Tumor Epidermal Growth Factor Receptor and EGFR PY1068 Are Independent Prognostic Indicators for Head and Neck Squamous Cell Carcinoma

Sarah Wheeler1, Doris R. Siwak2, Raymond Chai1, Courtney LaValle2, Raja R. Seethala3, Lin Wang3, Kathleen Cieply5, Carol Sherer3, Corwin Joy5, Gordon B. Mills5, Athanassios Arghiris4, Jill M. Siegfried2, Jennifer R. Grandis1,2, and Ann Marie Egloff1

Abstract

**Purpose:** To assess the prognostic value of epidermal growth factor receptor (EGFR) molecular characteristics of head and neck squamous cell carcinoma (HNSCC).

**Patients and Methods:** HNSCC tumors from patients prospectively enrolled in either an Early Detection Research Network (EDRN) study and treated with surgery without an EGFR-targeted agent (N = 154) or enrolled in a chemoradiation trial involving the EGFR-targeted antibody cetuximab (N = 39) were evaluated for EGFR gene amplification by FISH and EGFR protein by immunohistochemical staining. Fresh-frozen tumors (EDRN) were also evaluated for EGFR protein and site-specific phosphorylation at Y992 and Y1068 using reverse-phase protein array (n = 67). Tumor (n = 50) EGFR and EGFRvIII mRNA levels were quantified using real-time PCR.

**Results:** EGFR expression by immunohistochemistry (IHC) was significantly higher in the EDRN tumors with EGFR gene amplification (P < 0.001), and a similar trend was noted in the cetuximab-treated cohort. In the EDRN and cetuximab-treated cohorts elevated EGFR by IHC was associated with reduced survival (P = 0.019 and P = 0.06, respectively). Elevated expression of total EGFR and EGFR PY1068 were independently significantly associated with reduced progression-free survival in the EDRN cohort [HR = 2.75; 95% confidence interval (CI) = 1.26–6.00 and HR = 3.29; 95% CI = 1.34–8.14, respectively].

**Conclusions:** In two independent HNSCC cohorts treated with or without cetuximab, tumor EGFR levels were indicative of survival. Tumor EGFR PY1068 levels provided prognostic information independent of total EGFR.

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Introduction

In the United States 36,540 oral cavity and pharynx cancers and 12,720 laryngeal cancers were diagnosed in 2010 according to population-based estimates (1). The primary challenge in the successful treatment of these cancers, more than 90% of which are squamous cell carcinoma (head and neck squamous cell carcinoma (HNSCC)), is the high rate of tumor recurrence. Most HNSCC cases are diagnosed as locoregionally advanced disease (stage III or stage IV; ref. 1). Approximately 50% of HNSCC patients treated for a locoregionally advanced primary cancer will experience disease recurrence within 5 years and most will die as a result (1).

Standard of care for locally advanced HNSCC has included multimodality treatment involving surgery with curative intent followed by radiation therapy (RT) or chemoradiotherapy (CRT ref. 2). Even with combined modality treatment, 5-year survival rates for HNSCC have largely remained unchanged since the 1970s (1). Aggressive multimodality treatments are associated with significant morbidities including reduced swallowing and communication. These morbidities require consideration of the necessity for aggressive treatment. Efforts to define treatment-relevant subpopulations of HNSCC patients have been ongoing, and the status of the epidermal growth factor receptor (EGFR) in HNSCC tumors has been a primary focus.

EGFR was recognized as contributing to HNSCC development and progression as early as the 1990s. Consequently, molecular characterization of EGFR in tumors, especially protein expression and gene amplification, has been a focus of several studies intending to define prognostic markers for HNSCC (3–18). High levels of EGFR mRNA and protein have been found in 92% and 40% to 90% of HNSCC, respectively.
Epidermal growth factor receptor (EGFR) has been recognized as contributing to head and neck squamous cell carcinoma (HNSCC) development and progression, but the prognostic value of many specific EGFR molecular characteristics have not been evaluated alone or in combination. We assessed EGFR molecular characteristics including tumor EGFR gene amplification, EGFR gene expression, EGFRvIII gene expression, EGFR protein, and phosphoprotein for a patient cohort treated with surgery with curative intent. We identified tumor EGFR protein and EGFR PY1068 levels to be independent prognostic indicators and determined that EGFR gene amplification was not an indicator of prognosis in this surgical cohort. We validated the use of EGFR tumor protein expression but not EGFR gene amplification as an indicator of prognosis in an independent cohort treated with the anti-EGFR antibody therapeutic cetuximab, thereby defining elevated EGFR tumor protein level as a prognostic rather than predictive indicator. Defining EGFR molecular characteristics relevant to patient prognosis is an important step toward deciding treatment while considering the morbidities associated with aggressive multimodal therapies. In addition to identifying important prognostic indicators, the work presented here defines relationships between different tumor EGFR molecular characteristics, thus providing insights about the aberrant regulation of EGFR.

with tumor response to EGFR tyrosine kinase inhibitors in lung cancers, have not been reported in U.S. HNSCC populations (26–30).

This study was carried out to define the relationship between EGFR gene amplification, gene expression, and protein and phosphoprotein levels in prospectively collected tumor tissues from a cohort of HNSCC patients treated with surgery with curative intent. The overall goal was to define EGFR-specific prognostic molecular characteristics and to increase our understanding of the relationships between these molecular characteristics. We further sought to determine whether primary findings could be extrapolated to an independent patient population that had received cetuximab therapy.

Materials and Methods

Study subjects and tissue samples

Surgical patients who were treated with curative intent for pathologically confirmed HNSCC of the oral cavity, oropharynx, hypopharynx, or larynx were enrolled in this Early Detection Research Network (EDRN)-sponsored study before surgery (n = 154; Table 1). Patients gave written informed consent, donated tissues for study, and completed an administered questionnaire about tobacco use. Fresh-frozen tumors were available for a subset of subjects for reverse-phase protein array (RPPA; n = 67) and quantitative real-time PCR (qRT-PCR; n = 50) analyses (Table 1). EDRN tumors (n = 58) and paired histologically normal mucosal tissues (n = 30) were arrayed in triplicate in a previously described tissue microarray (TMA; ref. 31). Tumors were prioritized for TMA inclusion based on overlap with available fresh-frozen tissues and adequate tissue for triplicate cores. TMA-arrayed tumors were representative of the EDRN cohort with regard to patient age, sex, smoking status, and tumor site (Table 1). The majority of TMA-arrayed EDRN tumor samples were also evaluated by RPPA and qRT-PCR (n = 40). Arrayed paraffin-embedded tissues from a previously described cohort treated on protocol with induction docetaxel, cisplatin, and cetuximab followed by concurrent radiotherapy, cisplatin, and cetuximab were available for EGFR IHC analysis (32). All tissues were collected under a tissue bank protocol approved by the University of Pittsburgh Institutional Review Board.

Immunohistochemical staining and quantification

Immunohistochemical staining of TMA sections, deparaffinized with successive ethanol and xylene baths, was done for P16 (P16INK4a Ab G175-405, 1:200; BD Pharmingen) following antigen retrieval. EGFR staining was done without antigen retrieval using clone H11 antibody (EGFR M3563, 1:500; Dako), which has been previously validated and employed (33, 34). Signal amplification employed a proprietary antibody-conjugated micropolymer peroxidase (ImmPRESS; Vector). Immunoreactive cells were visualized with diaminobenzidine (DAB) chromogenic substrate (5 minutes at room temperature). Sections were counterstained with hematoxylin and lithium carbonate for morphologic detail. For EGFR, only plasma membrane and

Translational Relevance

Epidermal growth factor receptor (EGFR) has been recognized as contributing to head and neck squamous cell carcinoma (HNSCC) development and progression, but the prognostic value of many specific EGFR molecular characteristics have not been evaluated alone or in combination. We assessed EGFR molecular characteristics including tumor EGFR gene amplification, EGFR gene expression, EGFRvIII gene expression, EGFR protein, and phosphoprotein for a patient cohort treated with surgery with curative intent. We identified tumor EGFR protein and EGFR PY1068 levels to be independent prognostic indicators and determined that EGFR gene amplification was not an indicator of prognosis in this surgical cohort. We validated the use of EGFR tumor protein expression but not EGFR gene amplification as an indicator of prognosis in an independent cohort treated with the anti-EGFR antibody therapeutic cetuximab, thereby defining elevated EGFR tumor protein level as a prognostic rather than predictive indicator. Defining EGFR molecular characteristics relevant to patient prognosis is an important step toward deciding treatment while considering the morbidities associated with aggressive multimodal therapies. In addition to identifying important prognostic indicators, the work presented here defines relationships between different tumor EGFR molecular characteristics, thus providing insights about the aberrant regulation of EGFR.
Table 1. EDRN cohort subject and disease characteristics

<table>
<thead>
<tr>
<th></th>
<th>All cases</th>
<th>TMA cases</th>
<th>RPPA cases</th>
<th>qRT-PCR cases</th>
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<tr>
<td></td>
<td>n = 154</td>
<td>n = 58</td>
<td>n = 67</td>
<td>n = 50</td>
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<tr>
<td><strong>Gender</strong></td>
<td></td>
<td></td>
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<tr>
<td>Male</td>
<td>110 (71.4%)</td>
<td>41 (70.7%)</td>
<td>48 (71.6%)</td>
<td>36 (72.0%)</td>
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<td>17 (29.3%)</td>
<td>19 (28.4%)</td>
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<td>65 (97.0%)</td>
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<td>1 (4.4%)</td>
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<td>61 (23–80)</td>
<td>58 (23–80)</td>
<td>60 (23–80)</td>
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<td>Former smoker</td>
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<td>23 (34.3%)</td>
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<td>Active smoker</td>
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<td>Cigarette pack-years</td>
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<td>Never smoker</td>
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<tr>
<td>1–59 pack-years</td>
<td>57 (37.0%)</td>
<td>18 (31.0%)</td>
<td>21 (31.3%)</td>
<td>17 (34.0%)</td>
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<tr>
<td>&gt;60 pack-years</td>
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<td>28 (41.8%)</td>
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<td>Ever drinker</td>
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<td>49 (74.8%)</td>
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<td>Alcohol quantity†</td>
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<td>18 (26.9%)</td>
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<td>1–4</td>
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<td>≥5</td>
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<td>43 (86.0%)</td>
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<tr>
<td>Recurrence</td>
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<tr>
<td>Oral cavity</td>
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<td>23 (39.7%)</td>
<td>27 (40.3%)</td>
<td>16 (32.0%)</td>
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<td>Oropharynx</td>
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<td>12 (17.9%)</td>
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<tr>
<td>Larynx</td>
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<tr>
<td>Neck</td>
<td>4 (2.6%)</td>
<td>2 (3.4%)</td>
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<tr>
<td>Disease stage</td>
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<tr>
<td>I</td>
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<td>6 (10.3%)</td>
<td>6 (9.0%)</td>
<td>5 (10.0%)</td>
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<td>II</td>
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<td>13 (19.4%)</td>
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<tr>
<td>III</td>
<td>30 (19.5%)</td>
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<td>10 (14.9%)</td>
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<td>IV</td>
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<td>30 (44.8%)</td>
<td>23 (46.0%)</td>
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<td>Recurrence/Metastasis</td>
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<td>1 (1.7%)</td>
<td>1 (1.5%)</td>
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<td>41 (26.8%)</td>
<td>19 (32.8%)</td>
<td>20 (29.0%)</td>
<td>18 (36.0%)</td>
</tr>
<tr>
<td>CRT</td>
<td>27 (17.6%)</td>
<td>10 (17.2%)</td>
<td>11 (15.9%)</td>
<td>9 (18.0%)</td>
</tr>
<tr>
<td>No CRT</td>
<td>79 (51.6%)</td>
<td>27 (46.6%)</td>
<td>35 (50.7%)</td>
<td>21 (42.0%)</td>
</tr>
<tr>
<td>Unknown</td>
<td>6 (3.9%)</td>
<td>2 (3.4%)</td>
<td>3 (4.3%)</td>
<td>2 (4.0%)</td>
</tr>
<tr>
<td>Vital status</td>
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<td></td>
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<tr>
<td>Alive</td>
<td>79 (51.3%)</td>
<td>26 (44.8%)</td>
<td>30 (44.8%)</td>
<td>20 (40.0%)</td>
</tr>
<tr>
<td>Dead</td>
<td>73 (47.4%)</td>
<td>32 (55.2%)</td>
<td>37 (55.2%)</td>
<td>30 (60.0%)</td>
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<tr>
<td>Unknown</td>
<td>2 (1.3%)</td>
<td>0 (0.0%)</td>
<td>0 (0.0%)</td>
<td>0 (0.0%)</td>
</tr>
</tbody>
</table>

(Continued on the following page)
cytoplasmic staining were scored, as little to no nuclear staining was observed; for P16, combined nuclear and cytoplasmic staining was scored. A composite score was derived from the product of the percentage of stained tumor to the nearest 5% and staining intensity (0–3 integer scale), and scores were averaged over replicate cores to derive a final IHC score for each tumor.

**FISH**

Dual-color FISH analysis was done using a Spectrum Green–labeled chromosome 7 centromeric probe (CEN7) and a Spectrum Orange–labeled EGFR probe (Abbott Molecular) for EDRN tumor samples incorporated into a TMA. Nuclei were counterstained with 4',6-diamidino-2-phenylindole/antifade (Abbott Molecular). At least 60 cells were scored for each core. EGFR FISH analysis of the cetuximab-treated cohort tumor tissues has been previously described (32). Gene amplification was defined as present if the ratio of EGFR to CEN7 probe signals was greater than 2.0 in at least one core. Tissues were determined to be hypereploid if one or more cores had at least 4 or more copies of EGFR and CEN7 in at least 50% of cells examined. Tissues were defined as having high EGFR copy number if one of the following was present in at least one core: EGFR gene amplification, hyperploidy, or 15 or more EGFR gene copies in at least 10% of cells.

**Human papillomavirus evaluation**

EDRN human papillomavirus (HPV) tumor status was assessed using an HPV pan-specific DNA probe (Dako, Wide Spectrum HPV DNA Probe Cocktail, Biotinylated), which recognizes HPV subtypes 6, 11, 16, 18, 31, 33, 35, 45, 51 and 52, and bright field in situ hybridization. HPV status for the cetuximab-treated cohort has been previously described (32).

**Reverse-phase protein array**

RPPA was used to quantify EGFR proteins and phosphoproteins in fresh-frozen EDRN tumors. Fresh-frozen tumor tissues were not available for analysis for the cetuximab-treated cohort. Seven 2-fold dilutions of tumor protein lysate were spotted onto nitrocellulose-coated FAST slides. Antibodies for EGFR (SC-03, 1:1,000; Santa Cruz Biotechnology Inc.), EGFR PY992 (#2235, 1:100; Cell Signaling Technology) and EGFR PY1068 (#2234, 1:100; Cell Signaling) and Catalyzed Signal Amplification (CSA) System (DakoCytomation) were used for detection. The dilution series of each of the protein/phosphoprotein samples were quantified using computerized optical densities with local background adjustment (MicroVigene Software), and relative protein/phosphoprotein levels of each diluted sample were fitted and interpolated in the R Supercurve Package (MDA Bioinformatics & Computational Biology Department, http://bioinformatics.mdanderson.org/main/superCurve:Overview; ref. 35).

**Immunoblotting**

Fresh-frozen EDRN tumors were lysed in 1% TritonX, 10 mmol/L Tris-HCl pH 7.6, 5 mmol/L EDTA, and 50 mmol/L NaCl containing complete protease inhibitors (Roche) and PhosSTOP phosphatase inhibitor (Roche). Proteins/phosphoproteins were quantified in 40 μg of tumor protein lysates using the Odyssey Infrared Imaging System (Li-Cor Biosciences) and either goat anti-rabbit IRDye 680 or goat anti-mouse IRDye 800CW secondary antibodies (Li Cor Biosciences). Primary antibodies recognized β-actin (#4967S), Src PY416 (#2101S), STAT3 PY705 (#9131S), STAT3 (#9132S), EGFR PY992 (#2235S), or EGFR PY1068 (#2234S; Cell Signaling Technology), Src (B-12; Santa Cruz Biotechnology) or EGFR (#610017; BD Transduction Laboratories).

### Table 1. EDRN cohort subject and disease characteristics (Cont’d)

<table>
<thead>
<tr>
<th></th>
<th>All cases</th>
<th>TMA cases</th>
<th>RPPA cases</th>
<th>qRT-PCR cases</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n = 154</td>
<td>n = 58</td>
<td>n = 67</td>
<td>n = 50</td>
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<tr>
<td>Time to death, mo</td>
<td></td>
<td></td>
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<tr>
<td>Median (Range)</td>
<td>44.6 (1.5–112.3)</td>
<td>42.2 (1.5–112.3)</td>
<td>0.44^a</td>
<td>42.5 (1.5–112.3)</td>
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<td></td>
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<td>Disease progression</td>
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<td>0.41^b</td>
<td>26 (38.8%)</td>
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<tr>
<td>Disease progression</td>
<td>88 (57.1%)</td>
<td>36 (62.1%)</td>
<td>41 (61.2%)</td>
<td>34 (68.0%)</td>
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<td>0 (0.0%)</td>
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<tr>
<td>Progression-free survival, mo</td>
<td>33.8 (1.2–108.4)</td>
<td>26.4 (1.2–106.9)</td>
<td>0.51^c</td>
<td>26.8 (1.2–106.9)</td>
</tr>
</tbody>
</table>

*a*Analyzed versus unanalyzed cases.

^b^Fisher’s exact test.

^c^Rank sum test.

^d^Log-rank test.

^e^Typical number of alcohol drinks in 2-week period.
Measurement of EGFR and EGFRvIII mRNA levels using quantitative RT-PCR

cDNA was synthesized from RNA isolated from fresh-frozen EDRN tumors using random hexamers and SuperScript III First-Strand kit (Invitrogen). TaqMan real-time PCR quantification of EGFR, EGFRvIII, and beta-galuronidase (β-Gus) gene expression was done in duplicate using a 7700 Sequence Detector (Applied Biosystems Inc.) with an initial 12-minute 95°C denaturation followed by 40 cycles of 95°C denaturation and 60 seconds at 60°C. EGFR primers and probe were as follows: 5'-ATACCGCCGACGAACAG-3' (forward primer), 5'-GGAGCGTAATCCCAAGGATG-3' (reverse primer), and 5'-CATGGTCAGTTTTTCCTTG-CAGTGT-3' (probe). EGFRvIII primers and probe were as follows: 5'-CCTCTGGAGGAAAAAGGTAA-3' (forward primer), 5'-AGGCCCTTTCGACCCGTCTTAT-3' (reverse primer), and 5'-TGCGTCCGAGCCTGTGGG-3' (probe). β-Gus primers are probe were as follows: 5'-CTCTGGAGGAAAAAGGTAA-3' (forward primer), 5'-GAGCTGAGGAAATCCCAAGGATG-3' (reverse primer), and 5'-AGGCCCTTTCGACCCGTCTTAT-3' (probe). EGFR and EGFRvIII expression were measured relative to β-Gus using the comparative Ct method. EGFRvIII was scored as present or absent, EGFR mRNA was scored on a continuous scale.

Statistical analysis

Statistical analyses were carried out using STATA V9 (Statacorp), SPSS V14.0 (IBM) and Prism (Graphpad). Tests were 2-sided and significance was defined as P < 0.05. Correlations were assessed using Spearman’s rank correlation test and associations between categorical variables were tested using Fisher’s exact tests. The intraclass correlation coefficient (ICC) was used to assess EGFR IHC staining reproducibility. PFS was defined as time from first treatment to first subsequent upper aerodigestive cancer, metastasis, or death. Overall survival (OS) was defined as time from first treatment to death. Each EGFR molecular marker was tested for association with PFS by log-rank tests, and a log-rank test of trend was employed when 3 ordered categories were compared. Power was estimated for log-rank tests using the Freedman method (36). EGFR characteristics found to be associated with survival were tested in univariate Cox proportional hazards models and, if significantly associated, tested for association with survival in multivariable models adjusted for candidate prognostic variables associated with survival in this cohort (Wald P < 0.05). Candidate prognostic variables included age, sex, tumor HPV status, AJCC disease stage, smoking status, pack-year category, cancer site, and adjuvant treatment as defined in Table 1. The assumption of proportional hazards was tested by evaluation of scaled Schoenfeld residuals.

Results

EGFR protein by IHC but not by RPPA was higher in EDRN tumors with amplified EGFR

We previously reported that elevated tumor EGFR protein levels in EDRN TMA-arrayed tumors tended to be associated with reduced PFS (31). We assessed tumor EGFR gene amplification status to characterize relationships between tumor EGFR gene amplification and EGFR protein levels. EGFR gene amplification status was categorized as follows: (i) EGFR gene amplification, (ii) hyperploidy without EGFR gene amplification, and (iii) no hyperploidy or EGFR gene amplification. Numbers of tumors in each category are provided in Fig. 1A. No EGFR gene amplification was detected in histologically normal adjacent tissues (n = 30).

EGFR protein assessment by IHC showed reliability with an ICC of 0.86 [95% confidence interval (CI) = 0.77–0.92] for triplicate tumor cores. EGFR protein levels by IHC were significantly higher in EDRN HNSCC tumors with EGFR gene amplification (Fig. 1B). Of the 13 tumors with amplified EGFR, 10 tumors had high EGFR by IHC (IHC scores in the highest tertile: >30) and none had low levels (IHC scores equal to 0). Eighteen of 56 tumors with EGFR IHC scores had scores in the highest tertile. Of these 56% had EGFR amplification, 22% were hyperploid, and 22% were neither hyperploid nor had amplified EGFR, indicating that processes in addition to EGFR amplification contributed to high tumor EGFR protein levels. Our finding of increased EGFR tumor protein by IHC with increasing EGFR copy number has been observed for lung cancer (37).

Because P16 and HPV have been identified as prognostic indicators for HNSCC, EDRN tumors incorporated into the TMA were evaluated for P16 and HPV status. Only 4 of the evaluated 48 EDRN tumors were found to be positive for HPV: 2 oropharyngeal, 1 laryngeal, and 1 neck metastasis (Supplementary Table S1). All HPV-positive tumors had high P16 levels. Of the 4 HPV-positive tumors none had EGFR gene amplification nor exhibited hyperploidy and all had low EGFR protein levels by IHC (Supplementary Table S2).

EDRN tumor EGFR protein as measured by RPPA analysis of fresh-frozen tumors did not differ by EGFR amplification or tumor hyperploid status in TMA-arrayed tumors (Fig. 1C). To validate our RPPA results, 10 fresh-frozen EDRN tumors evaluated by RPPA were assayed by immunoblot for EGFR protein. We found that tumors with high EGFR protein levels by RPPA also had significantly higher EGFR protein levels by immunoblotting than those tumors with low EGFR by RPPA (Supplementary Fig. S1A). We did not find a statistically significant correlation between EGFR IHC protein levels and EGFR protein by RPPA (r = 0.16, P = 0.26).

EDRN tumor EGFR mRNA and EGFRvIII mRNA levels did not differ by EGFR gene amplification status

To determine whether EGFR mRNA levels were elevated in EDRN HNSCC tumors with EGFR gene amplification, we measured tumor EGFR mRNA levels by qRT-PCR. Tumor EGFR mRNA levels did not differ by EGFR amplification or hyperploidy status (Fig. 1D), and tumor EGFR protein levels by IHC and EGFR mRNA levels were not correlated (r = 0.28, P = 0.12). Similarly, there was no correlation between levels of tumor EGFR protein by RPPA and tumor EGFR mRNA (r = 0.04; P = 0.81). Thus EGFR protein levels are, at least in part, likely posttranslationally regulated.
Transcripts encoding EGFRvIII, a variant of EGFR that lacks exons 2 through 7 (38), were detected in 9 of 49 (18%) successfully evaluated tumors. Detection of EGFRvIII expression, which was confined to HPV-negative tumors (Supplementary Table S2), did not differ with tumor EGFR gene amplification or hyperploid status ($P = 0.69$, Fisher exact test). EGFRvIII was detected only in tumors with intermediate or high EGFR mRNA levels ($P = 0.004$, Fisher exact test).

**Analyzed tumor subsets were representative of the EDRN cohort**

Tissues selected for molecular analysis depended upon incorporation into a TMA or availability of fresh-frozen tissues. Of the 58 TMA tumors, 54 were analyzed by RPPA and 42 for EGFR mRNA levels by qRT-PCR. Overall, 40 tumor samples were analyzed using all methods. Patient and tumor characteristics of analyzed tissues did not differ from tissues not analyzed by sex, age, smoking/drinking histories, tumor type, or tumor site (Table 1). We noted a decrease in PFS for TMA-arrayed tumors that was not statistically significant and likely reflected the need for larger tumors to array sufficient material. Similarly, cases analyzed by RPPA differed from nonanalyzed cases with respect to disease stage, likely because advanced stage tumors provided sufficient tissue for evaluation (Table 1).

**EDRN cohort exhibited typical characteristics**

To compare our cohort to previously described surgical cohorts, we evaluated associations between OS and demographic factors, tobacco use, disease stage, and tumor site. Increasing age by category (<55, 55–65, or >65 years) tended to be associated with reduced OS [$P = 0.09$; log-rank test (LRT)]. The ratio of men to women in our cohort was typical and approximately 2.5:1, (5, 39), and sex was not associated with OS ($P = 0.77$; LRT). Increasing number of cigarette pack-years (PY) and active smoking status at first treatment were significantly associated with reduced OS ($P = 0.002$ and $P = 0.03$, respectively; LRT). Patients with higher AJCC tumor stage had shorter OS ($P = 0.0004$; LRT) as did patients with nodal disease ($P = 0.02$; LRT). OS differed by adjuvant CRT versus RT ($P = 0.001$; LRT) with patients who received RT only in addition to surgery having shorter OS. Eighty percent of stage IV and 40% of stage III patients received adjuvant RT or CRT. Tumor site was not significantly associated with OS ($P = 0.69$; LRT).

We did not observe statistically significant improved survival for patients with HPV-positive/P16 high tumors ($P = 0.27$; LRT; Supplementary Table S1), likely reflecting the low prevalence of HPV-positive tumors in our surgical cohort (8%). Median OS for patients with HPV-negative tumors was 45.1 months, whereas the median survival time was not reached for patients with HPV-positive tumors. Of
the 4 patients with HPV-positive tumors, one patient died 42.6 months after treatment. This patient was 1 of 2 HPV-positive patients who were active smokers at the time of first treatment.

Overall, our patient cohort was typical of a surgical HNSCC cohort with the usual associations of reduced survival with higher disease stage, presence of nodal disease, and heavier tobacco use.

**High tumor EGFR protein by IHC was associated with reduced survival in the EDRN cohort**

EGFR tumor protein levels by IHC were analyzed using tertiles to define high, intermediate, and low EGFR expressing tumors to represent the EDRN tumor data in more detail (31). PFS decreased significantly with increasing tumor EGFR levels by IHC (Fig. 2A). In our cohort, EGFR amplification was not a significant indicator of patient PFS (Fig. 2B). High EGFR copy number, which included tumors with high polysomy and/or EGFR amplification and has been shown to be associated with reduced PFS in a similar analysis (15), tended to be associated with reduced PFS in the EDRN cohort, but this did not reach statistical significance ($P = 0.09$). We estimated our power to detect a difference in PFS by EGFR copy number to be 55%, 68%, and 78% for HRs of 1.8, 2.0, and 2.2, respectively, indicating that we had limited ability to detect differences of lower magnitude. In a multivariable Cox proportional hazards models adjusted for age and nodal stage, EGFR IHC levels (low vs. intermediate/high), but not high EGFR copy number, was significantly independently associated with PFS ($P = 0.016$ and $P = 0.685$, respectively). Adjuvant therapy was found to not be statistically significantly associated with PFS ($P = 0.318$) and, as a result, was not included in the final multivariable model. Therefore, EGFR high copy number did not provide prognostic information independent of EGFR IHC. Levels of EGFR protein by RPPA, EGFR mRNA, and presence of EGFRvIII mRNA were also not significant predictors of PFS (Fig. 2C and D, and $P = 0.68$, respectively).

**An independent cetuximab-treated cohort exhibited reduced survival with increased tumor EGFR protein levels by IHC**

The cetuximab-treated cohort ($n = 39$) was previously evaluated for tumor EGFR gene copy number ($n = 26$) and HPV status ($n = 28$); 27% had increased EGFR gene copy number defined as EGFR gene amplification or hyperploidy and 64% of tumors were HPV positive (32). For this study, we evaluated EGFR tumor protein levels by IHC and EGFR gene amplification. Twenty-four tumors were evaluable for EGFR protein levels by IHC; large differences in EGFR levels across different tumors were observed (Supplementary Fig. S2). All 24 tumors had EGFR gene amplification and HPV mRNA level by tertile. Log-rank tests with associated $P$ values compare presence versus absence (B) or trend across low, intermediate, and high tertiles (A, C, and D).
that did not reach statistical significance (Fig. 3A). Neither EGFR protein levels nor presence of EGFR gene amplification differed by tumor HPV status ($P = 0.43$ and $P = 0.19$, respectively; rank sum test and Fisher exact test, respectively). Elevated EGFR tumor protein as defined by the median tended to be associated with reduced PFS (Fig. 3B). EGFR gene amplification was not associated with PFS (Fig. 3C). Neither EGFR gene copy number status nor tumor HPV status was associated with PFS in this cohort, as previously reported (32).

**Site-specific phosphorylation at EGFR PY1068 but not PY992 was associated with reduced survival in the EDRN cohort**

RPPA was used to measure EGFR site–specific phosphorylation at Y1068 and Y992 in fresh-frozen tumors from the EDRN cohort. We confirmed that tumors with high EGFR PY1068 or PY992 by RPPA had significantly higher levels of these EGFR phosphoproteins by immunoblotting (Supplementary Fig. S1B and C). Intermediate or high tumor EGFR PY1068 levels were associated with significantly reduced PFS, and a statistically significant trend of decreased PFS with increasing EGFR PY1068 expression was noted across the tertiles (Fig. 4A). EGFR PY992 tumor levels were not associated with PFS (Fig. 4B). EGFR PY1068 and PY992 levels did not differ significantly by tumor HPV status; 3 of 4 HPV-positive EDRN tumors had low EGFR PY1068 levels whereas 1 of 4 HPV-positive EDRN tumors had low levels of EGFR PY992 (Supplementary Table S2).

EGFR protein by RPPA was positively correlated with both PY1068 and PY992 levels ($P = 0.24$, $P = 0.053$; $P = 0.26$, $P = 0.034$, respectively). However, EGFR PY1068 and PY992 levels were not significantly correlated with each other ($P = 0.15$, $P = 0.24$), indicating tumors with high EGFR tended to have higher phosphorylated EGFR, but phosphorylation site–specific differences were present. With limited remaining tissue, we assessed levels of activated Src family kinase (SFK) and STAT3 by quantitative immunoblotting with anti-SFK PY416 or anti-STAT3 PY705, respectively, in 5 tumors ranked high by EGFR PY1068 and 5 tumors ranked low by EGFR PY1068 (Supplementary Fig. S3). SFK PY416 levels did not differ with EGFR PY1068 levels, but tumors with high EGFR PY1068 had higher levels of STAT3 PY705 (Supplementary Fig. S3), suggesting that activation of the STAT3 pathway may be an important downstream effector of EGFR PY1068 activity.

Cox proportional hazards models were used to determine whether EGFR PY1068 was associated with PFS when also considering tumor EGFR protein levels by IHC. Low versus intermediate/high levels of tumor EGFR protein by IHC and EGFR PY1068 were defined by the lowest tertile versus the intermediate and high tertiles for each marker. Intermediate/high tumor EGFR by IHC and intermediate/high tumor EGFR PY1068 were both independently associated with reduced PFS in a multivariable Cox proportional hazards model containing both (HR = 2.75; 95% CI = 1.26–6.00 and HR = 3.29; 95% CI = 1.34–8.14, respectively). Indicating that both contributed significantly as prognostic factors.

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**Figure 3.** High tumor EGFR protein by IHC tended to be associated with reduced PFS in the cetuximab-treated cohort. A, EGFR protein levels determined by IHC staining categorized by tumor EGFR gene amplification and ploidy status. Kruskal–Wallis $P$ value provided. B, Kaplan–Meier PFS plots by low versus high tumor EGFR protein by IHC level as defined by the median. C, Kaplan–Meier plot of PFS by tumor EGFR gene amplification status (presence vs. absence). Log-rank test–associated $P$ values are provided for B and C.
indicators. When combining EGFR by IHC and EGFR PY1068 levels into 3 groups, low in both, intermediate/high in one or intermediate/high in both, there was a significant trend toward reduced PFS across these 3 categories (Fig. 4C). In univariate Cox proportional hazards models, intermediate/high in both tumor EGFR protein by IHC and EGFR PY1068 was associated with significantly reduced PFS compared with low tumor levels of both EGFR protein by IHC and EGFR PY1068 (HR = 7.49; 95% CI = 2.11–26.48). This association was significant even after adjusting for nodal stage and patient age (HR = 5.55; 95% CI = 1.42–21.79).

Discussion

Of the EGFR molecular characteristics evaluated in paraffin-embedded formalin-fixed tumors, we found that elevated tumor levels of EGFR by IHC were significantly associated with PFS in a patient cohort treated with surgery with curative intent without an EGFR-targeted therapy. Although our IHC staining method did not detect nuclear EGFR, which has been previously reported to be associated with increased local HNSCC recurrence rates (34), our results are similar to a recent study finding high predominately plasma membrane and cytoplasmic tumor EGFR levels to be associated with reduced survival (40). We found a similar decrease in PFS with elevated tumor EGFR by IHC for patients treated with CRT and EGFR-targeted agent cetuximab. Our 2 cohorts differed in treatment type and HPV-positive tumor representation, suggesting that EGFR IHC levels may be prognostic for both HPV-positive and HPV-negative tumor types.

Although we found no significant association between EGFR gene amplification and PFS in either cohort, we did note a trend toward reduced PFS with increased EGFR gene copy number in the EDRN surgical cohort that was similar to the association reported by Chung and colleagues (15). Our finding of lack of significant association between increased EGFR gene copy number and PFS was probably not due to a minor difference defining high EGFR copy number in which we included 4 or more EGFR copies in at least 50% of cells, although Chung and colleagues delineated 40% as the cut-point (15). Although our follow-up time was longer than the Chung and colleagues study, our cohort was smaller, which may decrease power in our study to detect a difference in PFS by copy number status. Acknowledging these caveats, our data showed that tumor EGFR levels to be associated with reduced survival (40). We found a similar decrease in PFS with elevated tumor EGFR by IHC for patients treated with CRT and EGFR-targeted agent cetuximab. Our 2 cohorts differed in treatment type and HPV-positive tumor representation, suggesting that EGFR IHC levels may be prognostic for both HPV-positive and HPV-negative tumor types.

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the differences are largely technical in nature. Recent reports have shown that EGFR protein levels assessed by IHC versus immunoblotting methods can differ somewhat (33, 42), and that the magnitude of these differences varies depending upon the antibody used (33). We employed the anti-EGFR antibody clone H11 for our IHC studies. This clone H11 antibody was recently shown to have only a modest correlation between EGFR protein levels by automated quantitative analysis (AQUA) of IHC-stained cell lines and EGFR protein levels quantified from immunoblots of lysates from these same cell lines (33). Of 4 anti-EGFR antibodies tested in a study of 642 breast cancer tumors in this same report by Anagnostou and colleagues, only the clone H11 antibody showed prognostic value (P < 0.05), with shorter survival observed for patients whose tumors had high or intermediate tumor levels of EGFR as assessed by AQUA and IHC. Because of assay validation specifications, we used a different anti-EGFR antibody for our RPPA studies. Therefore, a portion of difference between IHC and RPPA results is likely attributed to differences in the antibodies performance.

In addition to inherent assay performance differences such as antibody differences and possible epitope availability differences in arrayed fresh-frozen tissue lysates compared with formalin-fixed tissues, pathologist-interpreted EGFR protein levels by IHC were confined to the cytoplasm and plasma membrane of tumor cells because nuclear EGFR was not detected using the clone H11 antibody. Subcellular architecture was lost when making lysates for RPPA. Therefore, it is possible that EGFR tumor protein in the cytoplasm, membrane, and nucleus may contribute differentially to signaling.

Although the stromal compartments of tumors are appreciated as important contributors to HNSCC development and progression, it is possible that stromal tissue present in RPPA samples contributed to the lack of correlation between IHC and RPPA analyses, though we were not able to retrospectively assess this. EGFR tumor levels by IHC were confined to the tumor portion of the specimen by the evaluating pathologist. EGFR levels by RPPA would represent tumor and stromal tissue levels. Our fresh-frozen tumor tissues contained at least 70% tumor; it is possible that up to 30% of our RPPA analyzed tumor tissues were stromal tissues. Our lack of concordance between tumor EGFR levels by IHC and EGFR in protein lysates was similar to previous reports comparing tumor EGFR levels by IHC and by ELISAs (43, 44).

We did find that high tumor levels of EGFR PY1068, but not EGFR PY992, in fresh-frozen tumor lysates contributed prognostic information alone and in addition to tumor EGFR levels by IHC, suggesting that EGFR PY1068 evaluation was not substantially hindered by subcellular localization or stromal contamination issues. Reports evaluating associations between clinical parameters and tyrosine-phosphorylated EGFR that is not site specific have yielded mixed results (3, 21–22). Our findings suggest that there are biologically relevant differences between phosphorylation at specific sites that could impact patient survival. Our data further suggest that STAT3 signaling downstream of EGFR PY1068 may be important. We evaluated only EGFR PY992 and PY1068 because the quality of these antibodies was sufficient for RPPA. It is possible that evaluation of additional EGFR phosphorylation sites will yield more information. EGFR PY1068 had prognostic value in our predominantly HPV-negative cohort. It will be important to assess its prognostic value in independent cohorts, including those with higher HPV-positive tumor representation.

The assessment of phosphoproteins in tissues is generally recognized as requiring special care because of the labile nature of the phosphorylation. We collected and processed tissues under a protocol that involved coordination of personnel and immediate transport of collected tissues to the pathology laboratory for examination, cataloging, and freezing to minimize time to freezing. Beginning in 2003, our tissue bank recorded time from surgical resection to freezing, and typical banking time was within 40 minutes of resection. For evaluations of EGFR PY1068 tumor levels, time to freezing logistics will need to be considered before general use.

EGFR transcription/translational regulatory mechanisms in HNSCC are likely complex and only just beginning to be defined. Our observation of association between EGFR gene amplification and elevated EGFR protein by IHC but lack of association of EGFR mRNA levels with either characteristic suggests complex regulation and contradicts somewhat a previously published report of elevated EGFR mRNA in EGFR FISH-positive lung cancer (45). Similar to a previous report by Sok and colleagues, we found EGFRvIII expression to be associated with EGFR wild-type expression (38). EGFRvIII expression, which has been associated with resistance to EGFR-targeted therapies (38), was not prognostic in our surgical cohort that was not treated with an EGFR-targeted therapy. However, our detection of EGFRvIII in approximately 20% of tumors that were EGFR-targeting agent naive suggests that EGFRvIII expression may have relevance for HNSCC de novo resistance to EGFR-targeted therapies.

Strengths of our study include the prospective enrollment of our subjects and limited heterogeneity of treatments within each of the 2 cohorts evaluated. For the EDRN cohort, evaluations extended beyond paraffin-embedded tumor tissues to include fresh-frozen tissues. This study presents a multifaceted evaluation of HNSCC that includes the assessment of molecular characteristics that currently require fresh-frozen specimens. A limitation of this study was our inability to assess all patient tumors for all parameters. This limitation reflects the challenges of obtaining sufficient fresh-frozen material for study. Importantly, there...
are few specimen selection biases, and the evidence indicates that studied specimens are representative of the general cohort.

In conclusion, we report EGFR tumor levels by IHC assessment, which is carried out routinely, are informative with regard to patient prognosis. Because independent cohorts treated with and without an EGFR-targeting agent had similar survival profiles by tumor EGFR IHC status, EGFR IHC likely provides prognostic rather than predictive value. We noted a trend toward reduced survival with high EGFR gene copy number; however, EGFR gene copy status did not provide prognostic information alone or in combination with tumor EGFR IHC data. We do not anticipate that EGFR FISH analysis will provide prognostic information above that acquired by tumor EGFR IHC analysis in the general HNSCC patient population. Of interest, we report that EGFR site–specific phosphorylation at PY1068 provided prognostic information that was independent of tumor EGFR levels by IHC. These data suggest a further exploration of EGFR site–specific phosphorylation events and EGFR PY1068-specific downstream signaling could provide additional insights into HNSCC progression.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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Sarah Wheeler, Doris R. Siwak, Raymond Chai, et al.


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