Epidermal Growth Factor Receptor Activation in Glioblastoma through Novel Missense Mutations in the Extracellular Domain

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Abbreviations: EGF, epidermal growth factor; EGFR, epidermal growth factor receptor; FISH, fluorescence in situ hybridization; IL-3, interleukin-3; MALDI-TOF, matrix-assisted laser desorption/ionization time-of-flight; SNP, single-nucleotide polymorphism

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ABSTRACT

Background

Protein tyrosine kinases are important regulators of cellular homeostasis with tightly controlled catalytic activity. Mutations in kinase-encoding genes can relieve the autoinhibitory constraints on kinase activity, can promote malignant transformation, and appear to be a major determinant of response to kinase inhibitor therapy. Missense mutations in the EGFR kinase domain, for example, have recently been identified in patients who showed clinical responses to EGFR kinase inhibitor therapy.

Methods and Findings

Encouraged by the promising clinical activity of epidermal growth factor receptor (EGFR) kinase inhibitors in treating glioblastoma in humans, we have sequenced the complete EGFR coding sequence in glioma tumor samples and cell lines. We identified novel missense mutations in the extracellular domain of EGFR in 13.6% (18/132) of glioblastomas and 12.5% (1/8) of glioblastoma cell lines. These EGFR mutations were associated with increased EGFR gene dosage and conferred anchorage-independent growth and tumorigenicity to NIH-3T3 cells. Cells transformed by expression of these EGFR mutants were sensitive to small-molecule EGFR kinase inhibitors.

Conclusions

Our results suggest extracellular missense mutations as a novel mechanism for oncogenic EGFR activation and may help identify patients who can benefit from EGFR kinase inhibitors for treatment of glioblastoma.

The Editors’ Summary of this article follows the references.
**Introduction**

The epidermal growth factor receptor (EGFR) is a receptor tyrosine kinase that regulates fundamental processes of cell growth and differentiation. Deletion of the EGFR gene is embryonically lethal in mice, and increased EGFR signaling has been linked to a variety of human malignancies. Mechanisms for oncogenic conversion of EGFR in cancer include EGFR gene amplification, structural rearrangements of the receptor, overexpression of epidermal growth factor (EGF)–family ligands by tumor cells and/or surrounding stroma, and—as was recently shown in lung cancer—activating mutations in the EGFR kinase domain [1].

The evidence for a role of EGFR in oncogenesis is particularly compelling in glioblastoma, the most aggressive human brain tumor with a two year survival of less than 5% despite surgery, radiation, and chemotherapy [2,3]. About 40% of glioblastomas show amplification of the EGFR gene locus [4], and about half of these tumors express a mutant receptor (EGFRvIII) that is constitutively active due to an in-frame truncation within the extracellular ligand-binding domain [5–7]. Perhaps the strongest evidence for a role of EGFR in the biology of glioblastoma stems from clinical trials in which 15%–20% of glioblastoma patients experienced significant tumor regression in response to small-molecule EGFR kinase inhibitors [8,9]. Our recent data indicate that expression of EGFRvIII in the context of an intact PTEN (phosphatase and tensin homolog) pathway is associated with these clinical responses [9].

To explore the possibility that EGFR might be the target of oncogenic mutations outside the kinase domain, we sequenced the entire EGFR coding region in a panel of 151 glioma tumors and cell lines.

**Methods**

**DNA Samples**

Genomic DNA was extracted from eight glioblastoma cell lines (A172, SF268, SF295, SF539, T98G, U87, U118, and U251) and 143 fresh frozen glioma samples. The clinical glioma samples comprised glioblastomas (n = 132), World Health Organization grade III anaplastic astrocytomas (n = 3), grade III mixed gliomas (n = 4), and grade III oligodendro-gliomas (n = 4). Germline genomic DNA was extracted from peripheral blood samples. To confirm the match between germline and tumor DNA for each patient, we performed mass spectrometric genotyping of 24 single-nucleotide polymorphism (SNP) loci. These loci included 23 SNP loci represented on both 50K Xba and Hind arrays (Affymetrix, http://www.affymetrix.com) and one AmelXY locus for sex determination (Table S1). Collection and analysis of all clinical samples was approved by the University of California Los Angeles Institutional Review Board.

**Reagents**

Erlotinib was purchased from WuXi Pharmatech (http://www.pharmatechs.com). The following antibodies were used in this study: anti-EGFR, anti-phospho-Y1068-EGFR anti-phospho-Y845-EGFR, and anti-phosphoinositide 3-kinase (PI3K) p85 (all from Cell Signaling Technology, http://www.cellsignal.com); anti-phosphotyrosine 4G10 (Upstate Biotechnologies, now Millipore, http://www.upstate.com); and anti-actin, anti-ERK1/2, and anti-P-ERK1/2 (all from Santa Cruz Biotechnology, http://www.scbt.com).

**Sequencing and Mass Spectrometric Genotyping**

PCR reactions for each exon and flanking intronic sequences contained 5 ng of genomic DNA, 1X HotStar Buffer, 0.8 mM dNTPs, 1 mM MgCl2, 0.2 U HotStar Enzyme (Qiagen, http://www.qiagen.com), and 0.2 μM forward and reverse primers in a 6 or 10 μl reaction volume. PCR cycling parameters were: one cycle of 95°C for 15 min; 35 cycles of 95°C for 20 s, 60°C for 30 s, and 72°C for 1 min; followed by one cycle of 72°C for 3 min.

The resulting PCR products were sequenced using bidirectional dye-terminator fluorescent sequencing with universal M13 primers. Sequencing fragments were detected via capillary electrophoresis using ABI Prism 3730 DNA Analyzer (Applied Biosystems, http://www.appliedbiosystems.com). PCR and sequencing were performed at Agencourt Bioscience Corporation (http://www.agencourt.com) or at the Broad Institute of Harvard and MIT (http://www.broad.mit.edu). Forward (F) and reverse (R) chromatograms were analyzed in batch with Mutation Surveyor 2.51 (SoftGenetics, http://www.softgenetics.com), followed by manual review.

A minimum of 21 of 28 (75%) EGFR exon sequence coverage was accomplished for 151 samples. An exon for each individual sample was considered covered if 90% of the sequence trace within the exon had a phred quality score of 30 or greater, a signal-to-background noise ration of 15% or less, and signal intensity greater than 25% of the signal intensity of the sequencing plate. High-quality sequence variations found in one or both directions were scored as candidate mutations. Exons harboring candidate mutations were reamplified from the original DNA sample and resequenced.

For mass spectrometric genotyping, PCR and extension primers (Table S2) were designed using SpectroDESIGNER software (Sequenom, http://www.sequenom.com). Unincorporated nucleotides from PCR reactions were dephosphorylated with shrimp alkaline phosphatase (Amersham, http://www.amersham.com) followed by primer extension with Thermosequence polymerase (Amersham). Primer extension reactions were loaded onto SpectroCHIPs (Sequenom) and analyzed using a MALDITOF (matrix-assisted laser desorption/ionization time-of-flight) mass spectrometer (SpectroREADER, Sequenom) [10]. Mass spectra were processed with SpectroTYPEr (Sequenom) to determine genotypes based on peaks intensities corresponding to the expected extension products.

**Affymetrix 100K SNP Arrays**

Genomic DNA was processed and hybridized following the guidelines of the manufacturer (Affymetrix) and arrays were scanned with a GeneChip Scanner 3000. Genotyping calls and signal quantification were obtained using GeneChip Operating System 1.1.1 and Affymetrix Genotyping Tools 2.0 software. Data were normalized at the probe level to a baseline array with median signal intensity using invariant set normalization. After normalization, the signal values for each SNP in each array were obtained with a model-based (perfect-match/mismatch) method [11]. Signal intensities at each probe locus were compared with a set of normal reference samples representing 36 ethnically matched individuals to...
generate log2 ratios. Log2 ratios were smoothed using the breakpoint analysis method in the R package GLAD (Gain and Loss Analysis of DNA) [12]. Regions were considered amplified if their smoothed log2 ratio exceeded 0.3 (half the variation seen with a single-copy gain).

Fluorescence In Situ Hybridization

Dual-probe fluorescence in situ hybridization (FISH) was performed on paraffin-embedded sections with locus-specific probes for EGFR and the centromere of Chromosome 7 as previously described [9].

Determination of EGFRvIII Expression

RNA was extracted from fresh frozen tumor samples and EGFRvIII expression determined by two independent RT-PCR assays for each sample. Primer pairs included: #1F 5′-CTTCGGGAGCAGGATGCGAC-3′, #1R 5′-ACCAATACCTATTCGTTACAC-3′, #2F 5′-GAGCTCTTGGGAGCAG-3′, and #2R 5′-GTGATCTGTCAACCACATAATTACCTTCTT-3′. EGFRvIII expression was also examined by immunohistochemistry and/or immunoblotting depending on the availability of tissue samples.

Quantification of Mutant EGFR Alleles

The abundance of missense and wild-type EGFR alleles in tumor DNA samples was determined by PCR-cloning and sequencing of respective EGFR exons. PCR products were ligated into PCR2.1-Topo vectors (Invitrogen) and transformed into E. coli. After transformation, bacteria were plated onto selection plates and grown overnight. For each DNA sample, 65–94 colonies were isolated using a colony picking robot (QPix2, Genetix Limited, http://www.genetix.com), grown overnight, and bidirectionally sequenced at the Broad Institute. Sequence traces were analyzed using Mutation Surveyor software (SoftGenetics).

EGFR Expression Constructs

Retroviral EGFR expression constructs containing puromycin (pBabe-puro-EGFR) [13] or neomycin-resistance genes (pLXSN-neo-EGFR) [14] were used for site-directed mutagenesis using the Quick-Change Mutagenesis XL kit (Stratagene, http://www.stratagene.com). pLXSN-neo-EGFR retroviral constructs for EGFR and EGFRvIII were generously provided by David Riese 2nd (Purdue University, West Lafayette, Illinois, United States) and Webster Cavenee (Ludwig Institute for Cancer Research, La Jolla, California, United States). pBabe-Puro-based viral stocks were generated by transfecting the Phoenix 293T packaging cell line (Orbigen, http://www.orbigen.com) with the pBabe-Puro retroviral constructs using Lipofectamine 2000 (Invitrogen, http://www.invitrogen.com). pLXSN-Neo-based viral stocks were generated by transfecting the human amphotropic 293-T cell line with pLXSN-Neo retroviral constructs using Lipofectamine 2000 (Invitrogen). Supernatants were col-
Expression of EGFR Alleles in NIH-3T3 Cells

Cells cultured in DMEM supplemented with 10% calf serum were infected with pBabe-Puro-based viral stock in the presence of polybrene. Beginning 2 d after infection, cells were selected in puromycin (2 μg/ml) for 3 d. Pooling NIH-3T3 cells stably expressing respective EGFR alleles at comparable EGFR protein levels were examined for their ability to induce colony formation in soft agar and tumor growth in nude mice. For soft agar assays, 1 × 10^5 NIH-3T3 cells were suspended in a top layer of DMEM supplemented with 10% calf serum and 0.4% Select Agar (Gibco/Invitrogen) and plated on a bottom layer of DMEM supplemented with 10% calf serum and 0.5% Select Agar. EGF (10 ng/ml) was added to the top agar where indicated. Pictures of colonies were taken 3–4 wk after subcutaneous inoculation into nude mice (n = 6 per cell line).

Expression of EGFR Alleles in Human Astrocytes

Viral supernatants (pLXSN-neo-EGFR) were used to infect immortalized human astrocytes expressing the catalytic subunit of the telomerase holoenzyme and human papillomavirus 16 E6/E7 [16]. Astrocytes were then selected in G418 (Invitrogen) for approximately 10 d.

Results

Missense Mutations in Glioblastoma Cluster in the Extracellular Domain of EGFR

Encouraged by the recent success in identifying oncogenic kinase mutations through resequencing of kinase-encoding genes [17–19], we sequenced the entire coding sequence of EGFR in 143 human glioma samples and eight glioblastoma cell lines. Analysis of the initial Sanger sequencing results in these 151 samples revealed several novel sequence variations in the coding region of the EGFR. To validate these candidate mutations via a complementary method, all DNA samples were reexamined using allele-specific genotyping by MALDITOF mass spectrometry.

In all, we identified EGFR missense mutations in 14.4% (19/132) of glioblastomas, 12.5% (1/8) of glioblastoma cell lines, and none (0/11) in lower-grade gliomas. Only one tumor sample harbored a missense mutation in the EGFR kinase domain (L861Q), the location of EGFR mutations in lung cancer, supporting the recent conclusion from other groups that EGFR kinase domain mutations appear to be a rare event in this disease [20–22]. The remainder of the EGFR mutations (18/132 glioblastomas) were located in the extracellular ligand-binding (I, III) or cysteine-rich (II, IV) domains of the receptor (Figure 1A). Two evolutionarily highly conserved amino acid residues (Figure S1) were affected by mutations in five samples each (R108 and A289). Examination of peripheral blood DNA, matched to the tumor DNA by genotyping of 24 SNP loci, showed that eight of the 12 distinct missense mutations were unambiguously somatic, and one mutation (E330K) was germline. Three additional missense mutations...
Table 1. EGFR Missense Mutations Identified in a Panel of 151 Glioma Samples

<table>
<thead>
<tr>
<th>Sample Identifier</th>
<th>Histology</th>
<th>Exon</th>
<th>Nucleotide Change</th>
<th>AA Change</th>
<th>Somatic Mutation Detection</th>
<th>Abundance of Mutant Allele</th>
<th>EGFR Gene Dose</th>
<th>EGFRvIII</th>
</tr>
</thead>
<tbody>
<tr>
<td>S001050 GBM 2</td>
<td>G136A, G187C</td>
<td>D46N, G63R</td>
<td>Somatic</td>
<td>Het</td>
<td>+</td>
<td>81/95 (85.3%)</td>
<td>AMP</td>
<td>2.63</td>
</tr>
<tr>
<td>S001073 GBM 3</td>
<td>G323A</td>
<td>R108K</td>
<td>Somatic</td>
<td>Hom</td>
<td>+</td>
<td>88/90 (97.8%)</td>
<td>AMP</td>
<td>2.52</td>
</tr>
<tr>
<td>S001076 GBM 3</td>
<td>G323A</td>
<td>R108K</td>
<td>Somatic</td>
<td>Het</td>
<td>+</td>
<td>10/82 (12.2%)</td>
<td>NON-AMP</td>
<td>n.d.</td>
</tr>
<tr>
<td>S001092 GBM 3</td>
<td>G323A</td>
<td>R108K</td>
<td>Somatic</td>
<td>Het</td>
<td>+</td>
<td>16/93 (17.2%)</td>
<td>AMP</td>
<td>2.5</td>
</tr>
<tr>
<td>S001094 GBM 3</td>
<td>G323A</td>
<td>R108K</td>
<td>Somatic</td>
<td>Het</td>
<td>+</td>
<td>7/90 (7.8%)</td>
<td>NON-AMP</td>
<td>n.d.</td>
</tr>
<tr>
<td>S003763 GBM 3</td>
<td>G323A</td>
<td>R108K</td>
<td>Unknown</td>
<td>Het</td>
<td>+</td>
<td>3/94 (3.2%)</td>
<td>AMP</td>
<td>2.058</td>
</tr>
<tr>
<td>S001067 GBM 7</td>
<td>A787C</td>
<td>T263P</td>
<td>Somatic</td>
<td>Hom</td>
<td>+</td>
<td>83/92 (90.2%)</td>
<td>n.d.</td>
<td>n.d.</td>
</tr>
<tr>
<td>S001102 GBM 7</td>
<td>A787C</td>
<td>T263P</td>
<td>Somatic</td>
<td>Het</td>
<td>+</td>
<td>69/92 (75.0%)</td>
<td>AMP</td>
<td>2.4</td>
</tr>
<tr>
<td>S001103 GBM 7</td>
<td>A787C</td>
<td>T263P</td>
<td>Somatic</td>
<td>Het</td>
<td>+</td>
<td>3/65 (4.6%)</td>
<td>AMP</td>
<td>n.d.</td>
</tr>
<tr>
<td>S001097 GBM 7</td>
<td>C866A</td>
<td>A289D</td>
<td>Unknown</td>
<td>Het</td>
<td>+</td>
<td>n.d.</td>
<td>AMP</td>
<td>0.72</td>
</tr>
<tr>
<td>S001095 GBM 7</td>
<td>G865A</td>
<td>A289T</td>
<td>Unknown</td>
<td>Het</td>
<td>+</td>
<td>n.d.</td>
<td>NON-AMP</td>
<td>0.17</td>
</tr>
<tr>
<td>S001090 GBM 7</td>
<td>C666T</td>
<td>A289V</td>
<td>Somatic</td>
<td>Het</td>
<td>+</td>
<td>3/82 (3.7%)</td>
<td>NON-AMP</td>
<td>n.d.</td>
</tr>
<tr>
<td>S001108 GBM cell line 7</td>
<td>C666T</td>
<td>A289V</td>
<td>Unknown</td>
<td>Het</td>
<td>+</td>
<td>31/92 (33.7%)</td>
<td>n.d.</td>
<td>n.d.</td>
</tr>
<tr>
<td>S004384 GBM 7</td>
<td>C666T</td>
<td>A289V</td>
<td>Unknown</td>
<td>Het</td>
<td>+</td>
<td>83/90 (92.2%)</td>
<td>AMP</td>
<td>2.1</td>
</tr>
<tr>
<td>S002024 GBM 7</td>
<td>G971T</td>
<td>R324L</td>
<td>Unknown</td>
<td>Hom</td>
<td>n.d.</td>
<td>n.d.</td>
<td>n.d.</td>
<td>0.4</td>
</tr>
<tr>
<td>S001026 GBM 8</td>
<td>G998A</td>
<td>E330K</td>
<td>Germine</td>
<td>Het</td>
<td>+</td>
<td>38/94 (40.4%)</td>
<td>NON-AMP</td>
<td>n.d.</td>
</tr>
<tr>
<td>S003577 GBM 15</td>
<td>C178T</td>
<td>P596I</td>
<td>Unknown</td>
<td>Het</td>
<td>+</td>
<td>37/89 (41.6%)</td>
<td>NON-AMP</td>
<td>n.d.</td>
</tr>
<tr>
<td>S001018 GBM 15</td>
<td>G1793T</td>
<td>G598V</td>
<td>Somatic</td>
<td>Hom</td>
<td>n.d.</td>
<td>48/94 (51.1%)</td>
<td>AMP</td>
<td>n.d.</td>
</tr>
<tr>
<td>S001005 GBM 15</td>
<td>G1793T</td>
<td>G598V</td>
<td>Unknown</td>
<td>Het</td>
<td>+</td>
<td>77/92 (83.7%)</td>
<td>NON-AMP</td>
<td>n.d.</td>
</tr>
<tr>
<td>S001071 GBM 21</td>
<td>T2582A</td>
<td>L861Q</td>
<td>Somatic</td>
<td>Het</td>
<td>+</td>
<td>n.d.</td>
<td>AMP</td>
<td>2.49</td>
</tr>
</tbody>
</table>

Tabulated are sample identification numbers, source of the DNA (primary tumor versus cell line), site of the mutation (exon number, nucleotide change, amino acid change), homozygous versus heterozygous occurrence of the mutation, genotype of corresponding germline DNA, mutation detection method (Sanger sequencing, MS genotyping), abundance of the mutant EGFR allele (see Methods section), EGFR gene dosage, and EGFRvIII status. The sample set included 132 glioblastomas, 11 WHO grade III gliomas, and eight glioblastoma cell lines.

AA, amino acid; AMP, amplified; GBM, glioblastoma; Het, heterozygous; Hom, homozygous; n.d., not determined (failed reaction or sample not available); NON-AMP, not amplified.

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(A289D, A289T, and R324L) were found in tumors for which no normal tissue was available (Table 1). None of the missense mutations were detected in germline DNA from 270 normal control individuals.

To define which fraction of the EGFR pool represented the mutant allele in gliomas with EGFR missense mutations, we employed a PCR-cloning strategy previously used by our laboratories for mutation detection in clinical samples [23]. The mutant EGFR allele represented 30%-98% of the receptor pool in two-thirds (10/16) of all examined cases and over 50% in at least one tumor representing the most common amino acid changes: R108K, T263P, A289V, and G598V (Table 1). Lower abundance of the mutant EGFR allele in other samples might be due to contaminating stromal tissue, because genomic DNA was extracted from frozen tumor aliquots without prior microdissection.

We also genotyped genomic DNA from 119 primary lung tumors to detect EGFR ectodomain mutations. While 13.4% (16/119) of these lung tumor samples harbored mutations in the EGFR kinase domain, we did not detect any of the glioma-related EGFR ectodomain mutations in this sample set.

**EGFR Ectodomain Mutations Are Associated with Increased EGFR Gene Dose**

Since EGFR is amplified in about 40% of human glioblastomas [4], we determined the relationship between EGFR missense mutation and EGFR gene dose in our tumor samples. Of 17 tumors with EGFR missense mutations, 58.8% (10) showed evidence for EGFR amplification by FISH and/or Affymetrix 100K SNP genotyping arrays (Figure 1B; Table 1). This distribution suggests that EGFR missense mutations are associated with EGFR amplification and raises the question of whether EGFR missense mutations in glioblastoma co-occur with or are mutually exclusive of the EGFRvIII mutation, which is found almost exclusively in glioblastomas with increased gene dosage [24]. Using at least two independent assays for the determination of EGFRvIII status, we identified the EGFRvIII allele in 28.3% (13/46) of gliomas without EGFR missense mutation and 6.3% (1/16) tumors with EGFR missense mutation (Figure 1C; Table 1); note that this tumor showed vastly lower levels of EGFRvIII (Figure 1C, lane 12). These findings suggest that EGFR ectodomain mutations occur independently of EGFRvIII in glioblastoma and provide an alternative mechanism for EGFR activation in this disease.

**EGFR Ectodomain Mutants Are Oncogenic**

To test the oncogenicity of the glioma-related EGFR missense mutations, we transduced NIH-3T3 fibroblasts with retroviruses encoding either wild-type EGFR or selected EGFR missense mutants (encoding R108K, T263P, A289V, G598V, and L861Q). Ectopic expression of all EGFR mutants examined in NIH-3T3 cells conferred anchorage-independent colony formation in soft agar (Figure 2A). In contrast, expression of wild-type EGFR induced a transformed phenotype only in the presence of exogenous EGF, as previously reported [25,26].

To further analyze the oncogenic potential of the EGFR mutants, NIH-3T3 subclones stably expressing the same missense mutant receptors (encoding R108K, T263P, A289V, G598V, and L861Q) were inoculated subcutaneously into nude mice. NIH-3T3 cells infected with empty vector or wild-type EGFR-expressing virus did not yield any measurable growth.
tumors within the four-week observation period. In contrast, NIH-3T3 cells expressing each of the tested EGFR missense mutants produced large tumors at the inoculation site in all mice within three to four weeks (Figure 2B).

**EGFR Ectodomain Mutants Are Basally Phosphorylated and Are Responsive to Ligand**

Signal transduction through EGFR is determined by its basal catalytic activity, receptor activation by ligand, and signal termination through intracellular compartmentalization of the receptor-ligand complex, receptor dephosphorylation, and degradation [27]. To explore the biochemical basis for the gain of function observed with EGFR ectodomain mutants, we first examined the basal catalytic activity of A289V-EGFR in transiently transfected 293T cells using EGFR autophosphorylation as a readout for receptor activation. EGFR autophosphorylation was determined by measuring the total phosphotyrosine content of the immunoprecipitated EGFR (left blots) and whole cell lysates (right blots).

**Figure 3. Basal Activation and Ligand Response of EGFR Ectodomain Mutants**

(A) Increased EGFR tyrosine phosphorylation of A289V-EGFR. 293T cells were transiently transfected with green fluorescent protein (GFP; control), wild-type EGFR, or A289V-EGFR. At 24 h after transfection, 24 cells were serum starved for 12 h and then lysed. Shown are immunoblots of immunoprecipitated EGFR (left blots) and whole cell lysates (right blots).

(B) Increased basal activity of EGFR missense mutants in human astrocytes. Immortalized human astrocytes were stably infected with wild-type EGFR or the indicated EGFR missense mutants. Shown are total phosphotyrosine (PY), Y1068-EGFR, total EGFR, and PI3K p85 (loading control) immunoblots of whole cell lysates from cells following 12 h of serum starvation. The solid arrow at the PY position represents tyrosine-phosphorylated EGFR, and the interrupted arrows indicated other differentially tyrosine-phosphorylated proteins. The inset shows an anti-EGFR immunoblot of parental astrocytes (far-left lane) and stable astrocyte subclones (designated in remaining five lanes) growing in full serum.

(C) Basal receptor phosphorylation and EGF-responsiveness of wild-type EGFR and four different EGFR ectodomain mutants stably expressed in Ba/F3 murine hematopoietic cells. Shown are immunoblots of stable Ba/F3 subclones after 12 h of serum starvation (– EGF) and 15 min following EGF-induction (0.5 or 5 ng/ml EGF).

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We have identified novel oncogenic missense mutations in the ectodomain of EGFR in glioma. The association of these mutations with increased EGFR gene dosage raises the possibility of independent clones arising from a common progenitor with EGFR amplification. We also identified the R108K EGFR mutation in 7% (1/15) gliomas that failed EGFR kinase inhibitor therapy, but loss of PTEN in this tumor provides a potential explanation for treatment failure (Table S3). Larger clinical trials are required to ascertain the contribution of EGFR missense mutants to EGFR kinase inhibitor response in glioblastoma.

**Discussion**

We have identified novel oncogenic missense mutations in the ectodomain of EGFR in glioma. The association of these mutations with increased EGFR gene dosage raises the
question of whether similar ectodomain missense mutations might exist in other malignancies with EGFR amplification or polysomy of Chromosome 7. More broadly, our results suggest that ectodomain missense mutations in other tyrosine kinase genes may be transforming events in multiple cancers, arguing for an extension of current kinase gene resequencing efforts beyond the kinase domains [40,41].

The ligand-independent basal phosphorylation of the EGFR missense mutants in our study is consistent with their ability to confer NIH-3T3 cells with the ability to grow in soft agar in the absence of exogenous EGF. Whether all EGFR ectodomain mutations share a common mechanism of oncogenic receptor conversion warrants further study. A common mechanism is suggested by the structural observation fact that many of the resulting amino acid substitutions map to interdomain interfaces. R108K and A289V/D/T occur at the domain I/II interface, P596L and G598V occur at the domain II/IV contact, and T263P occurs in domain II just before the extended loop that contacts domain IV (Figure 4B). Differences in constitutive receptor activity (G598V>A289V>T263P), on the other hand, point toward alternative mechanisms of oncogenic receptor conversion.

Three of the EGFR missense mutations (encoding P596L, G598V, and A289V) were previously observed in smaller cohorts of glioblastoma tumors [24,42]. The identification of additional ectodomain mutations in our study might have been facilitated by the large number of tumors, near-complete coverage of the EGFR coding sequence, and use of MALDI-TOF mass spectrometry genotyping in addition to Sanger sequencing. Since most of the patients in our study were of Northern European descent, we were unable to establish whether the prevalence of EGFR ectodomain mutations in glioblastoma might be affected by ethnicity as has been shown for EGFR kinase domain mutations. The distribution of EGFR missense mutations in glioblastoma (largely extracellular) and lung cancer (exclusive kinase domain) suggests fundamental differences in oncogenic EGFR signaling between these two tumor types. Importantly, however, both classes of mutants—as well as EGFRVIII—appear to sensitize transformed cells to EGFR kinase inhibitors in a preclinical model system that has been predictive of clinical responses [33,43]. Based on the experience with kinase inhibitors for chronic myeloid leukemia [44], the development of sensitive methodologies to monitor the EGFR pool before and during therapy will constitute an important step in advancing the current use of EGFR kinase inhibitors for cancer.

Supporting Information

Table S1. PCR and Extension Primers for MALDI-TOF Mass Spectrometry Genotyping of 24 SNPs

<table>
<thead>
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<td>The GenBank (<a href="http://www.ncbi.nlm.nih.gov">http://www.ncbi.nlm.nih.gov</a>) accession numbers of the proteins discussed in this paper are human EGFR protein (NM_005228), ERBB2 (NM_004448), ERBB3 (NM_001982), and the EGFR protein of Mus musculus (NM_001982), Rattus norvegicus (NM_001982), Sus scrofa (NM_214007), Danio rerio (NM_194424), Drosophila melanogaster (NM_057410), and Xiphophorus (X56319).</td>
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Competing Interests: RB owns shares in AstraZeneca, maker of gefitinib. MM does consulting for Novartis Pharmaceuticals and receives research support from Novartis Pharmaceuticals and Genentech. WRS is an employee of Novartis Pharmaceuticals.

References


Editors’ Summary

Background. Normally, cell division (which produces new cells) and cell death are finely balanced to keep the tissues and organs of the human body in working order. But sometimes, cells acquire changes (mutations) in their genetic material that allow them to divide uncontrollably to form cancers—life-threatening, disorganized masses of cells. Cancer treatments often involve drugs that kill rapidly dividing cells but, although these hit cancer cells hardest, they also damage some normal tissues. Now, though, some of the specific changes that allow cancer cells to divide uncontrollably have been identified and drugs that attack only these abnormal cells are being developed. One of these—erlotinib—inhibits the activity of epidermal growth factor receptor (EGFR), a “receptor tyrosine kinase” that sits in the cell membrane. The interaction of epidermal growth factor (EGF)—a messenger protein—with the extracellular portion (or domain) of EGFR activates its intracellular part (a kinase enzyme). This adds phosphate groups to tyrosine (an amino acid) in proteins that form part of a signaling cascade that tells cells to divide. Cancer cells often have alterations in EGFR signaling. Some have extra copies of the EGFR gene (EGFR amplification); others make a short version of EGFR that is always active because it lacks the extracellular domain that binds EGF; yet others contain EGFR that is permanently active because of mutations in its kinase domain.

Why Was This Study Done? Erlotinib can help only patients whose tumor growth is dependent on EGFR signaling. To identify these patients it is necessary to have a detailed catalog of the mutations that occur in EGFR in tumors and to know which mutations drive uncontrolled cell growth. In this study, the researchers have catalogued and characterized the mutations in EGFR that occur in glioblastoma, a deadly type of brain tumor. The researchers chose this tumor type for their study because EGFR amplification and loss of the extracellular domain of EGFR are both common in glioblastomas and because about one in five patients with glioblastoma responds well to EGFR kinase inhibitors.

What Did the Researchers Do and Find? The researchers sequenced the whole coding sequence of the EGFR gene in more than 100 glioblastomas. Nearly 15% of the tumors contained missense mutations—changes that alter the amino acid sequence of EGFR. Only one tumor had a mutation in the EGFR kinase domain; the rest had mutations in its extracellular domain. To test whether these newly identified mutations might contribute to cancer development (oncogenesis), the researchers introduced mutated or normal EGFR genes into nontumorigenic mouse cells. Only the cells that contained the mutated EGFR genes formed tumors when injected into mice, indicating that the nontumorigenic cells had been “transformed” into cancer cells by the mutated EGFR genes. Finally, the researchers showed that EGFR containing the extracellular missense mutations had kinase activity in the absence of EGF when expressed in human and mouse cells, and that the growth of cells transformed by expression of the mutated genes was sensitive to erlotinib.

What Do These Findings Mean? These findings identify missense mutations in the extracellular domain of EGFR as a new way to oncogenically activate this protein. Until now researchers have concentrated on the kinase domain of this and other receptor tyrosine kinases in their search for oncogenic mutations, but the results of this study suggest that future searches should be much broader. The distribution of EGFR missense mutations in glioblastoma contrasts with that in lung cancer, in which alterations in EGFR signaling are also implicated in cancer development but all the oncogenic mutations are in the kinase domain. Fortunately, EGFR kinase inhibitors like erlotinib have broad activity: They inhibit the growth of cells transformed by the expression of EGFR containing extracellular domain mutations or kinase mutations, or by the expression of the short EGFR variant. This bodes well for the use of these drugs in patients with glioblastoma. However, before these inhibitors become a standard part of cancer treatments, sensitive techniques need to be developed to analyze tumors for these mutations so that the patients who will benefit from these targeted therapies can be identified.

Additional Information. Please access these Web sites via the online version of this summary at http://dx.doi.org/10.1371/journal.pmed.0030485.
- MedlinePlus encyclopedia entries on cancer and on brain tumors
- US National Cancer Institute information for patients and professionals on brain tumors
- Wikipedia pages on protein kinases, epidermal growth factor receptor, and erlotinib (note that Wikipedia is a free online encyclopedia that anyone can edit)