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Lung Adenocarcinoma with EGFR Amplification has Distinct Clinicopathologic and Molecular Features in Never-Smokers

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Abstract

In a subset of lung adenocarcinomas the epidermal growth factor receptor (EGFR) is activated by kinase domain mutations and/or gene amplification, but the interaction between the two types of abnormalities is complex and unclear. We selected to study 99 consecutive never-smoking women of East Asian origin with lung adenocarcinomas that were characterized by histologic subtype. We analyzed EGFR mutations by PCR-capillary sequencing, EGFR copy number abnormalities by fluorescence and chromogenic in situ hybridization and quantitative PCR, and EGFR expression by immunohistochemistry with both specific antibodies against exon 19 deletion-mutated EGFR and total EGFR. We compared molecular and clinicopathologic features with disease-free survival. Lung adenocarcinomas with EGFR amplification had significantly more EGFR exon 19 deletion mutations than adenocarcinomas with disomy, low and high polysomy (100% vs 54%, P=0.009). EGFR amplification occurred invariably on the mutated and not the wildtype allele (median mutated:wildtype ratios 14.0 vs 0.33, P=0.003), was associated with solid histology (P=0.008), and advanced clinical stage (P=0.009). EGFR amplification was focally distributed in lung cancer specimens, mostly in regions with solid histology. Patients with EGFR amplification had a significantly worse outcome in univariate analysis (median disease-free survival 16 vs 31 months, P=0.01) and when adjusted for stage (P=0.027). Lung adenocarcinomas with EGFR amplification have a unique association with exon 19 deletion mutations and demonstrate distinct clinicopathologic features associated with a significantly worsened prognosis. In these cases, EGFR amplification is heterogeneously distributed, mostly in areas with a solid histology.

INTRODUCTION

A subset of non-small cell lung carcinomas (NSCLC) has activating mutations in the epidermal growth factor receptor (EGFR) that predict response to treatment with EGFR tyrosine kinase inhibitors (TKIs) (1-3). The highest prevalence of somatic EGFR mutations (up to 55%) is in never-smoking women of East Asian origin (4-6). In contrast, somatic K-RAS mutations occur...
more commonly in patients with a smoking history and appear to be exclusive of *EGFR* mutations (7,8).

*EGFR* mutations mostly occur in exons 18-21 and cluster in two major hot spots (1). The most common mutations, L858R substitution mutation in exon 21 (40% of *EGFR* mutations) and small in-frame deletions in exon 19 (>50%) are reported to be the most closely associated with radiographic responses with *EGFR* TKI therapy (9,10). Mutations in exons 18 and 20 account for 10% of *EGFR* mutations in NSCLC (1).

The *EGFR* gene is also one of a growing number of putative oncogenes that can undergo marked copy number changes (11). The significance of *EGFR* copy number changes in NSCLC has not been clearly established, but several clinical trials have demonstrated that a higher copy number of *EGFR* copies is associated with a better response to treatment with gefitinib (12-15).

*EGFR* mutant tumors and NSCLC cell lines sometimes have concurrent increases in *EGFR* copy number (8,16-19). Activating kinase domain mutations appear to be an early event in lung carcinogenesis (20,21) and several studies have hypothesized that increased *EGFR* copy number is associated with more aggressive and poorly differentiated lung carcinomas (18,22, 23).

Interestingly, studies in human NSCLC cell lines have demonstrated differential EGFR and downstream signaling activation based on the type of mutation and the presence of gene amplification (24). These findings, corroborated with clinical observations of improved survival in EGFR TKI-treated patients with exon19 deletion mutations (9,25) suggest that certain molecular abnormalities are associated with distinctive clinicopathologic characteristics. In this study, we explored kinase domain mutations and copy number abnormalities in lung adenocarcinomas from a cohort of patients known to have a high prevalence of *EGFR* mutations and examined their pathologic and clinical significance. We found that a subset of patients with lung adenocarcinomas have a distinct genetic profile, clinicopathologic characteristics and outcome.

**MATERIALS AND METHODS**

**Patient Selection**

Surgical pathology specimens were obtained from 99 consecutive never-smoking women with NSCLC treated initially by surgery at the Khaosiung Veteran General Hospital, Taiwan from 1999 to 2004. Of these, 65 cases were included in the study based on a pathologic diagnosis of lung adenocarcinoma, absence of neoadjuvant treatment, and the availability of sufficient tissue to examine molecular abnormalities, gene copy number alterations, and protein expression by immunohistochemistry. Hematoxylin and eosin staining was performed on 5 um sections from paraffin-embedded formalin-fixed tumor tissue. Adenocarcinomas were evaluated by two pathologists (LRC and LMS) and classified according to WHO criteria (26). In mixed subtype adenocarcinomas we assessed the percentage of each histologic pattern (acinar, papillary, solid and bronchioloalveolar) in 10-percent increments and recorded the most predominant histologic pattern (27). The study was approved by the institutional review board of the Kaohsiung Veteran General Hospital and Kaohsiung Medical University and all participants gave written informed consent.

**Analysis of the EGFR and KRAS mutations**

DNA was extracted from areas of paraffin slides containing more than 50% tumor and mutation analysis for EGFR exons 18-21 and KRAS exons 12-13 was performed using SURVEYOR (Transgenomic, Omaha, NE) digestion and/or restriction fragment length polymorphism
analysis followed by high-performance liquid chromatography on the Transgenomic WAVE Nucleic Acid High Sensitivity Fragment Analysis System (WAVE HS system, Transgenomic Omaha, NE) according to previously published protocols (28). Amplicons were fractioned to enrich for heteroduplexes, and collected fractions were amplified and sequenced. EGFR mutated and wildtype alleles were quantified using quantitative polymerase chain reaction (DxS EGFR Mutation Test Kit, DxS Ltd., Manchester, UK) in cases with EGFR exon 19 deletion E746_E750 (n = 29) and L858R mutation (n = 10) for which sufficient DNA remained following mutation analysis.

**Analysis of EGFR Copy Number**

**Fluorescence in situ Hybridization**—FISH was performed on paraffin-embedded tissue sections according to protocols described previously (29). At least 50 cells were evaluated for each case by two pathologists (LMS and AJI). The EGFR gene copy number was classified according to previously published criteria (14,29) as: disomy, low polysomy (≤ 4 copies of EGFR in > 40% of cells), high polysomy (≥ 4 copies of EGFR in > 40% of cells, or gene amplification (homogenously staining regions with ≥ 15 copies in ≥ 10% of cells or a gene/chromosome ratio per cell of ≥ 2).

**Chromogenic in situ Hybridization**—CISH was performed on paraffin-embedded tissue sections and scored according to protocols described previously (29) using the EGFR amplification probe (Invitrogen/Zymed, South San Francisco, CA).

**Immunohistochemistry Analysis for EGFR Overexpression**

Immunohistochemistry for total EGFR protein was performed using Dako (Dako North America Inc., Carpinteria, CA) clone H11 at a 1:400 dilution following a 10 minute proteinase digestion step. EGFR expression was classified according to previously published criteria into one of four categories: 0 for no or only cytoplasmic staining; 1+ for partial membrane staining; 2+ for weak, complete membrane staining in > 10% of tumor cells; and 3+ for intense, complete membrane staining in > 10% of tumor cells (30,31). Expression scores of 2 or 3 were defined as EGFR protein overexpression.

Immunohistochemistry with mutation-specific antibodies for the detection of EGFR exon 19 deletion mutations was performed on 4 μm-thick tissue sections using E746_A750 EGFR deletion-specific RmAb (dEGFR, clone 6B6, Cell Signaling Technology, Inc, Danvers, MA) as previously described (32).

**Statistical Analysis**

Fisher’s exact test and Wilcoxon rank-sum test were used to analyze the association of EGFR copy number changes with each of the molecular, pathologic and clinical characteristics, respectively, for categorical and continuous data. Disease-free survival was measured from the date of surgery to the date of NSCLC recurrence or death, whichever occurred earlier, and was censored for patients still alive without a recurrence at their last follow-up. In order to adjust for the underlying prognosis due to differential stage, the logrank test was stratified by stage in the comparison of disease-free survival. The data analysis was conducted primarily using SAS 9.1 (SAS Institute, Cary, NC), while StatXact 6.1 (Cytel software Corp, Cambridge, MA) was used to compute an exact P-value for the stratified logrank test. All P-values are based on a two-sided hypothesis.
RESULTS

**EGFR** mutation status and **EGFR** copy number abnormalities

The results of **EGFR** molecular and copy number analyses are summarized in Figure 1 and illustrated in Figure 2A. As expected, this subset of patients (2,3,7) had a high prevalence of **EGFR** mutations: 52 (80%) of 65 analyzed patients had one **EGFR** mutation and 6 (9%) patients had two concomitant **EGFR** mutations (Fig 1). Overall, 39 tumors (60%) had an exon 19 deletion mutation, 15 adenocarcinomas (23%) had an exon 21 missense mutation, and 3 adenocarcinomas (5%) had a mutation in exons 18 or 20 (Table 1). **K-RAS** mutations were present in only three (5%) adenocarcinomas, and were mutually exclusive of **EGFR** mutations, as previously reported (8). One case had both the L858R activating mutation and T790M resistance mutation (Fig 1).

The exon 19 deletion mutation was present in 47%, 63%, and 52% of adenocarcinomas with disomy, low polysomy, and high polysomy, respectively (overall average in non-amplified cases 54%) and in 100% adenocarcinomas with **EGFR** amplification (Fisher exact test, \(P = 0.009\), Table 2 and Fig 2A). An L858R mutation was also detected in an amplified case, but only in the presence of a coexisting exon 19 deletion mutation (Figs 1 and 2A).

A significant increase in the ratio of exon 19 deletion mutation **EGFR** allele to wildtype allele was detected only in the adenocarcinomas with **EGFR** amplification (median value 14, range 2 to162) when compared with adenocarcinomas with disomy, low polysomy, and high polysomy (median 0.3, range <0.1 to 7.0, \(P = 0.003\), Fig 2B). The mutant alleles could not be detected by quantitative PCR in two cases (one case with **EGFR** amplification and one case with high polysomy) of the 29 cases with exon 19 deletion mutation that were tested. We did not identify any case where the L858R-mutated allele was amplified (ratio of mutant to wild type allele \(\leq 1.0\)).

**Lung Carcinomas with EGFR Amplification Have Distinctive Clinical and Pathologic Characteristics**

**Clinical Features**—The clinical features of patients with lung adenocarcinomas with and without **EGFR** gene amplification are presented in Table 2. Patients with adenocarcinomas with **EGFR** amplification presented predominantly in advanced clinical stages: IIA two patients, IIIA five patients, and IV two patients. None of the patients with adenocarcinomas with **EGFR** amplification presented with stage I, whereas 52% of all other patients presented with stage I (\(P = 0.009\)). There were no significant differences between the stages at presentation of patients with adenocarcinomas with exon 19 deletion and those with L858R (data not shown). We found no significant differences in the types of adjuvant treatment between patients with or without **EGFR** amplification (\(P = 0.508\), Table 2).

**Histologic Features**—A predominant solid pattern was present in 5 (56%) of 9 adenocarcinomas with **EGFR** amplification in contrast to only 7 (13%) of 56 adenocarcinomas without amplification (\(P = 0.008\) Table 2 and Fig 2C). Predominant acinar and papillary patterns were present in similar proportions in adenocarcinomas from all other copy number categories and a BAC predominant pattern occurred most commonly in disomic cases (Table 2). Although solid histology was more frequently seen in adenocarcinomas with exon 19 deletion mutation than in those with the L858R mutation (20% v 9%), this difference was not significant (\(P = 0.66\)).

**Immunophenotype**—**EGFR** protein overexpression was significantly more prevalent in adenocarcinomas with **EGFR** amplification than adenocarcinomas with any other copy number alterations (Fig 2D). **EGFR** protein was overexpressed in 8 of 9 (89%) adenocarcinomas with
EGFR amplification, 7 of 23 (30%) with high polysomy, 3 of 16 (19%) with low polysomy, and one of 17 (6%) with disomy ($P < 0.001$, Table 2 and Fig 2D). Thirteen (93%) of 14 adenocarcinomas with exon19 deletion mutation identified by sequencing were positive by immunohistochemistry using the exon 19 deletion-specific antibody. Similar to the total EGFR antibody, the deletion mutation-specific antibody had increased expression in the tumors with EGFR gene amplification (Fig 3). Overexpression of EGFR with exon 19 deletion was heterogeneously distributed in EGFR gene-amplified lung cancer specimens, mostly in areas with a solid growth pattern.

**Survival**

Median follow-up time was 27 months. The disease-free survival rate was significantly better for patients who had pathologic Stage I carcinoma than it was for patients with more advanced stages (42.8% v 17.5% at 5 years, $P = 0.047$). The median disease-free survival time was significantly worse among patients with adenocarcinoma with EGFR amplification than it was among patients without amplification (16 v 31 months, $P = 0.01$, Fig 4). When adjusted for stage, patients with EGFR amplification had a significantly worse outcome ($P = 0.027$).

**EGFR Copy Number Is Heterogeneous within Individual Tumors**

We used chromogenic in situ hybridization (CISH), an alternative technique to FISH, in order to visually locate the regions with EGFR copy number abnormalities in the tumor samples. As we previously reported, EGFR copy number abnormalities assessed by CISH highly correlate with FISH (29). Of the adenocarcinomas with EGFR amplification by FISH, five specimens had a heterogeneous copy number distribution in different histologic patterns when examined by CISH (Fig 3). By CISH, the areas with BAC and acinar histology had low polysomy and areas with solid and papillary histology had EGFR amplification. EGFR protein expression using both the total EGFR antibody and the exon19 deletion-specific antibody was most consistently and strongly detected in the tumor cells with EGFR gene amplification. Absent or low EGFR protein expression (scores 0 and 1) were seen in the regions with BAC and acinar histology, in areas of low polysomy.

**DISCUSSION**

In this study we show that in this selected cohort of patients with lung adenocarcinomas EGFR amplification (1) is invariably associated with exon 19 deletion mutations, (2) occurs exclusively on the mutated allele, (3) is focally distributed mostly in regions with solid histology, and (4) is associated with worse outcome.

Our study has several unique features. Firstly, the demographic characteristics of the study population (never-smoking women of East Asian origin) favor the presence of somatic EGFR mutations, and we identified EGFR kinase domain mutations in 80% of the cases. As expected in this patient group, KRAS mutations were rare events. The homogeneity of the study population enabled us to identify highly significant associations between genetic, clinical, and pathologic features in the absence of a large population analysis. Secondly, we studied surgical resection specimens from patients who had no preoperative neoadjuvant treatment. Because lung tumors are heterogeneous, the availability of large tumor specimens eliminates the artifacts of sampling error. This is particularly problematic in assessing copy number abnormalities, which, as our study reveals, can vary even within a single microscopic field of tumor. Finally, using a novel exon 19 deletion-specific antibody recently described by our group (32) we were able to directly visualize the location of tumor cells with EGFR exon 19 deletion mutations and show heterogeneity in receptor overexpression among different tumor cells. These findings may have implications for the efficacy of TKI treatment in any given patient with an EGFR-mutant adenocarcinoma.
According to previously published criteria for classifying lung adenocarcinomas based on \textit{EGFR} copy number abnormalities, (13) 49\% of the cases in our study would be considered “FISH positive” (\textit{EGFR} high polysomy or gene amplification) (13). The importance of distinguishing between high polysomy and gene amplification is not well-established, however, in our study tumors containing \textit{EGFR} with high polysomy did not have significantly unique clinical or pathologic features and were therefore grouped with all other non-gene amplified tumors for statistical analyses.

We found that gene amplification occurred exclusively in the tumors with \textit{EGFR} exon 19 deletion mutations and did not occur in the tumors with wildtype \textit{EGFR} or other types of \textit{EGFR} mutations (Fig 2A). In accordance with other studies, (18,19,21,33) we found that \textit{EGFR} amplification occurs preferentially on the mutated allele, an observation that strongly supports the concept that kinase domain mutations are early events in lung adenocarcinoma tumorigenesis, whereas gene amplification occurs later (Fig 2B). In our study the increase in the ratio of mutated: wildtype alleles occurred exclusively in cases containing the exon 19 deletion mutation.

The exclusive association of exon 19 deletion mutations with gene amplification is a novel observation and contrasts with prior studies that have identified gene amplification in different mutational backgrounds. Gene amplification has been detected in cell lines harboring either exon 19 deletion mutations or L858R mutation (17,24). Previous studies have identified \textit{EGFR} amplification in other genetic backgrounds, including in tumors that are \textit{EGFR} wildtype and that harbor other \textit{EGFR} mutations (15). However, in contrast with our study of untreated tumors, these combined alterations were identified in patients who had received prior chemotherapy (15).

Recent published studies in selected NSCLC cell lines suggest mechanistic differences between tumors containing the exon 19 deletion mutation and those with the L858R mutation (24). Tumors cells containing the exon 19 deletion mutation demonstrate constitutive \textit{EGFR} autophosphorylation only in the presence of gene amplification, whereas cells containing the L858R mutation demonstrate constitutive autophosphorylation regardless of amplification status (24). These findings, in association with evidence that amplification occurs only on the mutated \textit{EGFR} allele (24,33) suggest that amplification provides a growth advantage for tumor cells harboring the exon19 deletion mutation.

Our analysis provides interesting clinical and pathologic correlations that validate the \textit{in vitro} studies of \textit{EGFR} receptor biology (24). We found that this subset of \textit{EGFR} amplified tumors was significantly more likely to contain high grade, solid-subtype adenocarcinoma (Fig 2C) (26). Interestingly, this tumor subtype has been previously associated with \textit{KRAS} mutations and a smoking history, (27) however analysis of histologic subtypes in an \textit{EGFR}-mutation enriched patient population has not been performed to date. We also found that \textit{EGFR}-amplified tumors are more likely to present at higher stages and have worse disease-free survival (Fig 4).

In this population of previously untreated lung adenocarcinomas, \textit{EGFR} gene amplification is predicated on the existence of an underlying exon 19 deletion mutation, suggesting that, in at least a subset of patients, there is a stereotypical tumor progression pathway, with kinase domain mutations occurring early and gene amplification occurring later. Previous reports have demonstrated that \textit{EGFR} mutations are detectable even in preinvasive lesions like atypical adenomatous hyperplasia, but increased \textit{EGFR} copy number are mostly present in invasive (22) and higher grade tumors (23). Using an antibody directed specifically at exon19 deletion-mutated \textit{EGFR}, we demonstrated that all histologic subtypes of the sequencing-proven mutant tumors contain at least low levels of mutant protein expression. Using CISH to evaluate copy
number changes by light microscopy, we demonstrated that gene amplification is heterogeneous, occurring preferentially in solid and high grade papillary components. The tumor areas containing gene amplification highly correlated with the areas of protein overexpression by immunohistochemistry whether detected using the total EGFR antibody or exon19 deletion-specific EGFR antibody. The fact that EGFR molecular alterations are heterogeneously distributed within lung adenocarcinomas specimens confirms previous reports (18,23) and suggests that thorough pathologic and molecular analyses of a resection specimen are required to provide the most accurate information regarding tumor biology. Because the studied population was restricted to East Asian patients, the applicability of these findings to Western patients remains unclear.

Our findings demonstrate that within a subset of EGFR-mutated lung adenocarcinomas, EGFR gene amplification is associated with tumor progression, reflected by higher histologic grade and clinical stage. Amplification appears to promote constitutive receptor activation in exon19 deletion-mutated NSCLC cell lines and as such may also provide a growth advantage for these cells. (24) These findings highlight the complexity of tumor morphogenesis and suggest that molecular classification of lung cancer by both mutation and copy number analyses may have important implications for selection of therapy. Our study provides support for the concept of tumor heterogeneity and suggests a mechanism for variable responses to directed therapy for lung adenocarcinoma.

Acknowledgments

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REFERENCES


Figure 1.
EGFR mutation status, copy number abnormalities and EGFR protein expression in lung adenocarcinoma and relationship with the predominant histology. Each row is a lung cancer sample. Black rectangles represent the results of EGFR sequencing (EGFR Sequence) or a predominant pattern (Dominant Histology). EGFR expression was categorized on a scale from 0 (absent staining) to 3 (strong staining) and illustrated on a grey scale from white (score=0), light grey (score=1), dark grey (score=2), and black (score=3). BAC, bronchioloalveolar histology.
Figure 2.
Comparison of the genetic alterations and pathologic characteristics among the lung adenocarcinomas according to the $EGFR$ copy number categories. Lung adenocarcinomas with $EGFR$ amplification have very distinct genetic profiles. **Panel A.** Prevalence of $EGFR$ mutations in the studied adenocarcinomas. Some adenocarcinomas have a concomitant mutation in the $EGFR$ gene (dotted bars). In the $EGFR$ amplified cancers there is a significant difference in the mutation frequency of $EGFR$ exon 19 deletions ($P = 0.009$) but not in other mutations. **Panel B.** Furthermore, in cancers with $EGFR$ exon 19 deletions, there is an increase in both wildtype and mutated $EGFR$ copies in low and high polysomy cases (mean deleted:wildtype ratios 1.14 and 1.21, respectively), whereas there is a preferential increase of the deleted allele in amplified cases (mean deleted:wildtype ratios 36.3). The y axis indicates the log10 ratio between deleted allele and the wildtype allele. **Panel C.** Proportion of solid histology in each carcinoma. Boxes represent the mean values and whiskers the standard error of the mean. **Panel D.** $EGFR$ protein expression.
Figure 3.
Heterogenous histology, EGFR copy number, and protein expression in a gene amplified lung adenocarcinoma. The top panel shows a tumor field containing acinar and solid subtypes of adenocarcinoma. The lower panels show hematoxylin and eosin stain (400X), EGFR CISH (600X), and EGFR protein expression by immunohistochemistry (IHC) (400X). Part (A) shows acinar histology with low polysomy by CISH and 1+ protein expression. Part B shows solid histology with gene amplification in the form of homogenous staining regions by CISH and 3+ protein expression.
Figure 4.
Kaplan-Meier estimates of disease-free survival among patients with stage II-IV lung adenocarcinoma. The median disease-free survival time was significantly worse among patients with adenocarcinoma with \( \text{EGFR} \) amplification than it was among patients without amplification (16 vs. 31 months, \( P = 0.01 \)).
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<th>High polysomy 4 (17)</th>
<th>Amplification 0 (0)</th>
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*Percentages were calculated on the basis of the number of cases in each copy number category. Percentages may not total 100 because 6 cases had two concomitant mutations.
Table 2

Clinical Characteristics of Patients with Lung Adenocarcinoma According to EGFR Copy Number Abnormalities

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<th>Characteristic</th>
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<th>High Polysomy (N=23)</th>
<th>Gene Amplified (N=9)</th>
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<td>62 (46-78)</td>
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*P-value is based on the comparison between patients with EGFR amplification and all other patients.

†Stage II-IV only