Molecular Pathways: Sensitivity and Resistance to Anti-EGFR Antibodies

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Running Title: Resistance to Anti-EGFR Antibodies and Means to Overcome It

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Abstract

Monoclonal antibodies targeting the EGF receptor (EGFR) tyrosine kinase, such as cetuximab and panitumumab, achieve clinically meaningful responses in patients affected by head and neck (HNC) and colorectal cancer (CRC). Despite this evidence of efficacy, no genomic abnormalities that robustly predict sensitivity to EGFR blockade have been yet identified. This suggests that, in some tumor contexts, EGFR dependency is not acquired during neoplastic transformation and rather reflects an aberrant declination of physiologic traits typical of normal tissue counterparts. Indeed, EGFR signals are crucial for the reconstitution of damaged mucosa in the context of acute inflammation, and their sustained activation is likely to turn into a prooncogenic cue during chronic inflammation. Although positive predictors of response to anti-EGFR antibodies remain unknown, multiple determinants of resistance have been described, including alterations interfering with antibody-receptor interaction, deregulation of parallel signaling pathways, and mutations in downstream transducers. These findings provide new opportunities for the optimization of therapeutic strategies based on drug combinations. However, the emerging notion that genetic interactions and compensatory mechanisms may impact – both positively and negatively – the efficacy of targeted therapies complicates the rational design of combinatorial approaches, and implies a rethinking of the criteria required to prioritize laboratory findings for clinical validation in investigational trials.
EGFR belongs to the ERBB family of receptor tyrosine kinases (RTKs). Beside EGFR itself (also known as ERBB-1/HER1), the ERBB receptor family comprises ERBB2 (neu, HER2), ERBB3 (HER3) and ERBB4 (HER4) (1, 2). EGFR is activated through autocrine or paracrine stimulation by ligands that either bind specifically to the receptor (EGF, transforming growth factor α (TGFα) and amphiregulin (AREG)) or bind to both EGFR and ERBB4 (betacellulin (BTC), heparin-binding growth factor (HB-EGF), and epiregulin (EREG)) (2, 3). Ligand binding triggers receptors’ homo- or heterodimerization, which is followed by the activation of mitogenic and antiapoptotic signaling cascades, mainly via the RAS-RAF-MEK-ERK and the PI3K-AKT-mTOR axes (3, 4). In addition to interacting with the other members of the family, EGFR has been also reported to crosstalk with other cancer-relevant RTKs, such as the hepatocyte growth factor receptor MET and the insulin-like growth factor receptor 1 (IGF1R) (5, 6), whose signaling converges on downstream pathways similar to those activated by EGFR (Fig. 1). Besides these core signaling interactions, alternative networks have been proposed, including kinase-independent signaling activities related to receptor internalization (7, 8). A more detailed picture of EGFR-related signals is shown in Fig. 1 and is comprehensively reviewed elsewhere (2).

EGFR was originally proposed as a target in cancer due to generic biological indication (i.e., its frequent over-expression in tumors) (9) and the inclusion of anti-EGFR inhibitors into the toolbox of clinical oncologists was primarily based on evidence of efficacy (10). Two strategies for EGFR inhibition led to the development of agents that are approved for clinical use either as monotherapies or in combination with chemotherapeutic agents (11): anti-EGFR antibodies and small-
molecule EGFR tyrosine kinase inhibitors. Anti-EGFR antibodies, such as cetuximab and panitumumab, bind to the extracellular portion of the receptor causing its internalization and displacing ligand-receptor interactions, thereby interfering with EGFR activation (12); small-molecule kinase inhibitors (such as erlotinib, gefinitib and afatinib) inhibit EGFR autophosphorylation and downstream signaling by competing with ATP (12).

Interestingly, the two classes of inhibitors are endowed with largely non-overlapping clinical activities. On one side, small molecules have been approved for treatment of non-small cell lung cancer (NSCLC). In line with the concept of oncogene addiction, response to EGFR inhibitors in NSCLC is strongly associated with the presence of activating mutations in the target gene (13). On the other side, anti-EGFR antibodies are used for the treatment of colorectal (CRC) and head and neck cancers (HNC) (14), for which no univocal genetic determinants of sensitivity to EGFR inhibition have been yet identified.

The dependency of CRC and HNC on EGFR-signals is reminiscent of an aberrant declination of physiological or para-physiological traits typical of normal tissues. In vertebrates, EGFR is a crucial regulator of cellular homeostasis and controls the organogenesis of multiple epithelial tissues, including lining epithelia of endodermal origin (15, 16). It is tempting to speculate that the reason for the functional dependency on EGFR activity in HNC and CRC may be related to the close interaction of their epithelium of origin with mucosa-associated lymphoid tissues (MALTs), which are large-capacity receptacles of inflammatory cells. Indeed, in the adult intestine, EGFR signaling has a key function in mediating mucosal regeneration and inflammatory responses (17, 18). The abrogation of the EGFR signaling axis
impairs or reduces the regenerative potential of the intestine (18) and decreases the propensity of epithelial cells to undergo neoplastic transformation in the presence of chronic inflammation (19). In line with the assumption that cancer is a wound that never heals (20), it is likely that the upregulation of EGFR activity - normally involved in tissue repair in the context of acute inflammation - is turned into a prooncogenic cue during chronic inflammation. This would select for cancer cells relying on EGFR-driven signals for their growth, explaining why a fraction of CRCs are strictly dependent on EGFR activity even in the absence of genetic alterations of the receptor. Accordingly, the autocrine production of selected ligands (namely, AREG and EREG) and the upregulation of EGFR itself are not only key mediators of intestinal regeneration during inflammation (21), but also positive predictors of sensitivity to EGFR inhibition in CRC (22-25). Although less data are available, a similar scenario seems to apply also to HNC. Indeed, a strict crosstalk between inflammatory cytokines and EGFR signaling to foster tissue regeneration has been repeatedly reported for epithelial tissues in general (26), and for squamous epithelia in particular (27-29).

Clinical-Translational Advances

Resistance to anti-EGFR antibodies: causes and therapeutic opportunities

If EGFR signaling is a physiologic cue for epithelial repair that is usurped in cancer for growth and survival, then any tumor would be in principle sensitive to anti-EGFR antibodies, unless some specific event happens to cause resistance, either by interfering with the pharmacologic activity of the drugs or by subsidizing alternative ways to activate equivalent downstream effectors. Unfortunately, too little information is available about the potential determinants of resistance to anti-EGFR
antibodies in HNCs. Instead, more data exist for CRC, which are consistent with the proposed model. The known mechanisms of primary and acquired resistance to approved anti-EGFR agents in CRC are largely superimposable (30) and can be categorized into three classes (see Fig. 1 and Table 1): (i) reduced antibody-receptor interaction; (ii) activation of parallel substitute pathways; (iii) constitutive activation of downstream signals.

**Class I—multiple EGFR inhibition**

The most frequent cause of resistance to first-generation small molecules targeting EGFR in NSCLC is a mutation in EGFR (T790M), which reduces the affinity between the ATP-binding domain of the kinase and the inhibitor, impairing the ATP-competitive activity of the drug (31, 32). In such case, cancer cells remain dependent on EGFR signaling yet escape the therapeutic activity of the drug by modifying its pharmacodynamics. Similarly, a mutation in EGFR extracellular domain (S492R) causes resistance to cetuximab by impeding binding of the antibody to the receptor (33). Notably, cells bearing the S492R mutation in EGFR are still sensitive to treatment with panitumumab, which recognizes different receptor epitopes (33, 34).

Some EGFR ligands, such as EGF and TGFα, can compete with cetuximab for binding to EGFR. In particular, strong overexpression of TGFα has been shown to correlate with reduced sensitivity to cetuximab (24). Interestingly, TGFα-overexpressing tumors are not fully resistant to cetuximab; instead, they show an intermediate phenotype, characterized by partial desensitization to treatment (25). It is likely that, similar to mutations of the extracellular domain, TGFα does not intrinsically release dependency on EGFR, but reduces cetuximab binding efficacy (35). This suggests that more powerful inhibition of EGFR by combining multiple
EGFR-directed drugs might be efficacious in tumors in which EGFR signaling is necessary for proliferation but cetuximab activity per se is weaker for pharmacodynamic reasons. This is witnessed by the observation that, in patient-derived xenografts (PDXs) of CRC tumors, addition of the EGFR small-molecule inhibitors lapatinib or erlotinib to cetuximab can turn tumor growth inhibition into overt tumor shrinkage (>75% reduction in tumor volume upon treatment) in more than 25% of the cases that respond to cetuximab alone with disease stabilization (25). At the clinical level, a recent study has demonstrated encouraging activity of combined treatment with cetuximab and erlotinib in 37 chemorefractory patients with KRAS wild-type mCRC tumors (36): the response rate (41%) was definitely higher than that achieved by single-agent anti-EGFR antibodies, which is normally around 15-17% (2, 37, 38). An analogous improvement in efficacy has been described when combining the dual HER1/HER2 inhibitor afatinib with cetuximab in EGFR-mutant NSCLCs resistant to erlotinib monotherapy (30% overall response rate) (39), suggesting a wide range of applicability of “on-target” combination strategies for EGFR inhibition. A similar ‘diversification’ strategy can be also pursued by designing ad hoc antibody mixtures targeting multiple epitopes of the same receptor. A successful example of this approach is represented by SYM004 (40), which is currently tested in several phase II trials (NCT01117428).

Class II—co-targeting parallel pathways

Another mechanism adopted by cancer cells to escape oncogene dependency is the activation of parallel signaling cascades impinging on similar downstream effectors. Some such pathways have been clinically validated to trigger resistance to EGFR antibodies in CRC, including hyperactivation of HER2 and MET (22, 41, 42). In both
cases, preclinical evidence indicates that combined inhibition of the resistance-conferring pathway and EGFR itself can induce objective responses or prolonged disease control in most instances (22, 41, 42). For the specific case of \textit{HER2} amplification causing \textit{de novo} resistance to cetuximab and panitumumab, a phase II trial is ongoing to test a combination of the anti-\textit{HER2} antibody trastuzumab and lapatinib (EUDRACT 2012-002128-33, clinicaltrialsregister.eu). \textit{Interim} results are promising, with more than 30% objective responses among heavily pretreated patients (median, 5 prior therapies) (43).

Besides causing overt drug resistance, parallel signals can also induce partial desensitization to treatment. For example, insulin-like growth factor 2 (IGF2) is highly overexpressed in a fraction of CRCs (44); however, the frequency of IGF2 overexpressors among cetuximab responders is null or very low (25), pointing to IGF2-mediated activation of the cognate receptor IGF1R as a means to desensitize CRC cancer cells to EGFR inhibition. Indeed, increased IGF1R signaling has been repeatedly documented to associate with low sensitivity to EGFR blockade (45, 46). Of note, IGF2 overexpressors are highly enriched among cases responding to cetuximab treatment with disease stabilization ($p<0.001$ by Fisher’s exact test), but not among those that are fully resistant to treatment (25). Thus, similar to the autocrine production of TGF$\alpha$, IGF2 overexpression behaves as a response modifier, reducing but not abating EGFR dependency. Accordingly, addition of an IGF1R kinase inhibitor potentiated the anti-tumor effects of cetuximab in IGF2-overexpressing PDXs, suggesting that these tumors can be targeted successfully by a combined treatment against IGF1R and EGFR.
Despite this promising preclinical evidence, recent clinical trials in patients with KRAS wild-type CRC have shown that combined therapy with anti-EGFR and anti-IGF1R antibodies did not improve response compared with EGFR-targeted monotherapy (47, 48). The reasons for these discrepancies are currently not fully understood and there is still considerable discussion about the validity of IGFs and IGF1R as viable therapeutic targets in cancer. On one side, the apparent lack of efficacy shown by IGF/IGF1R inhibitors in the clinic could be due to the fact that no attempts were made to select for potential responders through molecular stratification based on predictive biomarkers (49). On the other side, preclinical studies could not adequately represent the clinical situation: differences could be ascribed to (i) the use of different pharmacologic modalities to inhibit IGF1R in PDX experiments versus clinical trials and/or to (ii) host-related modifiers, since the tumor microenvironment of xenografts is of mouse origin. Whatever the case, dedicated retrospective and prospective clinical studies are necessary to rigorously address this issue.

Class III—inhibition of downstream effectors

Most of the genetic alterations causing de novo and secondary resistance to anti-EGFR agents trigger constitutive activation of downstream signaling pathways. These include mutations in KRAS and NRAS (exon 2 to 4), BRAF (exon 15), and PIK3CA (exon 20), as well as gene amplification of KRAS (30). Results of randomized phase III studies on chemorefractory mCRC treated with cetuximab or panitumumab monotherapy led to the limitation in the use of anti-EGFR antibodies, together with chemotherapy, to patients bearing KRAS wild-type tumors (50).
KRAS is the most sought-after target for new therapies, being alone responsible for resistance in more than 40% of the overall cases. However, given the lack of robust approaches for direct inhibition of KRAS signaling activity, different strategies based on blockade of downstream effectors, such as MEK and ERK, have been proposed. Disappointingly, results obtained in preclinical models and then confirmed in the clinical setting have been fairly modest (51, 52), possibly because of feedback activation of subsidiary pathways, which sustain cancer cell viability during treatment. These compensatory mechanisms have been reported in CRC as well as in other cancer types, and involve upregulation of diverse RTKs, including EGFR, HER2, HER3 and MET (53). Based on such evidence, drug combinations have been tested preclinically, in which MEK or ERK inhibition is complemented by co-targeting the RTK responsible for the feedback activation (53). Some of these combination therapies are currently undergoing clinical evaluation (53), with two phase I trials recently completed (NCT01287130) (54).

A further layer of complexity emerged from the observation that most genetic causes of resistance to EGFR inhibitors lead to hyperactivity of the MEK-ERK axis; a phenomenon recalling the Darwinian definition of ‘convergent evolution’ (30). On these bases, it has been proposed that the MEK-ERK hub represents a culprit signaling node, whose inhibition can be exploited to prevent or retard the emergence of resistance. Consequently, clinical trials have been designed to test the concomitant upfront inhibition of EGFR and MEK/ERK, with the aim to extend the time-to-progression by anticipating the blockade of the most probable funnel of resistance-related signals.

Conclusions
The treatment paradigm for a patient should not be decided on the sole basis of the mutational status of a single gene with potential cancer-causing function, but rather on the basis of the heterogeneous context in which that mutation is found. Due to this complexity, drug combinations rather than monotherapies are likely required to provide long-lasting benefit. However, the amount of conceivable treatment hypotheses based on drug permutations largely exceeds the number of clinically testable choices, due to costs, ethical implications and logistic restraints. This calls for efficacious preclinical models for evidence-based prioritization of clinical experimentation. In this context, evidence is emerging that comparative testing of multiple combination strategies in PDXs can be exploited to select for the most effective therapeutic strategy among different options based on a similar rationale (22). For example, the observation obtained in PDXs that a combination of trastuzumab and lapatinib, but not treatment with either drug alone, can induce effective tumor shrinkage of HER2-amplified CRC is being confirmed in the clinical setting (43); again in line with observations obtained in PDX, trials have failed to demonstrate clinical efficacy of trastuzumab-based regimens in CRC (55). Similarly, the efficacy of the afatinib/cetuximab combination was effectively predicted by genetically modified mouse models of NSCLC and then confirmed by clinical data (39, 56). Another relevant example of effective anticipation of clinical findings by preclinical studies is the lack of efficacy against KRAS- and BRAF-mutant CRCs demonstrated by MEK and PI3K inhibitors, a notion that was anticipated by PDX-based data (52) and has been then supported by clinical evidences (51). Analogously, the efficacy of combined MEK/ERK inhibition in treating BRAF-mutated melanomas and preventing reactive squamous cell carcinomas was proposed by preclinical
studies (57) and has been now validated clinically (58, 59). This suggests that preclinical studies can effectively guide clinical experimentation when properly designed. However, discrepancies have also been observed between preclinical and clinical data, which argue against the general validity of this principle. We believe this disconnect between preclinical and clinical findings is ascribable to two main reasons: (i) the lack of a population-based contextualization of the findings obtained in most preclinical studies; (ii) the interference on treatment outcome produced by host-related modifiers of therapeutic response (immune system, species-specific ligand-receptor interactions, etc.) that are not properly recapitulated by traditional xenografts. Tackling such issues will require significant efforts and investments to achieve a better representation of the complexity and heterogeneity of cancer at the preclinical level. In particular, the progressive humanization of mouse models is generating great expectations. Humanization is a time- and labor-intensive process, which will require several technical challenges to be met before being widely exploited. However, encouraging preliminary results (60) suggest feasibility and effectiveness of this approach. Finally, a critical step will be the adoption of stringent criteria for clinical translation of preclinical findings (61), so that only those hypotheses endowed with high probability of success will enter clinical investigation.

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**Table 1.** Resistance to anti-EGFR antibodies and strategies to overcome it: preclinical evidences and clinical trials
Figure 1. EGFR signaling pathways and causes of resistance to anti-EGFR antibodies. Ligand binding to EGFR is followed by the activation of several downstream signaling cascades, which are categorized by colored outlines. Color fills represent the correlations between gene overexpression or genetic alterations and sensitivity to cetuximab treatment. Mutations causing resistance to cetuximab are represented as red circles; similarly, the genes that cause resistance when amplified are filled in red; genes that, when overexpressed, cause desensitization to treatment are depicted in yellow; finally, genes whose upregulation correlates with sensitivity to treatment are represented in green.

1) The RAS-RAF-MEK-ERK pathway (blue-colored): GRB2, through SHC, recruits SOS to the cell membrane. SOS induces Ras activation, which in turn triggers a RAF-dependent phosphorylation cascade involving MEK and causing ERK translocation to the nucleus, where transcription factors such as ELK1 are phosphorylated/stabilized to transactivate immediate early genes, for example, MYC.

2) The PI3K-AKT-mTOR cascade (pink-colored): PI3K is recruited to active EGFR through mediators such as GAB1 and subsequently mediates the conversion of phosphatidylinositol (3,4)-bisphosphate (PIP2) lipids to phosphatidylinositol (3,4,5)-trisphosphate (PIP3). This allows PDK1 to phosphorylate AKT, which in turn impinges on mTOR, MDM2 and XIAP. On one side, mTOR promotes protein synthesis through the phosphorylation of the ribosomal protein S6. On the other side, MDM2 and XIAP act as anti-apoptotic cues through inhibition of P53 and CASP respectively.

3) The JAK-STAT pathway (green-colored): Recruitment of JAKs upon EGFR activation induces c-SRC binding, which is then responsible for STAT phosphorylation. Phosphorylated STATs translocate to the nucleus and initiate the transcription of specific target genes.

4) The PLCγ-PKC cascade (grey-colored): phospholipase C gamma (PLCγ) catalyzes the production of DAG and IP3; the latter binds to the endoplasmic reticulum causing the release of calcium.
These events induce the activation of CaMK and PKC, leading to NF-κB transcription factor activation via IKK.

5) The Rho family GTPases pathway (orange-colored): VAV mediates the activation of RHO and RAC, which control actin/myosin filament contraction and lamellipodia protrusion, promoting cell motility and invasion.

6) JNK pathway (light-yellow-colored): PAK1, following its recruitment to EGFR through the adaptor NCK, activates a signaling cascade involving MAP2Ks family, i.e. MEKK1, and MAP3Ks, i.e. MKK4 and MKK7. The cascade converges to JNKs, which in turn modulate the transcription of target genes, such as c-JUN and c-FOS, regulating cell proliferation, differentiation and survival.

7) Receptor internalization, degradation and recycling (light-green and red-colored): LAPTM4B can induce the endosomal accumulation of kinase-inactive EGFR, which drives BECLIN-dependent initiation of autophagy, a mechanism of resistance to starvation (light green). Alternatively, the phosphorylated receptor undergoes ubiquitination and degradation in the presence c-CBL (red), or recycling in its absence.
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