Mutations of the Epidermal Growth Factor Receptor Gene in Lung Cancer: Biological and Clinical Implications

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ABSTRACT

Recently it has been reported that mutations in the tyrosine kinase domain of the epidermal growth factor receptor (EGFR) gene occur in a subset of patients with lung cancer showing a dramatic response to EGFR tyrosine kinase inhibitors. To gain further insights in the role of EGFR in lung carcinogenesis, we sequenced exons 18–21 of the tyrosine kinase domain using total RNA extracted from unselected 277 patients with lung cancer who underwent surgical resection and correlated the results with clinical and pathologic features. EGFR mutations were present in 111 patients (40%). Fifty-two were in-frame deletions around codons 746–750 in exon 19, 54 were point mutations including 49 at codon 858 in exon 21 and 4 at codon 719 in exon 18, and 5 were duplications/insertions mainly in exon 20. They were significantly more frequent in female (P < 0.001), adenocarcinomas (P = 0.0013), and in never-smokers (P < 0.001). Multivariate analysis suggested EGFR mutations were independently associated with adenocarcinoma histology (P = 0.0012) and smoking status (P < 0.001), but not with female gender (P = 0.9991). In adenocarcinomas, EGFR mutations were more frequent in well to moderately differentiated tumors (P < 0.001) but were independent of patient age, disease stages, or patient survival. KRAS and TP53 mutations were present in 13 and 41%, respectively. EGFR mutations never occurred in tumors with KRAS mutations, whereas EGFR mutations were independent of TP53 mutations. EGFR mutations define a distinct subset of pulmonary adenocarcinoma without KRAS mutations, which is not caused by tobacco carcinogens.

INTRODUCTION

Non–small-cell lung cancer (NSCLC) frequently overexpresses receptors of the erbB family including the epidermal growth factor receptor (EGFR) encoded by erbB-1 (HER1; ref. 1, 2). The EGFR is a 170 kilodaltons receptor tyrosine kinase (TK) that dimerizes and phosphorylates several tyrosine residues after binding of several specific ligands (1). These phosphorylated tyrosines serve as the binding sites for several signal transducers that initiate multiple signaling pathways resulting in cell proliferation, migration, and metastasis, evasion from apoptosis, or angiogenesis, all of which are associated with cancer phenotypes (1). Downstream pathways include ras-ras-MEK-ERK (raf-mitogen-activated protein kinase kinase-extracellular signal-regulated kinase), phosphatidylinositol-3 kinase-AKT and PAK-JNK-JNK (p21-activated protein kinase–c-Jun NH2 terminal kinase kinase–c-Jun NH2 terminal kinase; ref. 1). Gefitinib is an orally administered small molecule that specifically inhibits EGFR tyrosine phosphorylation (3). Clinical trials revealed that there was a significant variability in response to gefitinib. Good clinical response has been observed most frequently in women, nonsmokers, patients with adenocarcinomas, and Japanese patients (4, 5). However, it has not been possible to predict gefitinib sensitivity by levels of EGFR overexpression as determined by immunohistochemistry (6) or immunoblotting (7). The factor(s) that determine gefitinib sensitivity has long been an enigma. It has been reported recently that activating mutations of EGFR are present in a subset of pulmonary adenocarcinomas and that tumors with EGFR mutations are highly sensitive to gefitinib (8, 9). Furthermore, the incidence of EGFR mutations is higher in Japanese than in Caucasian patients (8). In this study, we searched for EGFR mutations in a large cohort of unselected Japanese NSCLC to correlate them with clinical and pathologic features including KRAS or TP53 mutations.

MATERIALS AND METHODS

Patients. Primary tumor samples were obtained from 277 unselected patients with lung cancer who underwent potentially curative pulmonary resection at the Department of Thoracic Surgery, Aichi Cancer Center Hospital from May, 2000 through November, 2000 and from January, 2001 through December, 2002, after obtaining appropriate approval from the institutional review and patients’ written informed consent. These cases corresponded to 82% of all consecutive cases. Inclusion of the cases into this study was dependent on availability of frozen tumor material. About 20 cases were excluded because tumor cells were too few to sufficiently extract tumor RNA because of inflammation and/or necrosis. There were 159 males and 118 females with an age at diagnosis ranging from 26 to 89 (median 64) years. One hundred fifteen-nine patients had stage I disease, 39 had stage II, 74 had stage III and 5 had stage IV diseases. There were 224 adenocarcinomas, 35 squamous cell carcinomas, 9 large cell carcinomas, 5 adenosquamous carcinomas, 3 small cell carcinomas, and 1 carcinoid. There were 115 never-smokers and 162 ever-smokers including current and former smokers. Smoking history was obtained by interviewing each patient at admission or first outpatient visit.

Molecular Analysis of Lung Cancer Specimens. Tumor samples were obtained at the time of surgery, rapidly frozen in liquid nitrogen, and stored at −80°C. Frozen tissue of the tumor specimens were grossly dissected to enrich as much tumor cells as possible by a surgical pathologist (Y. Y.). We isolated total RNA using the RNAeasy kit (Qiagen, Valencia, CA). The first four exons (exons 18–21) of the seven exons (exons 18–24) that code for TK domain of the EGFR gene that includes all of the mutations reported thus far (8, 9) were amplified with primers F1 (5′-AGCTTGTG-GAGCCTTGTAAACC-3′) and R1 (5′-TAAAAATATTGATCATGGAATATCTC-3′), in a one-step reverse transcription-PCR setup with Qiagen OneStep reverse transcription-PCR kit (Qiagen, Valencia, CA). The cDNA sequence of EGFR gene was obtained from GenBank (accession number NM005288). Reverse transcription-PCR conditions were available after request. Reverse transcription-PCR products were diluted and cycle-sequenced with the Big Dye Terminator v3.1/1.1 cycle sequencing kit (Applied Biosystems, Foster City, CA). Sequencing reactions were electrophoresed on an ABI PRISM 3100 (Applied Biosystems). Both the forward and reverse sequences obtained were analyzed by BLAST and chromatograms by manual review.

KRAS and TP53 Gene Analysis. We had previously examined the same cohort for KRA5 mutations and TP53 mutations (10, 11). Briefly, TP53 gene (exon 4 through 10) and KRAS gene (exons 1 and 2) were amplified and directly sequenced with ABI PRISM 310 Genetic Analyzer (Applied Biosystems).

Statistical Analysis. For comparisons of proportions, the χ2 test or Fisher’s exact test were used. The Kaplan-Meier method was used to estimate the probability of survival as a function of time, and survival differences were
Forty-six of the 54 point mutations were from a T to a G transversion.

It is noted that, in all cases, such alterations were in-frame. A deletion
yielding various changes in amino acid sequences as shown in

However, 22 deletions were coupled with point mutations or inser-
tions of five amino acid residues ELREA from codon 746 to 750.

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All of the 52 deletion mutations occurred around codons 746–750
in exon 19. About half (25 of 52) of deletion mutations were simple
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in Figure 1. It is noted that, in all cases, such alterations were in-frame.

Forty-six of the 54 point mutations were from a T to a G transversion
at the second nucleotide of codon 858 in exon 21 resulting in substi-
tution of leucine with arginine residue. Four of the point mutations
occurred simultaneously. Furthermore, it is of note that only mutant
sequences were present in chromatograms in 19 of 52 deletions, 13 of
the patients nor with stage of diseases. There was no difference in
the patients nor with stage of diseases. There was no difference in

RESULTS

EGFR Mutations in Unselected Lung Cancer Specimens. Of
277 unselected patients who underwent surgical resection of their
tumors, we found that 111 patients (40%) had mutations in exons
18–21 of the EGFR gene. There were 52 deletion mutations, 54 point
mutations, and 5 duplication/insertion mutations. In 14 tumors, cor-
responding cDNA from normal lung tissue far from the tumors was
also sequenced, which confirmed that all these mutations were so-
matic. Details of the resulting changes in EGFR protein as a conse-
quency of these mutations are illustrated in Figure 1.

In Figure 1. Analysis of 111 EGFR mutations in the TK domain of the EGFR gene found
in unselected cases with lung cancer.

I. Deletions

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A) Simple deletions

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B) Deletion plus point mutations

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C) Deletion plus insertion

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Codon 719

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Codon 858

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Codons 768 and 769

S768L and S769L

Further Analysis of Patients with Adenocarcinoma. EGFR
mutations were found almost exclusively in adenocarcinomas with only
one exception; hence, we did more detailed analysis limited to this
subset of patients (Table 1). EGFR mutations were also significantly
frequent in female, nonsmoking patients. When we divided
never-smokers into 3 categories depending on smoke exposure, there was a
trend that the higher the exposure, the lower the incidence of EGFR
mutations. EGFR mutations were significantly more frequent in well
to moderately differentiated adenocarcinomas (58%) than in poorly
differentiated adenocarcinomas (30%; P < 0.001). There were five
bronchioloalveolar cell carcinomas (BAC) in our cohort, of which three harbored EGFR mutations (60%), according to the World Health
Organization classification of lung cancers (which states that BAC is
a true noninvasive cancer without stromal or pleural invasion; ref. 12).
It seemed that EGFR mutations were associated neither with age
of the patients nor with stage of diseases. There was no difference in
incidence of EGFR mutations between both sexes in patients of age 50
(average age of menopause in Japan) or younger, although the number
of patients of this age group was small (2 of 7 males, 2 of 7 females).

Our preliminary study indicated that patients with EGFR mutations
survived for a longer period after gefitinib treatment than those
without EGFR mutations. However, EGFR mutations also might
have prognostic impact on patients with pulmonary adenocarcinoma,
even when the patients were not exposed to gefitinib because EGFR
mutations defined subsets of pulmonary adenocarcinoma with distinct features as described. Therefore, we did survival analysis in patients excluding those who were treated with gefitinib when they had recurrent diseases. The Kaplan-Meier curve (Fig. 2) indicated that EGFR mutations did not affect prognosis of the patients (P/H11005 0.9933), although the follow up period was relatively short (median follow up, 788 days).

**KRAS and TP53 Gene Mutational Analysis.** Of 224 patients with adenocarcinoma, KRAS and TP53 data were available for 196 and 192 patients, respectively. KRAS mutations were present in 26 of 196 patients (13%; 22 at codon 12, 1 at codon 13, and 3 at codon 61). TP53 mutations were present in 79 of 192 (41%). KRAS and TP53 mutations were significantly more frequent in ever-smokers, respectively [20% versus 6% for KRAS (P = 0.0054) and 54% versus 30% for TP53 (P < 0.001)]. Interestingly, EGFR mutations were never found in tumors with KRAS mutations, showing a mutually exclusive relationship. By contrast, EGFR mutations and TP53 mutations seemed to occur independently. Figure 3 shows the relationship among the three mutations by a Venn diagram in 192 patients in whom information about the status of these three genes was available.

TP53 mutations seemed more widely distributed in tumors without EGFR mutations (Fig. 4). Of seven mutations either at codon 157, 248, or 273 in which strong and selective adduct formation of benzo(a)pyrene diol epoxide, one of the major tobacco carcinogens, occurs (13), six were in tumors without EGFR mutations (Fig. 3). Furthermore, of 16 mutations caused by a G to a T transversions characteristic of mutations caused by aromatic polycyclic hydrocarbons (14), 15 were in tumors without EGFR mutations (Fig. 3).

**DISCUSSION**

Adenocarcinoma is the most predominant histologic subtype, and its incidence is increasing in Japan. Registration of resected lung cancer in Niigata prefecture, Japan, revealed that the incidence of adenocarcinoma is 71% of 1211 patients operated on from 2001 to 2002 (15). In our institution, adenocarcinoma accounted for 54% of 975 patients who were operated on from 1965 through 1995, 69% of 522 from 1996 through 2000, and 76% of 407 from 2001 through 2003. Considerable evidence indicates that the EGFR pathway also plays an important role in both the pathogenesis and the progression of lung cancer (1).

We found that 40% of 277 unselected patients with lung cancer carried mutations in the TK domain of the EGFR gene. More than 90% of the mutations were either deletions around codons 746–750 in
Adenocarcinomas without EGFR mutations

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Adenocarcinomas with EGFR mutations

exon 19 or L858R in exon 21, which all flank the ATP-binding pocket that is important for TK activity (8, 9). We also noted that in about 30% of the cases with EGFR mutations, only bands derived from mutant allele were detected on chromatogram. This is somewhat puzzling considering the heterozygous nature of the EGFR mutations reported thus far (8, 9) and the presence of stromal cells in resected tumor specimens. This finding may suggest that loss of wild-type alleles or amplification of mutant alleles accompanied with mutations in these cases, as indicated by Minna et al. (16).

EGFR mutations were almost exclusively present in adenocarcinoma. Mutations were more prevalent in females and nonsmokers, confirming and extending the results of previous reports (8, 9). It is noteworthy that these characteristics and Japanese ethnicity are all predictors of gefitinib sensitivity at least by univariate analysis (4, 5). Multivariate analysis suggested that nonsmoking status and adenocarcinoma histology independently contributed to gefitinib sensitivity at least by univariate analysis (4, 5). We also noted that well to moderately differentiated adenocarcinomas showing BAC feature show higher incidence of EGFR mutations than poorly differentiated ones. This observation might be relevant to the difference in smoking status, because KRAS mutations were more frequent in smokers as reported previously (18). In contrast, the incidence of TP53 mutations was not associated with EGFR mutations, although TP53 mutations also occurred more frequently in smokers (17). However, TP53 mutations in tumors without EGFR mutations showed characteristics of mutations caused by tobacco carcinogens in terms of sites or base substitution patterns (13, 14).

We were able to confirm higher incidence of EGFR mutations in Japanese patients. Lynch et al. found EGFR mutation in 2 of 25 unselected United States patients (9), and Paez et al. (8) did so in 1 of 61 United States patients and 15 of 58 Japanese patients. The reason for this marked difference between Japanese and United States patients is not very clear. However, difference in incidence of nonsmoking patients between Japanese and American female patients with lung cancer may partly account for this. In our cohort, 83% of female patients and 10% of male patients were never-smokers. This trend is common in Japan. For example, Toyooka et al. (22) and Minami et al. (23) reported that the proportion of never-smoking women in lung cancer patients is 96% and 75%, respectively. This makes quite a contrast with the fact that only 15% of 706 United States female and 6% of 1,347 male patients with lung cancer are never-smokers (24).

We found that EGFR mutations and KRAS mutations known to play an important role in pathogenesis of adenocarcinoma of the lung (25) were strictly mutually exclusive, reminding us of a similar exclusionary relationship between retinoblastoma and p16 inactivation in lung cancer (26). This finding may be explained by the fact that the KRAS-mitogen-activated protein kinase pathway is one of the downstream signaling pathways of EGFR (1). Because it has been shown that L858R and dell747-P753insS are activating mutations that result in markedly increased phosphorylation of EGFR when EGF was added (8, 9), tumors with KRAS mutations that already have activated further downstream effectors do not need to have EGFR mutations. The high incidence of EGFR mutations in lung adenocarcinomas may explain why KRAS mutations are lower in Japanese than in Caucasian patients. In the present study, KRAS mutations were found in 13% of adenocarcinomas, whereas they were present in 33% of Dutch cases (25). This may be also at least partially attributable to the difference in smoking status, because KRAS mutations were more frequent in smokers as reported previously (18). In contrast, the incidence of TP53 mutations was not associated with EGFR mutations, although TP53 mutations also occurred more frequently in smokers (17). However, TP53 mutations in tumors without EGFR mutations showed characteristics of mutations caused by tobacco carcinogens in terms of sites or base substitution patterns (13, 14).

We also noted that well to moderately differentiated adenocarcinomas had a significantly higher incidence of EGFR mutations than poorly differentiated ones. This observation might be relevant to the fact that adenocarcinomas showing BAC feature show higher sensitivity to gefitinib (27). However, when we used the strict criteria as stated by the World Health Organization Classification of lung tumors (12), our cohort included only five BAC, of which three had EGFR mutations. Unfortunately, these strict criteria are not applied by many pathologists, leading to considerable confusion between BAC and adenocarcinoma with BAC features in the literature. Alternatively, we proposed terminal respiratory unit type adenocarcinoma that is characterized by morphological resemblance to type II pneumocytes, Clara cells, and/or bronchioloalveolar cells as well as expression of thyroid transcription factor-1 and surfactant proprotein B (refs. 28, 29). In the World Health Organization classification, most nonmucinous bronchioloalveolar, mixed bronchioloalveolar and acinar subtypes, and some papillary subtypes belong to the terminal respiratory unit type adenocarcinoma (28, 29). We found that most adenocarcinoma with EGFR mutations were categorized into terminal respiratory unit type adenocarcinoma.6

EGFR mutations were not associated with stage of disease, suggesting that EGFR mutations occurs relatively early in clinical course and are associated with pathogenesis of adenocarcinoma rather than progression.

In conclusion, we found a high incidence of EGFR mutations in Japanese patients with pulmonary adenocarcinoma, especially in those who never smoked. EGFR mutations were never present in tumors with KRAS mutations, indicating possibilities of genotype-oriented approach for pulmonary adenocarcinoma.

ACKNOWLEDGMENTS

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REFERENCES

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