Epidermal Growth Factor Receptor Expression Identifies Functionally and Molecularly Distinct Tumor-Initiating Cells in Human Glioblastoma Multiforme and Is Required for Gliomagenesis

Stefania Mazzoleni1,5, Letterio S. Politi2, Mauro Pala6, Manuela Cominelli7, Alberto Franzin3, Lucia Sergi Sergi4, Andrea Falini2, Michele De Palma4, Alessandro Bufone8, Pietro L. Poliani7, and Rossella Galli1

Abstract

Epidermal growth factor receptor (EGFR) is a known diagnostic and, although controversial, prognostic marker of human glioblastoma multiforme (GBM). However, its functional role and biological significance in GBM remain elusive. Here, we show that multiple GBM cell subpopulations could be purified from the specimens of patients with GBM and from cancer stem cell (CSC) lines based on the expression of EGFR and of other putative CSC markers. All these subpopulations are molecularly and functionally distinct, are tumorigenic, and need to express EGFR to promote experimental tumorigenesis. Among them, EGFR-expressing tumor-initiating cells (TIC) display the most malignant functional and molecular phenotype. Accordingly, modulation of EGFR expression by gain-of-function and loss-of-function strategies in GBM CSC lines enhances and reduces their tumorigenic ability, respectively, suggesting that EGFR plays a fundamental role in gliomagenesis. These findings open up the possibility of new therapeutically relevant scenarios, as the presence of functionally heterogeneous EGFRpos and EGFRneg TIC subpopulations within the same tumor might affect clinical response to treatment. Cancer Res; 70(19): 7500–13. ©2010 AACR.

Introduction

In the last 10 years, the identification of putative cancer stem cells (CSC) in different types of tumors has raised many expectations. CSCs represent a rare fraction of the tumor bulk, uniquely responsible for tumor initiation and progression and, as such, are envisioned as elective targets of therapy (1, 2). The CSC model of tumorigenesis has been convincingly validated in many hemopoietic malignancies (3) and in solid tumors such as breast and colon cancers (4–7). However, in other tumors, CSCs seem to make up the majority of cells within the tumor bulk and all exhibit tumor-initiating ability, thus being more appropriately called tumor-initiating cells (TIC; refs. 8–11).

This last model might also apply to glioblastoma multiforme (GBM), as soundly shown by recent studies in cultured CSC lines (12, 13). To test whether this concept might hold true in specimens from patients with primary GBM, we selected the epidermal growth factor receptor (EGFR) as a prospective GBM CSC marker (14, 15). EGFR expression in GBM has both diagnostic and prognostic significance (16–19) and is associated with tumor progression (20). Likewise, EGFR gene amplification is positively correlated with molecularly defined GBM subclasses, characterized by active proliferation and poor prognosis (21). Valuable preclinical information has also been obtained by modulating EGFR expression in standard serum-cultured glioma cell lines (22–25) and by using these in vitro cultures for testing different therapeutic approaches (26).

Here, we investigated the biological significance of EGFR expression in human primary GBM by assessing its functional role in tumor cell fractions purified from several GBM patient–derived specimens and by validating it in GBM CSC lines, which reproduce the genotypic and phenotypic characteristics of GBM more faithfully than standard glioma cell lines (27, 28). By this experimental strategy, we identified multiple subpopulations of GBM TICs, each characterized by a distinct gene signature and tumorigenic potential, and thus being able to reproduce the diverse pathologic and functional features of GBM, such as invasive and angiogenic behavior.
Our findings unequivocally associate EGFR expression with specific biological functions and molecular traits in distinct GBM cell subpopulations, thus providing relevant preclinical information to be exploited for the development of TIC subpopulation–targeted effective therapies.

Materials and Methods

Collection and processing of patients’ specimens

GBM specimens were collected from patients with histologic diagnosis of primary GBM (WHO grade 4 glioma) in accordance with the protocol approved by the institutional review board of San Raffaele Scientific Institute (01-CSC07). Tumor diagnosis and grading were blind-reviewed by different pathologists at two distinct institutions. Samples that did not satisfy the inclusion criteria of primary GBMs (e.g., GBM with oligodendroglioma features) were excluded from the study. See Supplementary Experimental Procedure for processing methods.

Immunohistochemical staining

Four-micrometer sections were cut from paraffin blocks and were stained with mouse antihuman EGFR, mouse anti-CD31 (all DakoCytomation), rabbit anti-SOX2 (Abcam), mouse anti-Bmi1, and mouse anti-CD15 (Becton Dickinson). Sections were then incubated with a secondary antibody (ChemMATE Envision Rabbit/Mouse, DakoCytomation).

Molecular analysis

Total RNA from GBM tumor specimens and from CSC lines was extracted using the RNeasy Micro and Mini Kits (Qiagen). cDNA was obtained by using Superscript RNaseH− reverse transcriptase (Invitrogen). All cDNAs were normalized to the β-actin reverse transcription-PCR (RT-PCR) product. Standard RT-PCR for EGFRvIII was done as described in ref. 29.

Fluorescence-activated cell sorting

Following enzymatic and mechanical dissociation, cells from primary GBM tissues and from experimental xenografts were stained with rabbit antihuman EGFR (clone EGRF1, AbD Serotec), rat antihuman CD34/CD45/CD11b (Becton Dickinson), antihuman AC133 (Miltenyi), mouse anti-CD15 (clone MMA, Becton Dickinson), and antihuman pan-HLA (Becton Dickinson). Cells were sorted on a Becton Dickinson FACSVantage SE FACSDiVa. The purity of each cell fraction ranged between 90% and 99%. Fluorescence-activated cell sorting (FACS) analysis of CSC lines was done as described above, without enzymatic digestion.

Culture propagation, population analysis, and cloning

Established GBM CSCs were cultured as previously described (27).

Microarray-based gene expression profiling

See Supplementary Experimental Procedure for details.

Evaluation of CSC tumorigenicity by orthotopic implantation

Tumorigenicity was determined by injecting all the distinct cell preparations orthopothetically in nu/nu mice (27). Magnetic resonance imaging (MRI) analysis was performed as described in Supplementary Experimental Procedure.

Immunofluorescence analysis was performed on cryostat sections using mouse monoclonal antihuman EGFR (1:100; Calbiochem). Details can be found in Supplementary Data.

Western blotting

Lysates from GBM tissues and CSCs were immunoblotted according to standard protocols. The primary antibodies used were rabbit anti-EGFR, rabbit anti–phosphorylated EGFR (Tyr1068; Cell Signaling), rabbit anti-ErbB2 (Calbiochem) and rabbit anti-ErbB3 (Santa Cruz Biotechnology), rabbit anti–phosphorylated mitogen-activated protein kinase (MAPK; Cell Signaling), and rabbit anti–phosphorylated Akt (Ser473) (Cell Signaling). As a loading control, a mouse anti–β-tubulin antibody was used (Sigma-Aldrich).

Lentiviral vector generation, production, and cell infection

Human wild-type (wt) EGFR cDNA (Upstate) was cloned into the monocistronic transfer lentivector pCCL.sin,cPPT.PGK.GFP.WPRE11. CSCs were transduced with 1 × 107 transduction units/mL of lentiviral vectors for 16 hours.

Lentiviral vectors coding for shRNAs targeted against the human EGFR were purchased from Sigma (Mission RNAi). Infection of CSCs was performed according to the manufacturer’s instructions.

Immunofluorescence and fluorescence in situ hybridization

Immunofluorescence was performed as described in ref. 27, using mouse antihuman EGFR (Calbiochem) and rabbit polyclonal anti-GFP (Molecular Probes). Fluorescence in situ hybridization (FISH) was performed using the kit from Dako, according to the manufacturer’s instructions. Filamentous actin (F-actin) was stained by TRITC-conjugated phalloidin (Chemicon).

Pharmacologic EGFR inhibition in CSCs

AG1478 (Calbiochem) was used at the indicated final concentrations in complete medium. DMSO was used at the same concentration as the vehicle control. Cell proliferation was measured by an MTT incorporation assay.

Invasion assays

Invasion assays were performed in Matrigel-coated 8-μm-pore Transwell chambers (Corning Costar). EGFRααααααα and EGFRmCSCs were seeded in sister cultures on the upper side of the chambers in complete medium and allowed to migrate for 5 and 7 days, respectively, with or without AG1478. Noninvaded cells on the upper side of the filters were or were not scraped off, and those that migrated to the lower side were fixed and stained by using DiffQuick (Dade Behring). The extent of cell migration was normalized.
to the total number of viable cells in the corresponding unscraped culture.

Results

EGFR expression identifies distinct cell subpopulations within human primary GBM and GBM CSC lines

Several GBM surgical specimens were tested for EGFR mRNA expression by both microarrays and semiquantitative RT-PCR and all were shown to express the transcript (Table 1). However, immunohistochemistry on corresponding paraffin-embedded sections showed that, in agreement with the literature, only 50% of specimens were characterized by diffuse EGFR staining, which was particularly intense in small-sized round tumor cells (EGFRpos tumor samples; Fig. 1A, Supplementary Fig. S1). Accordingly, the other specimens displayed negligible EGFR expression that was restricted mostly to tumor-infiltrating inflammatory cells (EGFRneg tumor samples; Fig. 1A). Western blotting (WB) analysis confirmed the immunohistochemistry findings (Fig. 1B). Hence, EGFR protein distribution identifies two main distinct subtypes of human GBM (16).

By FISH, a subset of EGFRpos tumor specimens showed EGFR gene amplification and expression of mutant EGFRVIII that, in some patients, correlated with EGFR protein levels (Fig. 1C and D; Table 1). Interestingly, EGFRpos tumors contained small and thin CD31-positive vessels (Fig. 1E), whereas EGFRneg tumors were characterized by an actively proliferating vasculature [mean vessel area (±SEM), 833.1 ± 214.1 and 2,500.2 ± 615.1 µm² in EGFRpos and EGFRneg GBMs, respectively; P > 0.05, Student’s t test; n = 7; Fig. 1E]. All specimens expressed similar levels of stem cell–associated proteins, such as Sox2 and BMI1 (Fig. 1F), and of glial fibrillary acidic protein (GFAP; data not shown).

Interestingly, whereas immunohistochemistry indicated that EGFR was expressed in the totality of GBM cells, flow cytometry suggested that EGFR expression could be retrieved only in a smaller proportion of cells. Of note, within this EGFRpos cell fraction, a conspicuous subset of cells colabeled with the endothelial marker CD34 and the hematopoietic markers CD45 and CD11b (Fig. 1G), indicating that they were stromal cells. The CSC marker CD133 (30) was more expressed in proper tumor cells than in stromal cells in EGFRpos tumors, whereas the opposite was detected in EGFRneg tumors. On the contrary, CD15 was always more expressed in the stromal cell compartment in both EGFRpos and EGFRneg tumors (refs. 31, 32; Supplementary Table S1).

Thus, the frequency of EGFRpos proper tumor cells in GBM, calculated after the exclusion of stromal cells, ranged from 0% to 35% of the total tumor cell number (Table 1). Of note, some EGFRpos proper tumor cells also labeled with AC133 and/or CD15 markers, whereas EGFRneg cells did not (Fig. 1F and H; Supplementary Table S2).

To formally show that EGFR might also play a role in the biology of GBM CSCs in vitro, we tested 13 GBM CSC lines previously validated for being bona fide CSC lines (Supplementary Fig. S2). All CSC lines expressed EGFR mRNA, whereas only 5 of 13 CSC lines also expressed the EGFR protein (Table 2). Among the EGFRpos CSC lines, only 6% to 70% of cells expressed the receptor, suggesting that multiple GBM subpopulations could also be identified based on EGFR expression in CSC lines.

Interestingly, many EGFRpos and EGFRneg CSC lines contained AC133pos and CD15pos cells (Table 2; Supplementary Table S3). However, one of five EGFRpos CSC lines and four of eight EGFRneg CSC lines did not contain any AC133pos and CD15pos cells at all.

EGFR expression identifies GBM subpopulations with a distinctive gene signature

To molecularly analyze the above-described GBM subpopulations, we purified them from (a) EGFRpos single patients’ tumor specimens, (b) EGFRneg specimens, and (c) EGFRpos CSC lines.

EGFRpos patient samples T1224, T0131, T0222, and T0321 contained (a) EGFRpos/AC133neg cells (region R1), (b) EGFRpos/AC133pos cells (R2), and (c) EGFRneg/AC133neg (R3) cells. Two of them also contained a small proportion of EGFRpos/CD15pos cells (Fig. 2A and B; Supplementary Table S2). Stromal cells were excluded from sorting.

Immediately after cell sorting and purity assessment, without any in vitro manipulation, the different GBM fractions were subjected to transcriptional profiling by whole-transcript microarrays (Fig. 2C). EGFRpos cell subpopulations displayed a specific molecular signature clearly distinguishable from that of double-negative cells (R3). Of note, a subset of 163 genes was differentially expressed between EGFRpos and EGFRneg cell subpopulations, even when isolated from distinct patient specimens, suggesting that EGFR expression in GBM might affect common molecular determinants (Supplementary List S1). In addition to EGFR, the differentially expressed genes (DEG) upregulated in EGFRpos versus EGFRneg GBM fractions were related to biological processes such as tumor invasion and progression [e.g., peristin (POSTN), LMO3, and AQP4]. Conversely, genes overexpressed in EGFRneg GBM fractions were mostly involved in the interaction of tumor cells with the microenvironment [e.g., PDGFRB, Notch3, PTPRK, luciferin (LUM), and endothelin receptor A (EDNRA)]. Thus, GBMs contain molecularly distinct subpopulations of tumor cells.

When the same freshly isolated cell fractions were cultured in vitro by the NeuroSphere Assay under limiting dilution conditions (33), EGFRpos cell fractions gave rise to a higher frequency of secondary neurospheres than EGFRneg cells (Fig. 2D).

Cell subpopulations expressing different levels of EGFR were also purified from EGFRpos CSC lines (Fig. 2E–G). Immediately after sorting, EGFRhigh (R4), EGFRlow (R5), and EGFRneg (R6) CSC subpopulations were validated by WB (Fig. 2H) and subjected to transcriptional profiling, which indicated that each subpopulation was molecularly distinct from the others (Fig. 2I; Supplementary List S2). Of note, genes upregulated in EGFRhigh and EGFRlow versus EGFRneg fractions were also highly expressed in the most malignant
molecular subclasses of primary GBM (i.e., the proliferative and mesenchymal subtypes, as identified in refs. 21 and 34; Supplementary Fig. S3). Likewise, genes downregulated in EGFRpos fractions were also downregulated in the same malignant molecular subtypes.

As shown by clonogenic assays performed under limiting dilution conditions and by long-term population analysis, EGFRlow and EGFRneg cell fractions displayed the highest proliferative capacity, whereas EGFRhigh cell subpopulations showed a transiently reduced growth ability that required a few subculturing passages to be completely restored to the presorting levels (Fig. 2J). All subpopulations contained the same percentage of Bmi1- and Sox2-expressing cells, which was not affected by cell differentiation (Supplementary Fig. S4). When tested immediately after sorting, EGFR high and EGFRlow fractions contained 100% of EGFRpos cells, whereas EGFRneg fractions were devoid of any EGFRpos cells (Fig. 2K). However, after several subculturing passages, each cell

Table 1. EGFR expression in GBM patients’ tumor specimens

<table>
<thead>
<tr>
<th>Patient code</th>
<th>WHO tumor stage</th>
<th>Age/sex</th>
<th>EGFR wt mRNA</th>
<th>EGFR vIII mRNA</th>
<th>EGFR gene amplification</th>
<th>EGFR protein expression (% of positive cells)</th>
<th>EGFR protein expression (membrane staining intensity)</th>
</tr>
</thead>
<tbody>
<tr>
<td>T0131</td>
<td>IV</td>
<td>58/M</td>
<td>2+</td>
<td>0</td>
<td>High amplification</td>
<td>70–90</td>
<td>3+</td>
</tr>
<tr>
<td>T0222</td>
<td>IV</td>
<td>57/F</td>
<td>2+</td>
<td>1+</td>
<td>High amplification</td>
<td>80–100</td>
<td>3+</td>
</tr>
<tr>
<td>T1210</td>
<td>IV</td>
<td>56/M</td>
<td>2+</td>
<td>0</td>
<td>High amplification</td>
<td>80–100</td>
<td>3+</td>
</tr>
<tr>
<td>T1224</td>
<td>IV</td>
<td>59/M</td>
<td>2+</td>
<td>1+</td>
<td>High amplification</td>
<td>70–90</td>
<td>3+</td>
</tr>
<tr>
<td>T0418</td>
<td>IV</td>
<td>63/M</td>
<td>1+</td>
<td>0</td>
<td>High polysomy</td>
<td>70–90</td>
<td>2+</td>
</tr>
<tr>
<td>T0625</td>
<td>IV</td>
<td>74/F</td>
<td>1+</td>
<td>0</td>
<td>Low amplification</td>
<td>70–90</td>
<td>2+</td>
</tr>
<tr>
<td>T0321</td>
<td>IV</td>
<td>59/M</td>
<td>2+</td>
<td>1+</td>
<td>High amplification</td>
<td>70–90</td>
<td>3+</td>
</tr>
</tbody>
</table>

EGFRpos GBMs

<table>
<thead>
<tr>
<th>Patient code</th>
<th>Total EGFRpos cells (%)</th>
<th>EGFRpos tumor cells (%)</th>
<th>EGFRpos stromal cells (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>T0131</td>
<td>20.8</td>
<td>4.0</td>
<td>16.8</td>
</tr>
<tr>
<td>T0222</td>
<td>76.8</td>
<td>35.2</td>
<td>41.6</td>
</tr>
<tr>
<td>T1210</td>
<td>13.7</td>
<td>10.7</td>
<td>3.0</td>
</tr>
<tr>
<td>T1224</td>
<td>78.1</td>
<td>20.3</td>
<td>57.8</td>
</tr>
<tr>
<td>T0418</td>
<td>36.6</td>
<td>12.4</td>
<td>24.2</td>
</tr>
<tr>
<td>T0625</td>
<td>22.4</td>
<td>8.9</td>
<td>13.5</td>
</tr>
<tr>
<td>T0321</td>
<td>39.1</td>
<td>21.7</td>
<td>17.4</td>
</tr>
</tbody>
</table>

EGFRneg GBMs

<table>
<thead>
<tr>
<th>Patient code</th>
<th>Total EGFRneg cells (%)</th>
<th>EGFRneg tumor cells (%)</th>
<th>EGFRneg stromal cells (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>T0104</td>
<td>4.9</td>
<td>0.9</td>
<td>4.0</td>
</tr>
<tr>
<td>T0109</td>
<td>17.3</td>
<td>0.0</td>
<td>17.3</td>
</tr>
<tr>
<td>T0125</td>
<td>19.0</td>
<td>1.6</td>
<td>17.4</td>
</tr>
<tr>
<td>T0130</td>
<td>25.3</td>
<td>3.3</td>
<td>22.0</td>
</tr>
<tr>
<td>T0325</td>
<td>0.0</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td>T0512</td>
<td>4.4</td>
<td>0.0</td>
<td>4.4</td>
</tr>
<tr>
<td>T1003</td>
<td>7.5</td>
<td>0.0</td>
<td>7.5</td>
</tr>
</tbody>
</table>

NOTE: FISH scores: high gene amplification, >10 gene copies in >10% of the cells; low gene amplification, 6 to 10 gene copies in >10% of the cells; high polysomy, >4 gene copies in >40% of the cells; low polysomy, >4 gene copies in >10% but <40% of the cells; no amplification, 1 to 4 gene copies. Immunohistochemistry scores: 3+, very intense membrane staining; 2+, intense membrane staining; 1+, moderate staining; 0, no staining.
Figure 1. EGFR expression identifies distinct cell subpopulations within primary human GBM. A, EGFRpos GBM tumors show diffuse and intense reactivity for EGFR in small and round neoplastic cells (T1224). EGFRneg GBM specimen shows EGFR staining restricted to tumor-infiltrating inflammatory cells (black arrow; T0109). Magnification, ×400 and ×800. B, WB confirms EGFR protein levels in GBM patients’ specimens. C, FISH analysis indicates that the EGFR gene is amplified only in EGFRpos tumors. D, the mutant EGFRvIII can be detected in a subset of EGFRpos tumors by RT-PCR. E, EGFRneg tumors contain modestly proliferating vessels (arrows), whereas EGFRpos tumors show an enlarged and proliferating vasculature (arrows). H&E and CD31 staining; magnification, ×200 and ×400. F, EGFRpos and EGFRneg tumors contain similar numbers of Sox2 and Bmi1pos cells. CD15pos proper tumor cells can be detected only in EGFRpos (arrow at bottom right, CD15pos monocytes within a vessel). Magnification, ×400. G, in EGFRpos tumors, many EGFRpos cells are proper tumor cells, whereas in EGFRneg tumors the few EGFRpos cells are stromal/inflammatory cells. H, the EGFRpos fractions from EGFRpos specimens contain AC133pos and CD15pos cells (top middle), which are either tumor cells or stromal cells. On the contrary, EGFRneg fractions (top right) and EGFRneg GBM tumors (bottom) contain only stromal AC133pos and CD15pos cells.
fraction regenerated the same frequency of EGFR pos and EGFRneg cells found in the parental bulk population, recapitulating the original cellular heterogeneity (Fig. 2K).

EGFR expression confers increased tumorigenic capacity to GBM cells

To assess whether EGFR expression might affect the tumorigenic ability of GBM cells, R1, R2, and R3 fractions, purified from EGFRpos GBM specimens, were transplanted into the brain of nu/nu mice, without any prior in vitro manipulation (Fig. 3A; Supplementary Fig. S1). MRI-based volumetric analysis showed that EGFRpos cells were characterized by enhanced tumorigenic capacity (Fig. 3A). However, EGFRneg/AC133neg cells were also capable of initiating tumors, although these developed significantly more slowly than those generated by EGFRpos GBM cells (Kaplan-Meier analysis; Fig. 3B).

Notably, EGFR expression was retrieved not only in xenografts derived from EGFRpos cells but also in those derived from EGFRneg fractions (Fig. 3C–E). Importantly, the latter xenografts never contained either AC133pos cells (Fig. 3E) or CD15pos cells (Fig. 3F, Supplementary Fig. S1). Thus, as recently shown for other stem cell markers in melanoma (35), EGFR expression in GBM TICs is dynamically regulated, given that EGFRneg cells can become EGFRpos on transplantation. Most importantly, EGFR expression positively correlates with gliomagenesis.

Although R1-, R2-, and R3-derived xenografts showed the same expression of SOX2 and Bmi1 (Fig. 3G and data not shown), they were molecularly different (Fig. 3H). By microarray-based analysis, proinvasive genes were overexpressed in EGFRpos cell–derived xenografts, whereas genes involved in angiogenesis were upregulated in EGFRneg cell–derived xenografts (Supplementary Fig. S5).

In agreement with these latter findings and with molecular data obtained on EGFRpos and EGFRneg subpopulations (Fig. 2C), xenografts from EGFRpos cells were shown to be highly invasive, with cells spreading preferentially along the gray matter while avoiding white matter fiber tracts (Fig. 3C and G; Supplementary Figs. S1 and S6). On the contrary, tumors formed by EGFRneg cells showed well-demarcated boundaries, with cells migrating preferentially along white matter tracts (Fig. 3C and G; Supplementary Figs. S1 and S6). Accordingly, EGFRpos cell–induced xenografts were characterized by thin, regularly shaped blood vessels and a low proliferative index, whereas tumors from EGFRneg cells contained enlarged and proliferating vessels and a higher frequency of mitotic cells (Supplementary Figs. S1 and S6).

Thus, EGFR expression confers different invasive, angiogenic, and tumorigenic abilities to GBM cells in vivo.

Notably, the same functional differences observed between xenografts generated by EGFRpos and EGFRneg TICs purified from GBM specimens could also be detected in xenografts

### Table 2. Characterization of EGFR<sup>pos</sup> and EGFR<sup>neg</sup> GBM CSC lines for their expression of the putative CSC enrichment markers AC133 and CD15

<table>
<thead>
<tr>
<th>CSC line code</th>
<th>EGFR wt mRNA</th>
<th>EGFR vIII mRNA</th>
<th>EGFR gene amplification (FISH)</th>
<th>PTEN expression (WB)</th>
<th>EGFR&lt;sup&gt;pos&lt;/sup&gt; cells (%)</th>
<th>AC133&lt;sup&gt;pos&lt;/sup&gt; cells (%)</th>
<th>CD15&lt;sup&gt;pos&lt;/sup&gt; cells (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>EGFR&lt;sup&gt;pos&lt;/sup&gt; CSC lines</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>L0627</td>
<td>2+</td>
<td>0</td>
<td>High amplification</td>
<td>2+</td>
<td>25.8 ± 3.5</td>
<td>42.9 ± 15.2</td>
<td>22.3 ± 2.9</td>
</tr>
<tr>
<td>L0804</td>
<td>2+</td>
<td>0</td>
<td>Low polysomy</td>
<td>0</td>
<td>7.7 ± 1.2</td>
<td>5.9 ± 0.9</td>
<td>2.7 ± 1.0</td>
</tr>
<tr>
<td>L0306</td>
<td>2+</td>
<td>0</td>
<td>Low polysomy</td>
<td>3+</td>
<td>21.1 ± 3.0</td>
<td>0.0</td>
<td>28.1 ± 2.9</td>
</tr>
<tr>
<td>L0201</td>
<td>2+</td>
<td>0</td>
<td>High polysomy</td>
<td>1+</td>
<td>79.1 ± 3.9</td>
<td>3.1 ± 1.5</td>
<td>13.7 ± 0.9</td>
</tr>
<tr>
<td>L0605</td>
<td>2+</td>
<td>0</td>
<td>Low polysomy</td>
<td>0</td>
<td>8.5 ± 2.8</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td><strong>EGFR&lt;sup&gt;neg&lt;/sup&gt; CSC lines</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>L0104</td>
<td>1+</td>
<td>0</td>
<td>No amplification</td>
<td>0</td>
<td>2.0 ± 0.8</td>
<td>30.1 ± 13.8</td>
<td>50.8 ± 3.2</td>
</tr>
<tr>
<td>L0223</td>
<td>1+</td>
<td>0</td>
<td>No amplification</td>
<td>3+</td>
<td>0.0</td>
<td>0.0</td>
<td>10.7 ± 1.3</td>
</tr>
<tr>
<td>L0125</td>
<td>1+</td>
<td>0</td>
<td>No amplification</td>
<td>1+</td>
<td>0.0</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td>L1210</td>
<td>1+</td>
<td>0</td>
<td>No amplification</td>
<td>0</td>
<td>2.4 ± 1.2</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td>L0314</td>
<td>1+</td>
<td>0</td>
<td>No amplification</td>
<td>3+</td>
<td>0.0</td>
<td>0.0</td>
<td>5.9 ± 1.7</td>
</tr>
<tr>
<td>L0325</td>
<td>1+</td>
<td>0</td>
<td>No amplification</td>
<td>0</td>
<td>0.0</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td>L0512</td>
<td>1+</td>
<td>0</td>
<td>No amplification</td>
<td>3+</td>
<td>1.7 ± 0.6</td>
<td>2.1 ± 1.4</td>
<td>11.7 ± 2.9</td>
</tr>
<tr>
<td>L0418</td>
<td>1+</td>
<td>0</td>
<td>No amplification</td>
<td>0</td>
<td>0.0</td>
<td>18.2 ± 4.5</td>
<td>0.0</td>
</tr>
</tbody>
</table>

**NOTE:** EGFR wt and EGFRvIII mRNA levels were measured by semiquantitative RT-PCR. EGFR, AC133, and CD15 expression was measured by flow cytometry. High gene amplification, >10 gene copies in >10% of the cells; low gene amplification, 6 to 10 gene copies in >10% of the cells; high polysomy, >4 gene copies in >40% of the cells; low polysomy, >4 gene copies in >10% but <40% of the cells; no amplification, 1 to 4 gene copies. The frequency of EGFR<sup>pos</sup> cells within EGFR<sup>pos</sup> CSC lines remained stable throughout extensive subculturing. Likewise, EGFR<sup>neg</sup> CSC lines were never shown to comprise EGFR<sup>pos</sup> cells even at very high subculturing passages.
Figure 2. EGFR expression identifies GBM subpopulations with distinctive gene signatures and different growth characteristics in vitro. A and B, EGFR\textsuperscript{pos}/AC133\textsuperscript{-} (R1), EGFR\textsuperscript{pos}/AC133\textsuperscript{pos} (R2), and EGFR\textsuperscript{pos}/AC133\textsuperscript{-} (R3) cells were isolated from EGFR\textsuperscript{pos} tumor specimens by FACS (IgGs, isotype controls). C, global gene expression data in R1, R2, and R3 fractions purified from patients’ specimens (left). The expression of a selection of coregulated genes is highlighted in the heatmaps (right). D, limiting dilution clonogenic assay of R1, R2, and R3 fractions immediately after sorting. E, different CSC lines comprise variable amounts of EGFR\textsuperscript{pos} cells. Magnification, ×200 (insets, ×600). F, some EGFR\textsuperscript{pos} CSCs display EGFR gene amplification. G, different CSC subpopulations could be isolated by FACS from EGFR\textsuperscript{pos} CSC lines based on their EGFR expression (region R4, EGFR\textsuperscript{high} CSCs; R5, EGFR\textsuperscript{low} CSCs; R6, EGFR\textsuperscript{neg} CSCs; L0627). H, WB analysis shows that EGFR is activated in EGFR\textsuperscript{high} and EGFR\textsuperscript{low} CSCs but is absent in EGFR\textsuperscript{neg} CSCs. I, global gene expression data of R4, R5, and R6 GBM fractions purified from EGFR\textsuperscript{pos} CSC lines. Semi-quantitative RT-PCR validation of DEGs. J, clonogenic assay and long-term growth curves of R4, R5, and R6 CSCs immediately after sorting and after in vitro culture. K, EGFR expression in CSC fractions immediately after sorting (top) and on in vitro culture (bottom; EGFR, green; magnification, ×200).
Figure 3. EGFR expression identifies TICs with different tumorigenic capacities. A, EGFR<sup>pos</sup> cell–derived tumors, independently of the coexpression of AC133, were significantly larger than tumors induced from EGFR<sup>neg</sup>AC133<sup>neg</sup> cells. P < 0.05, one-way ANOVA with Bonferroni test (n = 5, six independent experiments). B, Kaplan-Meier survival curves (P < 0.01). C, EGFR expression detected by an antihuman EGFR is retrieved in all xenografts, including EGFR<sup>neg</sup>AC133<sup>neg</sup> cell–derived tumors (EGFR, green). EGFR<sup>pos</sup> cell–derived tumors are characterized by an infiltrative pattern of growth. Tumor cells disperse within the gray matter, avoiding the corpus callosum (white arrow). EGFR<sup>pos</sup>AC133<sup>pos</sup> cells give rise to expanding tumors, mostly confined within the injection site, which migrate and invade along white matter tracts (white arrowhead). D, WB confirms EGFR protein expression in all xenografts. E, the same distinct EGFR<sup>pos</sup> and EGFR<sup>neg</sup> subpopulations as detected in the parental tumor were retrieved in the corresponding xenografts by flow cytometry. CD15<sup>pos</sup> cells (F) were not retrieved in any xenografts by immunohistochemistry. G, a similar frequency of Sox2 and Bmi1 immunoreactive cells could be retrieved in R1– and R3–derived xenografts. H, global gene expression data of R1– and R3–derived xenografts. I to J, EGFR expression confers enhanced tumorigenic potential to EGFR<sup>pos</sup> fractions from EGFR<sup>pos</sup> CSC lines (one-way ANOVA with Bonferroni test, n = 5, three independent experiments). P < 0.01, Kaplan-Meier survival curves. K, EGFR expression was retrieved in all xenografts, whereas ErbB2 was highly expressed only in EGFR<sup>pos</sup> CSC–derived tumors (WB).
generated by in vitro expanded EGFR\textsuperscript{pos} and EGFR\textsuperscript{neg} CSC lines (Supplementary Fig. S2; ref. 36).

Because EGFR expression in EGFR\textsuperscript{neg} cell–derived xenografts might be due to contaminating EGFR\textsuperscript{pos} tumor cells, we purified EGFR\textsuperscript{neg} tumor cells from EGFR\textsuperscript{neg} specimens that were totally devoid of EGFR\textsuperscript{pos}, AC133\textsuperscript{pos}, and CD15\textsuperscript{pos} proper tumor cells (Fig. 1A, G, and H; Supplementary Table S1). FACS-purified EGFR\textsuperscript{pos}/AC133\textsuperscript{neg} cells generated xenografts that expressed EGFR but were negative for AC133 and CD15, thus confirming that EGFR might indeed play a prominent role in glioma formation (Supplementary Fig. S7). Notably, both in vivo limiting dilution analysis and serial transplantation proved that all GBM subpopulations identified based on EGFR expression could be considered bona fide TICs (Supplementary Fig. S8).

The tumorigenic potential of EGFR\textsuperscript{high}, EGFR\textsuperscript{low}, and EGFR\textsuperscript{neg} cells purified from different EGFR\textsuperscript{pos} CSC lines (Figs. 2G and 3I and J and Supplementary Fig. S9 for L0627 and Supplementary Fig. S9 for L0605) was also tested. As observed for xenografts obtained from GBM specimen–derived subpopulations (Fig. 3A–E), tumors derived from EGFR\textsuperscript{high} and EGFR\textsuperscript{pos} CSCs were larger than those generated from EGFR\textsuperscript{neg} cell fractions, which, again, displayed tumor-initiating ability (Fig. 3I and J). Again, EGFR\textsuperscript{neg} CSC fraction–derived tumors expressed EGFR, confirming that EGFR upregulation occurred during experimental tumorigenesis (Fig. 3K). ErbB2 expression was detected only in EGFR\textsuperscript{high}–cell–derived tumors, suggesting that the xenografts were molecularly heterogeneous (Fig. 3K).

To understand the relationship between the expression of EGFR and that of the CSC markers CD15 and AC133 in terms of tumor-initiating potential, EGFR\textsuperscript{pos}/CD15\textsuperscript{pos} (R4), EGFR\textsuperscript{neg}/CD15\textsuperscript{neg} (R5), EGFR\textsuperscript{pos}/CD15\textsuperscript{pos} (R6), and EGFR\textsuperscript{neg} CD15\textsuperscript{neg} (R7) as well as EGFR\textsuperscript{pos}/CD15\textsuperscript{neg}/AC133\textsuperscript{neg} (R1) and EGFR\textsuperscript{neg}/CD15\textsuperscript{neg}/AC133\textsuperscript{neg} (R3) fractions were purified from L0627 and L0605 (Supplementary Fig. S9). Interestingly, EGFR\textsuperscript{pos} subpopulations, independent of the coexpression of AC133 and/or CD15, generated tumors that developed much earlier and grew larger than those generated by EGFR\textsuperscript{neg} fractions. Consistent with previous findings, CSC lines/subpopulations negative for EGFR, AC133, and CD15 generated xenografts that did not express either of the two markers in vivo but did express the EGFR (Supplementary Figs. S2 and S9).

Thus, all of our GBM CSC lines, taken as a whole or fractionated into subpopulations and independent of their basal EGFR expression, gave rise to xenografts that upregulated the EGFR significantly (Fig. 3K; Supplementary Figs. S2 and S9). To understand the mechanism underlying EGFR expression in EGFR\textsuperscript{neg} cell–derived xenografts, we hypothesized that because EGFR\textsuperscript{neg} GBM cells retain EGFR transcript expression (Tables 1 and 2; Fig. 2C and I), in vivo EGFR expression might be regulated posttranscriptionally. Indeed, when we simulated in vitro the mitogen-reduced adult brain microenvironment by starvation, EGFR\textsuperscript{neg} CSCs efficiently reexpressed the EGFR protein (Supplementary Fig. S2). Accordingly, when the same CSCs were reexposed to standard mitogen concentrations, they downregulated EGFR expression, as may occur in vivo during tumor progression when tumor-infiltrating stromal cells secrete mitogens in a paracrine fashion (37).

**Enforced EGFR expression by gene transfer increases the malignant behavior of CSCs in vitro and in vivo**

Lentiviral vector–mediated EGFR expression in three distinct EGFR\textsuperscript{neg} CSC lines allowed the expression of a fully functional receptor (Fig. 4A). Of note, the majority of EGFR-transduced cells acquired a fibroblastoid shape and developed stress fibers and actin-driven lamellipodia, all known markers of epithelial-mesenchymal transition and enhanced malignancy (Fig. 4B; Supplementary Table S4). Consistently, the average cell size was increased in most EGFR-transduced cells (Fig. 4C; Supplementary Table S4).

Gene expression profiling of naive, mock, and EGFR-overexpressing CSC lines identified a common subset of DEGs that was altered in both L0104 and L0125 CSC lines, suggesting that enforced EGFR expression affected the same molecular determinants in different patient-derived CSC lines (Fig. 4D and E). In addition to EGF, LIF, and ITGA3, genes previously shown to be also highly expressed in FACS-purified EGFR\textsuperscript{pos} CSC fractions (Fig. 2I; Supplementary List S2), proinvasive genes such as CXCL10 and ICAMI (38, 39) were upregulated in EGFR-transduced CSCs (Fig. 4D–E) and also overexpressed in the proliferative and mesenchymal subtypes of human GBM (ref. 2; Supplementary Fig. S3). Accordingly, tumor suppressors such as SPARCL1 (Fig. 2I), ERBB4, ASCL1, and EDNRB, which were downregulated in EGFR-transduced CSCs, were also downregulated in GBM malignant subtypes.

Notably, all EGFR-transduced CSC lines formed experimental tumors that were larger than those induced by the corresponding mock lines (Fig. 4F).

**Genetic loss of function of EGFR reduces the malignancy of CSCs in vitro and in vivo**

To silence EGFR expression stably, we exploited line L0201 and line L0627, which express high levels of EGFR in 70% and 30% of the cells, respectively (Table 2). The shRNA clones 204 and 206 induced EGFR protein knockdown with an efficiency of 60% and 70% in lines L0201 (Fig. 5A) and L0627 (data not shown), respectively. WB analysis confirmed the flow cytometry results and indicated an inhibition of downstream signaling pathways on EGFR silencing (Fig. 5B).

EGFR-knockdown CSCs displayed morphologic changes in vitro, with neurospheres appearing as well-differentiated cells (Fig. 5C). Consistently, the frequency of differentiated cells detected in shRNA-transduced CSCs increased under both proliferative (Fig. 5D) and differentiative culture conditions (data not shown).

Of note, tumors generated from EGFR-knockdown CSCs developed more slowly and were significantly smaller than those generated by the CTRL subclone, thus resulting in the increased survival of EGFR-knockdown CSC–transplanted mice (Fig. 5E).
Figure 4. Overexpression of EGFR enhances the tumorigenic potential of CSCs. A, lentiviral-mediated EGFR gene transfer resulted in the expression of a functional EGFR, as indicated by phosphorylation at residue Tyr1068 and by the hyperactivation of downstream pathways. B, enforced EGFR expression in EGFRneg CSCs (EGFR, red) correlates with changes in cell morphology, which are absent in GFP-transduced CSCs (GFP, green). F-actin staining (phalloidin, red). Magnifications: top, ×400; insets, ×1,000; bottom, ×1,000. C, EGFR overexpression in EGFRneg CSCs induces a significant increase in their size. FSC-A and SSC-A. D, global gene expression data in naïve, mock-transduced, and EGFR-transduced CSC lines identify a subset of DEGs that are coregulated in different patient-derived CSC lines and modulated by enforced EGFR expression (EGFR gene signature). E, semiquantitative RT-PCR validation of DEGs. F, ectopic expression of EGFR in EGFRneg CSC lines increases their tumorigenic potential and reduces mouse survival (Student’s t test, n = 5, three independent experiments).
Figure 5. Inhibition of EGFR expression and activity negatively affects the malignant behavior of CSCs. A and B, flow cytometry and WB of L0201 shRNA 204 and shRNA 206 CSC subclones indicate efficient knockdown of EGFR protein and downregulation of MAPK and Akt downstream pathways. C and D, EGFR knockdown induces CSC differentiation. Tuj1, red; GFAP, green. Magnifications: top, ×200; bottom, ×400. *, \( P > 0.05 \), Student’s t test. E, EGFR silencing in CSCs significantly decreases their tumorigenicity (one-way ANOVA with Bonferroni test, \( n = 4 \), two independent experiments). P < 0.01, Kaplan-Meier survival curves. F, AG1478 treatment inhibits the phosphorylation status of EGFR and Akt in CSCs (WB). G, EGFR\(^{\text{pos}}\) CSC lines respond to treatment by decreasing their proliferation/survival, whereas EGFR\(^{\text{neg}}\) CSC do not. *, \( P > 0.05 \); **, \( P > 0.01 \), Student’s t test. H and I, EGFR inhibition by AG1478 negatively affects the invasive ability of CSCs. **, \( P > 0.01 \), Student’s t test. J, CSC responsiveness to TKI is independent of PTEN expression (WB).
EGFRpos and EGFRneg CSC lines differentially respond to pharmacologic inhibition of EGFR

To pharmacologically inhibit EGFR activity, we exploited the EGFR tyrosine kinase inhibitor (TKI) AG1478. WB analysis of two different EGFRpos CSCs that were exposed to AG1478 for 2, 5, and 16 hours showed effective inhibition of EGFR autophosphorylation and a significant decrease in AKT phosphorylation, a hallmark of drug sensitivity (Fig. 5F).

Pharmacologic treatment of EGFRpos CSC lines with AG1478 for up to 72 hours in vitro resulted in a significant decrease in CSC survival/proliferation (Fig. 5G). Relevantly, the survival and proliferation of EGFRneg CSC lines were not affected by AG1478, even when the same lines were transduced with EGFR-coding vectors before treatment, suggesting that EGFR-overexpressing EGFRpos CSC lines did not become addicted to EGFR (data not shown). Likewise, exposure of EGFRpos CSCs to AG1478 strongly reduced their invasive capacity as compared with controls (Fig. 5H and I). Again, the invasive ability of EGFRneg CSC lines was not affected by AG1478 exposure.

Interestingly, all the EGFRpos CSC lines responded to pharmacologic treatment independently of the expression of PTEN, a putative molecular determinant of TKI responsiveness in patients with GBM (Fig. 5; ref. 40).

Thus, EGFRpos CSCs are responsive to pharmacologic inhibition by TKIs, whereas EGFRneg CSCs are not.

Discussion

EGFR expression contributes to GBM heterogeneity

GBM is characterized by a high degree of heterogeneity, which is efficaciously reflected in the definition “multiforme.” However, the intrinsic heterogeneity of GBM might refer not only to the well-known molecular diversity of GBM subtypes but also to the existence of genetically and functionally distinct cohorts of TICs within the same tumor.

In line with recent reports that provide new interpretations of the process of tumorigenesis in mouse hematopoietic malignancies (8), mouse colon cancer (41), human melanoma (10, 11), and brain tumors (42), our findings indicate that the initiation and progression of GBM may not depend on the presence of a single and rare fraction of CSCs, as proposed by the hierarchical model of tumor development (43). On the contrary, our data propose a different biological context, in which all GBM cells can be considered TICs with different degrees of stemness as proven by their different tumorigenic ability and by their distinct phenotypic and molecular features (44). In fact, all of our GBM-derived TIC subpopulations satisfy the requirements for bona fide CSCs: they self-renew in vitro and in vivo and give rise to experimental tumors that recapitulate the phenotypic traits of the tumor of origin under limiting dilution conditions and on serial transplantation.

Based on these observations, GBM tissue heterogeneity might be explained by the presence of a hierarchy of distinct TICs, as recently suggested for in vitro generated GBM CSC lines (13). These distinct TICs distribute along a gradient of tumorigenic potential that is strictly associated with EGFR expression.

Thus, our study provides conclusive evidence that the majority of GBM cells have tumorigenic capacity and that the hierarchical model of tumorigenesis might not fully apply to GBM.

Mechanisms underlying EGFR-dependent GBM heterogeneity

Tumor cells might modify their phenotype during tumor progression, with multiple cohorts of TICs being generated (45). In this study, we have shown that EGFR expression contributes to GBM cell diversity by generating different TIC populations. As to the mechanisms involved in the generation of EGFR-dependent phenotypic heterogeneity in GBM, the contribution of tumor microenvironment needs to be taken into consideration. Paracrine EGFR ligands, such as epidermal growth factor, are released by tumor stromal cells that, in this way, contribute to the activation of the EGFR signaling in both proper tumor cells and endothelial cells (37). When stroma-produced epidermal growth factor is secreted, EGFR protein downregulation occurs in target cells by receptor internalization, followed by lysosomal degradation.

In line with this view, it is tempting to speculate that the EGFRpos cell component detected in EGFRpos GBM might be generated from GBM cells that were originally EGFRpos through receptor downregulation induced by excessive ligand stimulation during tumor progression, as we simulated in vitro by modulation of mitogen concentration. In addition, termination of EGFR signaling in EGFRneg GBM cells might lead to the acquisition of compensatory additional genetic events, which might account for the molecular differences detected between EGFRpos and EGFRneg TICs. For instance, the expression of other receptor tyrosine kinases, such as PDGFRs, observed in EGFRpos TICs might contribute to their tumorigenic ability by synergizing with the EGFR re-upregulation required for experimental gliomagenesis. Indeed, PDGFR pathway activation has been recently shown to identify a GBM subtype that does not express the EGFR (46), thus suggesting that the latter GBM subtype might be sustained by EGFRneg PDGFRpos TICs.

EGFRpos and EGFRneg TICs can both give rise to experimental tumors that phenocopy the tumor of origin, and therefore, they both can be considered bona fide TICs. However, because EGFRpos TICs are characterized by enhanced tumorigenic potential and highly invasive behavior, they might be envisioned as the “actual” GBM CSCs. Conversely, EGFRneg TICs, which form tumors with low efficiency and need to re-upregulate the EGFR to be tumorigenic, might be better defined as “potential” GBM CSCs, which might be kept in a dormancy-like state by EGFR downregulation, being reactivated on exposure to appropriate stimuli when exposed to the in vivo microenvironment. In line with this notion, it has been recently shown that GBMs, which were EGFRneg in origin, expressed the EGFR on recurrence (47).
Therapeutic implications of EGFR-dependent GBM heterogeneity

The role of EGFR in the malignant progression of GBM and its effect on patient survival have been highly debated. Despite the controversial prognostic significance of EGFR expression in GBM, pharmacologic targeting of EGFR by means of TKIs has been proposed as a possible therapeutic strategy (40).

To date, single-agent EGFR inhibition in GBM did not achieve complete therapeutic efficacy. This failure has been ascribed primarily to the maintenance of a high level of Akt-dependent signaling in PTEN-mutated tumors (48) and to coactivation in the same tumor cell of multiple receptor tyrosine kinases, which might compensate for the effective inhibition of EGFR-dependent pathways (49).

By complementing these explanations, our findings suggest that the simultaneous presence of distinct TICs within the same tumor might also influence the outcome of EGFR-targeted therapies in GBM. Indeed, whereas effective inhibition of EGFR in our EGFRpos CSC lines can be achieved independently of PTEN expression, EGFRneg CSCs do not respond to treatment. By translating these results into a clinical perspective, in spite of the inhibition of the EGFRpos cell component in EGFRpos GBM, the nonresponsiveness of the EGFRneg TIC fraction to EGFR inhibitors might allow these cells to survive treatment and to support tumor relapse. Therefore, an effective therapeutic regimen should take into consideration the role of residual, nonresponder TICs. To this end, the development of a combination therapy targeted not only against the most aggressive “actual” TIC populations but also against the less malignant “potential” TICs will be necessary to improve the management of GBM.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Acknowledgments

We thank Alessio Palini and Chiara Villa for technical assistance with FACS. Antonella Iadanza for technical assistance with MRI, and Carol Stayton for editing of the manuscript.

Grant Support


The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked advertisement in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

Received 06/28/2010; accepted 07/18/2010; published OnlineFirst 09/21/2010.

References


Epidermal Growth Factor Receptor Expression Identifies Functionally and Molecularly Distinct Tumor-Initiating Cells in Human Glioblastoma Multiforme and Is Required for Gliomagenesis

Stefania Mazzoleni, Letterio S. Politi, Mauro Pala, et al.

Cancer Res 2010;70:7500-7513. Published OnlineFirst September 21, 2010.

Updated version
Access the most recent version of this article at:
doi:10.1158/0008-5472.CAN-10-2353

Supplementary Material
Access the most recent supplemental material at:
http://cancerres.aacrjournals.org/content/suppl/2010/09/20/0008-5472.CAN-10-2353.DC1

Cited articles
This article cites 49 articles, 17 of which you can access for free at:
http://cancerres.aacrjournals.org/content/70/19/7500.full.html#ref-list-1

Citing articles
This article has been cited by 23 HighWire-hosted articles. Access the articles at:
/content/70/19/7500.full.html#related-urls

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.