Emergence of Multiple EGFR Extracellular Mutations during Cetuximab Treatment in Colorectal Cancer

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Abstract

Purpose: Patients with colorectal cancer who respond to the anti-EGFR antibody cetuximab often develop resistance within several months of initiating therapy. To design new lines of treatment, the molecular landscape of resistant tumors must be ascertained. We investigated the role of mutations in the EGFR signaling axis on the acquisition of resistance to cetuximab in patients and cellular models.

Experimental Design: Tissue samples were obtained from 37 patients with colorectal cancer who became refractory to cetuximab. Colorectal cancer cells sensitive to cetuximab were treated until resistant derivatives emerged. Mutational profiling of biopsies and cell lines was performed. Structural modeling and functional analyses were performed to causally associate the alleles to resistance.

Results: The genetic profile of tumor specimens obtained after cetuximab treatment revealed the emergence of a complex pattern of mutations in EGFR, KRAS, NRAS, BRAF, and PIK3CA genes, including two novel EGFR ectodomain mutations (R451C and K467T). Mutational profiling of cetuximab-resistant cells recapitulated the molecular landscape observed in clinical samples and revealed three additional EGFR alleles: S464L, G465R, and I491M. Structurally, these mutations are located in the cetuximab-binding region, except for the R451C mutant. Functionally, EGFR ectodomain mutations prevent binding to cetuximab but a subset is permissive for interaction with panitumumab.

Conclusions: Colorectal tumors evade EGFR blockade by constitutive activation of downstream signaling effectors and through mutations affecting receptor–antibody binding. Both mechanisms of resistance may occur concomitantly. Our data have implications for designing additional lines of therapy for patients with colorectal cancer who relapse upon treatment with anti-EGFR antibodies. Clin Cancer Res; 21(9); 2157–66. ©2015 AACR.
Mutational analysis in tissue samples

DNA extraction from tumoral samples was performed as previously described (12). Mutational analysis of KRAS (exons 2, 3, and 4), BRAF (exon 15), NRAS (exons 2 and 3), PIK3CA (exons 9 and 20), and EGFR (exon 12) was performed by Sanger sequencing using BigDye v3.1 (Applied Biosystems) following manufacturer’s instructions and analyzed on a 3500Dx Genetic Analyzer (Applied Biosystems). KRAS (exons 3 and 4) and NRAS (exons 2, 3, and 4) were also analyzed by pyrosequencing (Qiagen) and KRAS (exon 2) was also assessed by Therascreen real-time PCR (Qiagen) following the manufacturer’s instructions. All cases were also screened by pyrosequencing using a next generation sequencing (NGS) 454 GS Junior platform (Roche Applied Science). Processed and quality-filtered reads were analyzed using the GS Amplicon Variant Analyzer software version 2.5p1 (Roche). Mutations detected by NGS were confirmed by competitive allele-specific TaqMan PCR (CAST-PCR, Applied Biosystems) when specific assays were available.

Cell culture and generation of resistant cells

DiFi cells were cultured in F12 medium (Invitrogen) supplemented with 5% FBS; OXCO-2 cells were cultured in Iscove medium (Invitrogen) supplemented with 5% FBS; LIM1215 cells were cultured in RPMI1640 medium (Invitrogen) supplemented with 5% FBS and insulin (1 μg/ml); NCHi508 cells were cultured in RPMI1640 medium (Invitrogen) supplemented with 5% FBS; HCA-46 cells were cultured in DMEM (Invitrogen) supplemented with 5% FBS and CCK81 cells were cultured in MEM (Invitrogen) supplemented with 5% FBS. All media also contained 2 mmol/L L-glutamine and antibiotics (100 U/mL penicillin and 100 mg/mL streptomycin), and cells were grown in a 37°C and 5% CO2 air incubator. The DiFi and OXCO-2 cell lines were a kind gift from Dr. J. Baselga in November 2004 (Oncology Department of Vall d’Hebron University Hospital, Barcelona, Spain) and Dr V. Cerundolo in March 2010 (Weatherall Institute of Molecular Medicine, University of Oxford, Oxford, United Kingdom), respectively. The LIM1215 parental cell line has been described previously (18) and was obtained from Prof. Robert Whitehead (Vanderbilt University, Nashville, TN) with permission from the Ludwig Institute for Cancer Research (Zurich, Switzerland). The NCHi508 cell line was purchased from ATCC (LGC Standards S.r.l). HCA-46 cell lines were obtained from European Collection of Animal Cell Cultures (distributed by Sigma-Aldrich Srl). CCK81 cell line was obtained from Health Science Research Resources Bank. The identity of each cell line was tested and authenticated by Cell ID System and by Gene Print 10 System (Promega), through short tandem repeats (STR) at 10 different loci (D5S818, D13S317, D7S820, D16S539, D21S11, vWA, TH01, TPOX, CSF1PO, and amelogenin). Amplicons from multiplex PCRs were separated by capillary electrophoresis (3730 DNA Analyzer, Applied Biosystems) and analyzed using GeneMapperID software from Life Technologies. Resulting cell line STR profiles were cross-compared and matched with the available STR from ATCC, ECACC, and CellBank Australia repositories online databases. All cell lines were tested and resulted negative for mycoplasma contamination with Venor GeM Classic Kit (Minerva Biolabs).

Generation of resistant cells utilized in this article has already been previously described (6, 9). CCK81 cetuximab-resistant derivatives were obtained by increasing the cetuximab dosage stepwise from 680 nmol/L to 1.4 μmol/L during the course of 6 months.
Mutational analysis in cell lines
Genomic DNA samples were extracted by Wizard SV Genomic DNA Purification System (Promega). For Sanger sequencing, all samples were subjected to automated sequencing by ABI PRISM 3730 (Applied Biosystems). Primer sequences are listed elsewhere (6, 9). The following genes and exons were analyzed: KRAS (exons 2, 3, and 4), NRAS (exons 2 and 3), PIK3CA (exons 9 and 20), BRAF (exon 15), EGF (exon 12). All mutations were confirmed twice, starting from independent PCR reactions.

Drug assays
Cetuximab was obtained from the Pharmacy at Niguarda Ca’ Granda Hospital, Milan, Italy. Cell lines were seeded in 100 μL medium at the following densities (2 × 10^3 for DfiR, 1.5 × 10^3 for LIM1215, HCA-46, NCIE508, and OXCO-2, 3 × 10^3 for CCR81) in 96-well culture plates. After serial dilutions, cetuximab in serum-free medium was added to cells, and medium-only wells were included as controls. Plates were incubated at 37°C in 5% CO2 for 6 days, after which cell viability was assessed by ATP content using the CellTiter-Glo Luminescent Assay (Promega).

DNA constructs and mutagenesis
The pLX301-EGFR WT construct was a generous gift from Dr. C. Sun and Prof R. Bernards (NKI, Amsterdam, the Netherlands). EGF mutants containing the 6 point mutations (R451C, S464I, G465R, K467T, I491M, and S492R) were constructed using the QuikChange II site-directed mutagenesis kits from Agilent Technologies with pLX301-EGFR WT plasmid as the template DNA. The presence of mutations was confirmed by DNA sequencing. The system was parameterized using the Amber12 force field (20).

Molecular simulations
Input coordinates for the structure of cetuximab bound to wild-type EGFR (extracellular part) were taken from PDB:1YY9 (19). The system was parameterized using the Amber12 force field (20) and solvated and neutralized in a TIP3P water box. Molecular dynamics was extended for 100 ps of energy minimization was conducted under NPT conditions at 1 atm, 300K, and a cutoff of 9 Å, with rigid bonds and PME for long-range electrostatics. Potential energy minimization was run for 2 ps. During minimization, the heavy protein atoms were not restrained. The simulation was run using ACEMD (21) on a local Graphics Processing Unit (GPU)-equipped workstation.

Flow cytometry
To measure cetuximab and panitumumab binding to cells expressing mutant EGFR, we harvested by trypsinization and washed the cells twice with PBS. We incubated the cells with Fc blocking solution for 15 minutes on ice to block nonspecific Fc binding of immunoglobulins. We then washed the cells and incubated them with the monoclonal antibodies for EGFR binding during 30 minutes on ice. To visualize the primary antibody a goat anti-human IgG phycoerythrin-conjugated (Invitrogen) was used as a secondary antibody. EGFR binding was analyzed using the FACScan flow Cytometer.

Protein detection
We subjected total cell lysates to Western blot analysis as previously reported (12). The phospho-EGFR antibody (Y1068) was purchased from Cell Signaling Technology.

Results
Emergence of EGFR ectodomain mutations in patients treated with cetuximab
Thirty-seven consecutive patients with mCRC who had acquired resistance to cetuximab after an initial response to the treatment and had good quality paired pre- and posttreatment specimens were included in this study. Tumor biopsy obtained during the regular diagnosis procedure was used as the pretreatment sample. In most cases, this sample was obtained from the primary tumor during routine colonoscopy. Biopsies at progression were taken from liver (21 samples), lung (6), bone (2), peritoneum (3), colon-rectum (3), retroperitoneal lymph node (1), and subcutaneous node (1) with ultrasound guidance, CT scan guidance, or colonoscopy in the case of colon-rectum lesions. There were no major biopsy-related complications. Clinical characteristics of the patients are showed in Supplementary Table S1. All pretreatment biopsies were screened for mutations in KRAS, NRAS, and BRAF by Sanger and pyrosequencing as part of routine clinical practice at Hospital del Mar (Barcelona, Spain). Mutations in PIK3CA and EGFR were also assessed as part of this study. All pretreatment biopsies were wild-type except for three samples that harbored mutations in PIK3CA. As PIK3CA mutations do not preclude response to anti-EGFR therapy, these patients were treated with cetuximab-based regimens. Posttreatment tissue samples were analyzed for the same mutations using the same sequencing platforms. In total, we detected the emergence of 31 mutations in posttreatment biopsies from 20 patients (Table 1). The additional 17 posttreatment samples did not reveal variants in any of the genes we analyzed. In 7 cases, mutations in different genes were detected in the same tissue sample (median of detected mutations within the same specimen 2, range 1–5; Table 1).

Acquired mutations were found in NRAS (9 events) and KRAS genes (8 events) followed by mutations in PIK3CA (6 events) and BRAF (3 events). Interestingly, mutations in RAS frequently occurred in exons 3–4 (67% of NRAS and 50% of KRAS, with a cutoff of 9 Å, with rigid bonds and PME for long-range electrostatics. Potential energy minimization was run for 2 ps. During minimization, the heavy protein atoms were not restrained. The simulation was run using ACEMD (21) on a local Graphics Processing Unit (GPU)-equipped workstation.
NOTE: KRAS, NRAS, BRAF, PIK3CA, and EGFR mutations were analyzed in paired tissue samples obtained at diagnosis (pre-treatment) and at progression (post-treatment). Black boxes indicate the presence of mutations detected by clinical routine sequencing procedures.

Table 1. EGFR pathway mutations in tissue samples from patients with mCRC treated with cetuximab

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EGFR ectodomain mutations and acquired resistance to cetuximab in colorectal cancer cell models

We previously reported that acquisition of resistance in colorectal cancer cells is associated with emergence of KRAS, BRAF, and NRAS-activating mutations (6, 9, 12). To discover additional mechanisms of resistance to EGFR blockade, we exploited 5 colorectal cancer cell lines (DiFi, LIM1215, HCA-46, NCIH508, OXCO-2, and CCK81), which are highly sensitive to cetuximab (Supplementary Fig. S2). These cell lines are wild-type for KRAS, NRAS, and PIK3CA with the exception of NCIH508, which displays the p.E545K PIK3CA mutation. Altogether, these cell models recapitulate the molecular features of tumors from patients with colorectal cancer likely to respond to anti-EGFR therapies. For each line, at least five million cells were exposed continuously to cetuximab until resistant populations emerged (Supplementary Fig. S2). To define molecular mechanisms underlying acquisition of resistance, we initially performed Sanger sequencing of genes involved in regulation of the EGFR signaling pathway (EGFR, KRAS, BRAF, NRAS, and PIK3CA). In accordance with our previous reports, resistant populations often displayed KRAS, BRAF, and NRAS mutations (Table 2; ref. 9). All of these alleles were detected in the resistant cells but not in the corresponding parental population from which they originated. Importantly, in several occasions multiple genetic alterations were concomitantly present in the resistant cell population (Table 2) indicating their polyclonal status. To assess the molecular features of individual clones, we performed limited cell dilutions of LIM1215 and CCK81 as these cell lines are amenable to this procedure. We then subjected single clones to Sanger sequencing for candidate genes (EGFR, KRAS, BRAF, NRAS, and PIK3CA). Notably, mutation profiling of clones identified three novel EGFR variants: S464L, G465R, and I491M (Supplementary Fig. S3). Considering that the resistant derivatives are polyclonal, and in light of the limited sensitivity of the Sanger sequencing method, we postulated that variants present in less than 20% of the cell populations might have remained undetected. To identify mutations present at low frequency, we employed ddPCR, which is known to have a mutant/wild-type sensitivity of 1:20,000. ddPCR probes were designed and individually validated using control mutant DNA to detect EGFR variants previously identified in tumor biopsy or cell lines (Supplementary Table S2). This analysis...
unveiled the presence of 3 new EGFR variants (S464L, G465R, and I491M) that were not detected by Sanger sequencing in resistant cell populations (Table 2 and Supplementary Table S3). The ddPCR approach could not be performed in tissue samples, as there was no sufficient material available. Overall, the mutational landscape of cell lines with acquired resistance to cetuximab recapitulates the molecular profiles of tumors that relapsed upon cetuximab treatment.

**Structural model analysis of EGFR ectodomain mutations**

To understand how the EGFR ectodomain mutations detected in tumor samples and cell lines could drive resistance to EGFR blockade, we performed computational structure-based analyses. With the exception of R451C, the EGFR mutations are located in the receptor region, which has been shown to interact with cetuximab, thus providing functional characterization successfully minimizes to a C451-C475 disulfide bond. Indeed, a system setup in this configuration successfully minimizes to a C451-C475 disulfide bond. We verified that the distance in the crystal structure between these residues (C451-C475, carbon alpha distance 6.8 Å) is compatible with the formation of a disulfide bond. Indeed, a system setup in this new configuration successfully minimizes to a C451-C475 distance of 5.2 Å. Overall, all identified mutations in EGFR (except R451C) were located in the cetuximab-binding epitope.

**Biochemical and functional analyses of EGFR ectodomain mutations**

To experimentally assess the impact of the EGFR ectodomain mutations on the ability of the receptor to interact with cetuximab, we performed forward genetic experiments on the newly discovered mutations. Wild-type and mutant EGFR cDNAs were ectopically expressed in NIH 3T3 cells that lack endogenous EGFR. Flow cytometry was used to establish the extent of cetuximab binding to cells expressing the mutants; wild-type EGFR and S492R served as positive and negative controls, respectively. These experiments clearly showed that the newly discovered EGFR K467T, R451C, S464L, G465R, and I491M mutations were not permissive for binding to cetuximab thus providing functional...
evidence of their role in driving acquired resistance to EGFR blockade. Of note, the effect of EGFR R451C on cetuximab binding was less prominent compared with the other mutants (Fig. 2).

To further characterize the functional properties of the EGFR mutations we performed biochemical studies in cells expressing individual mutations. As expected, cetuximab abrogated ligand-mediated activation of the wild-type receptor, while had no or very limited impact in cells carrying mutated EGFR (S464L, G465R, K467T, I491M, and S492R; Fig. 3). Notably, in R451C-mutant cells, cetuximab was still capable of inhibiting EGFR phosphorylation (Fig. 3).

We then examined whether panitumumab, the other anti-EGFR drug approved to treat colorectal cancer, was active in cells overexpressing EGFR mutations. As previously described, S492R-mutant cells efficiently bound to panitumumab (12). We found that the K467T and R451C mutants were to some extent permissive for panitumumab binding, whereas S464L, G465R, and I491M mutants did not bind to this antibody (Fig. 2). Accordingly, biochemical analyses showed that panitumumab prevents EGFR activation in S492R, K467T, and R451C mutants (Fig. 3).

Discussion

We present a comprehensive analysis of mutational changes affecting key members of the EGFR signaling pathway emerging in tumor biopsies of patients treated with cetuximab and in cell models, which acquired resistance to cetuximab in vitro. We found that colorectal cancer cells evade EGFR blockade through two main strategies. The main mechanism of resistance involves downstream pathway reactivation that occurs in 43% of patients' samples and 58.8% of the cells, respectively. The second entails EGFR extracellular domain mutations that were detected in 10.8% of patients' samples and 29% of the cells. Although the specific mutations partially differ among cell lines and patients, they overlap in terms of activated cellular pathways observed in preclinical models and patients samples (22). The cell-based findings may be translated back into the clinic. For example, the EGFR ectodomain alleles, initially discovered in cells, might reasonably also be present in patients who relapse upon EGFR blockade and this could be verified using tissue and liquid biopsies.

The molecular landscape of acquired resistance to EGFR blockade revealed the emergence of multiple point mutations in the ectodomain of EGFR. In particular, we detected two novel EGFR exon 12 mutations (EGFR p.R451C and p.K467T) in 2 patients. The previously reported EGFR S492R mutation was detected in 3 of 37 postcetuximab tissue samples (8%), whereas a recent study reports 16% of S492R EGFR mutation detection in 239 postcetuximab plasma samples (11). Such differences may be explained by different sensitivity of the detection techniques as well as the ability of plasma samples to capture the heterogeneity of solid tumors as compared with single biopsies of one tumoral lesion (8, 16, 23). Plasma samples of the patients included in the current study were not systematically collected and therefore we could not analyze the prevalence of EGFR mutations in circulating tumor DNA in the cohort. Accordingly, studies in larger cohorts of patients treated with cetuximab or panitumumab are warranted to define the exact frequency of the other newly identified EGFR ectodomain mutations. Of note, most samples harboring the...
EGFR S492R mutation also exhibited EGFR gene amplification (12), similar to lung cancer tumors harboring the T790M mutation of resistance to tyrosine kinase inhibitors, where the T790M allele appears to be selectively amplified (24). Interestingly, our in vitro analysis showed that panitumumab was effective in a subset of EGFR mutants. As the binding epitopes of cetuximab and panitumumab overlap but are not identical, it is foreseeable that mutations arising in EGFR after anti-EGFR treatment will differentially disrupt binding of cetuximab and/or panitumumab to the receptor (25), with relevant clinical implications for the treatment of cetuximab-resistant patients.

Activating mutations in EGFR downstream signaling effectors were the most frequent event in both cell models and patients. Emergence of KRAS and NRAS mutations occurred in 42% of patients, similar to what we have previously reported in tissue samples, but lower than previously reported in plasma samples (6–10). Again, this may be due to the advantage of circulating DNA in capturing the heterogeneity of solid tumors compared with biopsy of one tumoral lesion (8, 16, 23), indicating that diagnostic tools such as liquid biopsies are required to capture the complexity of the disease. As recently reported, RAS mutations often occurred outside of exon 2 in clinical samples and cell models (26, 27). The finding that codon 61 and 146 KRAS mutations occur more frequently in the acquired resistance setting than in the general colorectal cancer population is worth further studies. Of note, all samples harboring a PIK3CA mutation also displayed other mechanisms of resistance. The role of PIK3CA mutations in driving acquired as well as primary resistance remains controversial and needs to be further characterized. We did not identify emergence of molecular alterations in 20% of patients, suggesting limitations in the sensitivity of the detection technique, tumor heterogeneity, as well as other mechanisms of resistance such as ligand overexpression or c-MET amplification (15, 28, 29).

**Figure 2.**
EGFR mutations differentially affect binding to cetuximab and panitumumab. A, NIH 3T3 cells stably expressing wild-type or the indicated EGFR mutations were incubated with cetuximab or panitumumab, and antibody binding was analyzed by flow cytometry using a secondary antibody to human IgG conjugated with phycoerythrin (PE). NIH 3T3 cells expressing the empty vector were used as a negative control (empty). Graphs show results of one representative experiment. B, the percentage of cells binding to the antibody are shown as relative values compared to EGFR wild-type (wt) cells (percentage of EGFR wt cells set to 1) and are mean values of two independent experiments. While cetuximab binding was affected in cells expressing EGFR mutants, panitumumab was able to bind to cells expressing the S492R and K467T EGFR mutation. The R451C mutation had a moderate impact on binding to either cetuximab or panitumumab.
Importantly, multiple mechanisms of resistance were often present in the samples from relapsed tumors and often displayed more than one molecular alteration. This was also observed in cell lines resistant to cetuximab, strongly suggesting their polyclonal status. This likely reflects the heterogeneity of colorectal cancers and supports the role of circulating DNA to comprehensively characterize the molecular landscape of resistance to EGFR blockade in patients. Activation of EGFR–RAS signaling axis as well as EGFR ectodomain mutations frequently co-occurred. These findings suggest the design of clinical trials that include concomitant inhibition of EGFR downstream signaling together with direct inhibition of the EGFR receptor. Considering that panitumumab seems to be ineffective on a subset of the newly discovered mutations, drugs inhibiting EGFR through different mechanism will also be needed.

Our results have implications for the care of patients as they support the necessity of reassessing the molecular landscape of tumors after progression to anti-EGFR drugs, which currently is not routinely done in clinical practice. The plasticity of tumor cells and their high capacity of adaptation under selective drug pressure, emphasizes the need for sequential tumor or plasma biopsies to better monitor and personalize treatment.

In summary, our study highlights the importance of reassessing the molecular profile of the overall disease burden longitudinally during therapy, and provides evidence that acquired resistance to anti-EGFR therapy in patients with mCRC arises from the emergence of heterogeneous and overlapping molecular changes. Such complexity converges on two main mechanisms of resistance: activating mutation in EGFR downstream signaling and mutations in EGFR ectodomain that disrupt antibody–receptor binding. In light of these findings, pharmacologic studies combining inhibition of both EGFR and EGFR downstream signaling effectors to bypass cetuximab resistance are warranted.

**Figure 3.** Ligand-dependent activation of EGFR mutants in the presence of cetuximab and panitumumab. NIH 3T3 cells expressing WT EGFR or the indicated EGFR mutations were cultured in the presence of cetuximab (Ctx) or panitumumab (Pnm) for 2 hours and stimulated with EGF (5 ng/mL) for 15 minutes. Immunoblotting was performed using antibodies to the indicated proteins.
Disclosure of Potential Conflicts of Interest

A. Bardelli is a consultant/advisory board member for BioCartis, Horizon Discovery, and Trovagene. C. Montagut is a consultant/advisory board member for Merck. No potential conflicts of interest were disclosed by the other authors.

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Other (general projections and grant writing): G. De Fabritiis

Acknowledgments

The authors thank Dr. Salvatore Siena, Dr. Andrea Santoro Bianchi, and members of the laboratory of Molecular Genetics for critical reading and editing of this article. The authors also thank Fundacio Cellex (Barcelona) for a generous donation to the Hospital del Mar Medical Oncology Service.

Grant Support

This work was supported by RD12/0036/0051, P11/00895, P12/00680, PT13/00100/0005, 2014 SGR 567 and 2014 SGR 740 grants and by the Xarxa de Banc de Tumors de Catalunya [to C. Montagut]. The European Community’s Seventh Framework Programme under grant agreement no. 259015 COLTHERES (to A. Bardelli); Associazione Italiana per la Ricerca sul Cancro (AIRC) IG grant no. 12812 (to A. Bardelli); AIRC MFAG no. 11349 (to F. Di Nicolaontio); grant D’Farmacoenergetica—5 per mille 2009 MIUR—Fondazione Piemontese per la Ricerca sul Cancro—ONLUS (to F. Di Nicolaontio); AIRC 2010 Special Program Molecular Clinical Oncology 5 per mille, project no. 9970 (to A. Bardelli). FP7 5 per mille 2010 and 2011 Ministero della Salute (to A. Bardelli); Ministero dell’Istruzione, dell’Università e della Ricerca, progetto PRIN 2010-2011 (to A. Bardelli). J. Albanel is a recipient of intensification program ISCIII/FEADER.

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