[62]. The BRAF protein is one of the main effectors of KRAS, because it is immediately downstream of KRAS and it must be phosphorylated by KRAS to be activated. The point mutation V600E causes a classic CTG to CAG substitution at codon 600, which results in constitutive activation of the RAS/RAF/MEK/ERK pathway similar to KRAS mutations. KRAS and BRAF mutations are mutually exclusive in CRC^[62].

Di Nicolantonio *et al*^[62] performed a retrospective analysis of 113 tumour samples treated with cetuximab or panitumumab with or without chemotherapy. Seventy-nine patients with KRAS-WT were identified. In this cohort, 11 (13.9%) patients were BRAF mutants. None of them reported an objective tumour response.

In the CRYSTAL study^[37], 9% (59 of 625) of patients had BRAF mutations and they had a shorter median OS in both the FOLFIRI (10.3 mo) and FOLFIRI/cetuximab (14.1 mo) arms compared with the KRAS-WT/BRAF-WT population in which survival was 21.6 and 25.1 mo, respectively. BRAF-MUT status was unrelated to cetuximab efficacy; thus the authors concluded that BRAF mutation is an indicator of poor prognosis, and that it did not predict the efficacy of cetuximab in their dataset. Also in the combined analysis of the CRYSTAL and OPUS results^[63], BRAF mutation was found to be a negative prognostic marker. In fact, PFS and OS were lower in the BRAF-MUT population irrespective of

treatment received.

Similarly, in a Dutch retrospective analysis of BRAF status conducted in patients treated with capecitabine/oxaliplatin/bevacizumab with or without cetuximab for mCRC, 8.7% of tested samples (45 of 519) had the BRAF V600E mutation^[64,65]. Patients with BRAF mutations showed a shorter median PFS irrespective of treatment group. In a retrospective pooled study from the European Consortium that included 761 chemorefractory patients treated with cetuximab plus chemotherapy, De Roock *et al*^[61] reported a 4.7% rate of BRAF mutation (35 patients with V600E mutations and 1 patient with mutation D548Gn). Compared with BRAF-WT subjects, BRAF-MUT patients had a significantly lower ORR (8.3% *vs* 38% for WT, OR = 0.15, $P = 0.0012$), and a shorter PFS (median, 8 wk *vs* 26 wk in WT, HR = 3.74, $P < 0.0001$) and OS (median, 26 wk *vs* 54 wk in WT, HR = 3.03, $P < 0.0001$).

BRAF mutation was a negative prognostic factor also in the PRIME trial^[59]. In fact, patients with RAS-WT but BRAF-MUT tumours had a worse PFS and OS compared with subjects with both RAS and BRAF wild-type disease. In RAS-WT/BRAF-MUT subgroup, the addition of panitumumab to chemotherapy produced a small, statistically not significant benefit in term of DFS and OS ($P = 0.12$ and 0.76 , respectively)^[59].

The only trial to report that BRAF mutation plays both a prognostic and predictive role is the PICCOLO phase III trial^[66], which was designed to evaluate the addition of panitumumab to single-agent irinotecan as second- or subsequent-line therapy in 1198 prospectively tested KRAS WT mCRC patients. BRAF-MUT tumours (13.6%) showed a worse OS than BRAF-WT tumours, and the addition of panitumumab to irinotecan had a detrimental effect on survival (HR = 1.84, 95%CI: 1.10-3.08, $P = 0.029$).

In conclusion, BRAF mutation seems to be a negative prognostic factor rather than a negative predictive marker of the efficacy of anti-EGFR mAb. BRAF-MUT patients have a worse survival than BRAF-WT patients irrespective of treatment received. They may benefit from anti-EGFR mAb, but to a significantly lesser extent than BRAF-WT patients.

NEUROBLASTOMA-RAS

Neuroblastoma-ras (NRAS) is a member of the RAS oncogene family and is located on chromosome 1. The product of this gene is a GTPase enzyme membrane protein that shuttles between the Golgi apparatus and the cellular membrane. KRAS, BRAF and NRAS mutations are mutually exclusive^[67]. In CRC, the NRAS mutation rate is 3%-5%^[61]. NRAS mutations are associated with lack of response to treatment with cetuximab^[61]. In the study by De Roock *et al*^[61], NRAS-mutant patients treated with either cetuximab or panitumumab (2.6% of 644 KRAS-WT subjects) had a significantly lower ORR than NRAS-WT patients (7.7% *vs* 38.1%). Progression-free

survival and OS did not differ statistically between mutated and not mutated patients. In contrast, in the COIN trial^[68], which failed to demonstrate a survival benefit with the addition of cetuximab to first-line oxaliplatin-based chemotherapy in exon 2 *KRAS*-WT mCRC patients, no benefit in OS was obtained with the combination treatment, even in the subgroup of *KRAS*/*NRAS*/*BRAF*-WT subjects. The presence of any mutation in the *KRAS*, *NRAS* or *BRAF* genes negatively affected OS, regardless of treatment received.

A retrospective evaluation of biomarkers in patients enrolled in the PRIME trial indicated that *NRAS* plays an important role in predicting the efficacy of panitumumab. Among the 656 patients with *KRAS*-WT exon 2, 108 (17%) had other mutations in *KRAS* exon 3 or 4, in *NRAS* exons 2, 3 or 4, or in *BRAF* exon 15^[59]. Patients with *KRAS*-WT exon 2 tumours bearing any other *RAS* mutation did not benefit from the addition of panitumumab to FOLFOX (median OS 17.1 mo *vs* 17.1 mo, $P = 0.12$). In contrast, patients with “all *RAS*” wild-type tumours (namely, wild-type for *KRAS* exons 2/3/4 and for *NRAS* exons 2/3/4) significantly benefited from the combination treatment (median OS 25.8 mo *vs* 20.2 mo, HR = 0.77, 95%CI: 0.64-0.94, $P = 0.009$).

The FIRE-3 phase III trial (AIO KKR-0306), conducted at 150 German and Austrian cancer centres, involved a head-to-head comparison of FOLFIRI plus either cetuximab or bevacizumab as first-line treatment in patients with mCRC. Of the 752 patients enrolled, *KRAS* wild-type tumours were identified in 592 patients who were then randomized 1:1 to receive first-line FOLFIRI every two weeks plus either cetuximab at 400 mg/m² on day 1 followed by 250 mg/m² weekly (arm A) or bevacizumab at 5 mg/kg every 2 wk (arm B). The primary analysis showed a median OS almost 4 mo longer in arm A *vs* arm B. The results of a pre-planned analysis of the effect of *KRAS* mutations in exon 3 (codon 59/61) and exon 4 (codon 117/146), of *NRAS* mutations in exon 2 (codons 12/13), exon 3 (codons 59/61) and exon 4 (codons 117/146), and of the *BRAF* V600E mutation on treatment efficacy were presented at the 2013 ESMO Congress^[69]. Mutational analyses were done by pyrosequencing in 396 of 592 randomised patients (66.9%). Among patients with “all *RAS*” wild-type tumours, OS was significantly longer with FOLFIRI/cetuximab than with FOLFIRI/bevacizumab (33.1 mo *vs* 25.6 mo, $P = 0.01$). The OS HR for adding cetuximab *vs* bevacizumab in patients with all *RAS*-WT tumours was 0.70 ($P = 0.01$). Overall survival was the same, 20.6 mo *vs* 20.3 mo, respectively, in patients with mutated *RAS* treated with either cetuximab or bevacizumab. A similar trend was observed in the association between PFS and mutational status; PFS was slightly longer in patients with *RAS*-WT treated with FOLFIRI/cetuximab than in those treated with FOLFIRI/bevacizumab: 10.4 mo *vs* 10.2 mo ($P = 0.54$) respectively. The HR for PFS in *RAS*-WT patients was 0.93 ($P = 0.63$). In the presence of any *RAS* mutation, PFS was significantly longer in patients adminis-

tered bevacizumab therapy than in patients treated with cetuximab: 12.2 mo *vs* 6.1 mo ($P = 0.004$). These findings may impact on clinical decisions because *RAS* mutational analysis may identify the subgroup of patients who are more likely to benefit from first-line cetuximab with respect to bevacizumab.

PI3KCA

Activation of phosphatidylinositol 3-kinase (PI3K) caused by TK located at the cytoplasmic surface of the cell wall, results in the phosphorylation of PIP2 to phosphatidylinositol 3-kinase (PIP3). Phosphatidylinositol 3-kinase activates AKT, which in turn triggers downstream pathways thereby promoting cell survival and proliferation. The *PIK3CA* gene encodes the catalytic subunit for PI3K, and mutations within this gene result in aberrant AKT stimulation, which in turn promote the growth of various cancers^[70,71]. Although *PIK3CA* mutations account for 10%-20% of CRC tumours, their effect on patient outcome is not yet clear^[21,29,72].

Ogino *et al*^[72] examined the tumour tissue of 450 patients with resected stage I-III colon cancer from two independent prospective cohort studies and found that 82 patients (18%) had *PIK3CA* mutations in exons 9 and 20^[72]. They concluded that *PIK3CA* mutation increases cancer-specific mortality in patients with *KRAS*-WT tumours (HR = 3.80, 95%CI: 1.56-9.27), but seemed to have no significant effect on mortality in *KRAS*-MUT patients (HR = 1.25, 95%CI: 0.585-2.96). In contrast, in the metastatic setting, a *PIK3CA* mutation was identified in 17.7% (14/85) of cetuximab-treated mCRC patients, but ORR, time-to-progression and OS did not differ between mutated and non-mutated patients^[73]. Moreover, the *PIK3CA* mutation was unrelated to outcome in *KRAS*-WT tumours treated in the cetuximab arm of the CAIRO 2 study^[74]: 5-year survival was 90% in *PIK3CA*-WT and 82% in *PIK3CA* mutants (log-rank $P = 0.075$).

Two European groups published opposite results regarding the predictive role of *PIK3CA* mutations in anti-EGFR mAbs resistance. Sartore-Bianchi *et al*^[70] analysed exons 9 and 20 *PIK3CA* mutational status in 110 mCRC patients treated with cetuximab or panitumumab. Fifteen patients (13.6%) had *PIK3CA* mutations, and none of them responded to treatment with anti-EGFR mAbs ($P = 0.038$). The correlation between *PIK3CA* mutations and lack of response was even stronger in the *KRAS*-WT subgroup of patients ($P = 0.016$). The authors concluded that *PIK3CA* mutations could help to distinguish potential non-responders to anti-EGFR mAbs within the *KRAS*-WT subpopulation. On the other hand, in a similar study, Prenen *et al*^[71] analyzed *PIK3CA* mutations in 200 patients with chemorefractory mCRC, and did not find a link between *PIK3CA* and anti-EGFR mAb resistance. Thirteen percent (5/39) of their patients with *PIK3CA* mutations responded to cetuximab, and 11% (18/160) did not ($P = 0.78$). The data from the largest European analysis^[61] conducted so far (773 DNA samples

from patients treated with cetuximab from 11 centres) explained the discrepancies between the Sartore-Bianchi *et al*^[70] and Prenen *et al*^[71] studies. In these studies, 14.5% of samples harboured *PIK3CA* mutations and a lower response rate to cetuximab was associated with *PIK3CA* exon 20 mutations but not to those with mutations in exon 9^[61]. The Sartore-Bianchi *et al*^[70] cohort had more exon 20 mutations (73%) than exon 9 mutations (27%), whereas the Prenen *et al*^[71] cohort had the opposite - 13% and 78%, respectively^[75].

Based on these results, *PIK3CA* mutations, even though promising, need further prospective studies before they can be used in clinical practice.

PTEN

PTEN functions as a key tumour suppressor gene that is involved in the homeostatic maintenance of PI3K/AKT signalling. In wild type cells, signal transduction events deriving from EGFR activation and directed *via* PI3K are balanced by the presence of this negative regulatory molecule. Loss of PTEN function causes increased levels of phosphatidylinositol-3,4,5-triphosphate (PIP-3), the major substrate of PTEN, thereby resulting in persistent activation of PI3K effectors^[76,77]. PTEN activity can be altered by gene mutations (5%), allelic losses at chromosome 10q23 (23%), and epigenetic mechanisms such as hypermethylation of the PTEN promoter region (19.9% in CRC with MSI-H *vs* 2.2% in MSI-L)^[78]. Loss of PTEN protein expression evaluated by immunohistochemistry is present in between 20% and 40% of unselected CRC cases^[32]. Moreover, it is associated with *KRAS*, *BRAF* and *PIK3CA* mutations, and EGFR polysomy. Interestingly, while there is concordance of *KRAS* status in primary and distant tumours^[79,80], PTEN expression is concordant in the primary tumour and metastases only in 60% of cases^[35,79] because PTEN loss is more frequent in distant metastases than in the primary tumour. Preclinical analyses have also shown that PTEN loss provokes resistance to cetuximab-induced apoptosis in CRC cell lines^[28].

Frattini *et al*^[31] found that none of 11 patients expressing lower levels of PTEN responded to combination treatment with irinotecan and cetuximab, whereas 10 (63%) of 16 patients with intact PTEN protein expression had a partial response. Loupakis *et al*^[35] recently reported that low expression of PTEN as measured by immunohistochemistry in the primary tumour did not affect response rate, PFS or OAS of mCRC patients treated with cetuximab plus irinotecan. By contrast, when PTEN was measured in the metastatic samples, ORR and PFS were significantly better in patients with high PTEN expression than in those with low PTEN expression: 26% *vs* 5% ($P = 0.007$) and 4.7 mo *vs* 3.3 mo ($P = 0.005$), respectively. Sartore-Bianchi *et al*^[70] found that loss of PTEN was related to lack of response to cetuximab and panitumumab ($P = 0.001$), and to a shorter PFS and worse OS in 81 tumour specimens of mCRC. Differently, Laurent-Puig *et al*^[81] showed PTEN protein expression

did not affect ORR or PFS in 162 *KRAS*-WT mCRC patients treated with cetuximab, but PTEN loss was associated with a shorter OS ($P = 0.013$). The reasons for these discrepancies are not clear. It is difficult to interpret these data because of the small sample size, the presence of *KRAS* mutant tumours and the fact that PTEN expression was evaluated in primary tumours and/or in metastatic sites. Moreover, evaluation of PTEN protein expression by immunohistochemistry or other methods (*i.e.*, western blot) is influenced by the subjective parameter of the interpreter in the definition of cut-off levels. Therefore, these data should be considered exploratory and the value of PTEN as a predictive or prognostic marker in CRC cannot yet be established.

CHEMOTHERAPY BACKBONE FOR ANTI-EGFR MABS

The choice of chemotherapy backbone may influence the efficacy of EGFR-targeted mAbs. The COIN study^[68] investigated the use of cetuximab in addition to oxaliplatin-based chemotherapy (66.1% with capecitabine and 33.9% with infusional 5FU) in the first-line setting for mCRC. Surprisingly, the addition of cetuximab to oxaliplatin-based chemotherapy did not increase OS or PFS compared with chemotherapy alone, even in the *KRAS*-WT subpopulation.

The CRYSTAL^[37] and OPUS^[42] studies, that demonstrated benefit from the addition of cetuximab to chemotherapy, both used infusional 5-FU regimens (FOLFIRI and FOLFOX, respectively). Similarly, in the COIN trial, the subgroup of patients treated with infusional 5FU benefited from cetuximab treatment (OS: HR = 0.72, 95%CI: 0.53-0.98), whereas those treated with capecitabine did not (OS: HR = 1.02, 95%CI: 0.82-1.26), although the formal test for interaction was not significant ($P = 0.10$)^[68]. The NORDIC VII^[82] trial also reported that no benefits came from adding cetuximab to oxaliplatin-based regimen (with bolus 5FU). The use of oral and bolus administration of fluoropyrimidines in COIN and NORDIC VII studies (instead of an infusional regimen) may explain the lack of benefit in survival. However, this hypothesis seems to be confuted by the FUTURE randomised phase II study, which compared cetuximab plus oxaliplatin + UFT (oral fluoropyrimidine) with cetuximab plus FOLFOX4 (infusional fluoropyrimidine) as first-line treatment for mCRC patients. In fact, in the *KRAS*-WT population, median PFS and OS were very similar (PFS: 9.2 mo *vs* 6.8 mo, $P = 0.18$; OS: 20.8 mo *vs* 20.1 mo, $P = 0.74$) in the two arms using oral or infusional fluoropyrimidine^[83].

Although the results of COIN and NORDIC VII studies seem to cast doubts on the efficacy of the oxaliplatin + cetuximab combination, significant benefits in survival from the addition of anti-EGFR mAbs to FOLFOX4 were reported in the PRIME^[39] and OPUS^[84] trials. Moreover, in the randomised phase II AIO 0104^[85] and CELIM^[86] trials, which used oral and infusional fluoro-

Table 1 New approach integrates novel molecular biomarkers with the pathologic features

Biomarker	Incidence	Prognostic value	Predictive value
B-RAF mutations	4%-15%	Poor prognosis ^[38,49,62,64,66,68,72,74,83]	Controversial data
K-RAS mutations	40%	Controversial data ^[36,65,68,72,86]	Major predictor of resistance to anti-EGFR mAbs ^[24,37,39,56,61]
Mut G13D	15%-20%		Weaker resistance ^[52]
N-RAS mutations	3%-5%		Predictor of resistance ^[59,69]
PI3KCA mutations	10%-20%	Conflicting results ^[28,30,61,65,70,71,73]	Controversial data ^[61,70,71,73]
PTEN status	20%-40%	Conflicting results ^[31,32,35,81,87]	Controversial data ^[51,70]

pyrimidines, respectively, the activity of cetuximab was similar in oxaliplatin- and irinotecan-containing regimens.

Lastly, it is now clear that cetuximab or panitumumab should not be added to an oxaliplatin-based chemotherapy regimen in patients with any mutation in exon 2/3/4 *KRAS* or *NRAS* genes or in patients with unknown mutational status, because it exerts a detrimental effect on survival (EMA protocol number 000741-II/50, 25 July 2013; EMA protocol number 702774/2013, 21 November 2013).

CONCLUSION

Before the era of personalised medicine, cancer prognosis and treatment decisions were made mainly based on the histopathologic characteristics of the tumour. The new approach integrates novel molecular biomarkers with the pathologic features of a tumour to improve the prediction of prognosis and treatment efficacy (Table 1). During recent years, attempts have been made to understand the molecular mechanisms underlying resistance to EGFR inhibitors to refine the selection of candidates for these treatments, and improve the clinical outcome of patients treated with anti-EGFR mAbs. Encouraging progress has been made in our understanding the behaviour of mCRC at molecular level, which led to the discovery of other biomarkers of resistance to anti-EGFR mAbs besides *KRAS*. The development of new technologies, such as next-generation sequencing, will enable the simultaneous analysis of many genes, and lead to the identification and validation of predictive biomarkers for existing and new target therapies. Translating discoveries from bench to clinical practice is a costly and time-consuming process, but the benefits of personalised medicine justify this effort.

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