Epidermal Growth Factor Receptor Mutations in Small Cell Lung Cancer

Akiko Tatematsu,1 Junichi Shimizu,2 Yoshiko Murakami,4 Yoshitsugu Horio,2 Shigeo Nakamura,5 Toyoaki Hida,2 Tetsuya Mitsudomi,3 and Yasushi Yatabe1

Abstract

Purpose: The vast majority of epidermal growth factor receptor (EGFR) mutations occur in lung adenocarcinoma, and even rare cases of other subtypes with this mutation, such as adenosquamous cell carcinoma, are associated with adenocarcinoma histology. According to this adenocarcinoma-specific nature of EGFR mutation, analysis of EGFR mutations with small cell lung cancers (SCLC) may provide a clue to its histogenesis.

Experimental Design: The mutational status of the EGFR gene was accessed in a cohort of 122 patients with SCLC; all patients were from a single institute. When the EGFR mutated, its gene copy number was also examined.

Results: EGFR mutations were detected in five SCLCs (4%). The patients were mainly in the light smoker and histologic combined subtype. All but one of the tumors harbored gene amplifications. Notably, in three tumors of the combined SCLC subtype, both components of adenocarcinoma and SCLC harbored an EGFR mutation, whereas gene amplification was detected only in the adenocarcinoma component. A partial response was achieved in a patient (with an EGFR mutation) who was treated with gefitinib.

Conclusions: Although EGFR mutations are rare in SCLC, a combined subtype of SCLC with adenocarcinoma in light smokers may have a chance of harboring EGFR mutations. For patients with an EGFR mutation, EGFR tyrosine kinase inhibitor can be a treatment option. In terms of molecular pathogenesis, it is suggested that some SCLCs may have developed from pre-existing adenocarcinomas with EGFR mutations, but the development may not be simply linear, taking into consideration the discordant distribution of EGFR amplification.

The vast majority of epidermal growth factor receptor (EGFR) gene mutations are detected in lung adenocarcinoma. A comprehensive analysis by Shigematsu and Gazdar reported that non–adenocarcinomatous lung cancers with EGFR gene mutations were restricted to <5% of lung cancers (1). Although it is rare in other histologic subtypes, adenosquamous cell carcinoma showed the highest frequency among lung cancers, followed by squamous cell carcinoma and large cell carcinoma. In contrast, small cell carcinoma was not listed among EGFR-mutated lung cancers following a comprehensive examination of 1,380 lung tumors, which suggests a different molecular pathogenesis for this type of cancer. However, two patients (who had never smoked), recently reported having EGFR mutations with small cell lung cancers (SCLC; refs. 2, 3). In the first case, published in The New England Journal of Medicine, the patient with adenocarcinoma was initially treated with erlotinib. The recurrent tumor in the brain consisted of small cell carcinoma, which also harbored an EGFR mutation. Because the mutational status of the EGFR gene in the initial adenocarcinoma was not addressed, the clonal relationship between the two tumors was not clear. Another case was also a never-smoker who developed widespread SCLC. Mutation analysis revealed a typical EGFR gene deletion at exon 19. The tumor responded well to gefitinib treatment, and both primary and metastatic tumors regressed dramatically (3).

The incidence of EGFR mutation is quite high among the Japanese (~ 30-40% of non–small cell lung cancers on average) in contrast to ~10% of patients in the United States and in European countries (1, 4, 5). The clinicopathologic characteristics of patients with EGFR mutations include female sex, not smoking, and less frequent p53 mutation (4–6), which are very different from those of SCLC. It is therefore expected that EGFR mutations are very rare or absent in SCLC. A comprehensive analysis of EGFR mutations in SCLCs has not been reported in the literature; however, we believe it is important to determine its incidence, especially in mutation-endemic countries. In this study, we comprehensively examined a total of 122 SCLCs to address mutation incidence in SCLC.
EGFR Mutations in SCLC

Translational Relevance

It is well known that epidermal growth factor receptor (EGFR) mutations are prevalent in female nonsmokers. However, EGFR mutations have recently been reported in some patients with small cell lung cancer (SCLC). In this study, we first examined a large series of SCLCs to address mutation incidence. Because the incidence of EGFR mutations differs between the United States and Japan, these data are important in determining the significance of ethnicity and frequency of EGFR mutations. As a result, a combined subtype of SCLC with adenocarcinoma in light smokers may have a chance of harboring EGFR mutations, although EGFR mutations are generally rare in SCLC. Notably, one such patient with an EGFR mutation achieved a partial response to gefitinib treatment. Although clinical relevance needs to be examined in more patients, EGFR tyrosine kinase inhibitor can be a treatment option for patients with SCLCs harboring an EGFR mutation.

Materials and Methods

Patients. Among 150 patients that were diagnosed with SCLC in the last 7 years at the Department of Pathology and Molecular Diagnostics, Aichi Cancer Center in Nagoya, Japan, specimens from 122 patients were available for molecular genetic analysis, and these were the subject for the current study. This series included 102 specimens obtained by biopsy, and 20 from surgically resected tumors. Histologic diagnosis of SCLC was based on the standard criteria defined by WHO classification (7). The study was a part of a comprehensive lung cancer research program, which had been approved by the institutional review board.

EGFR mutation analysis. All the specimens were fixed with formalin, and the EGFR mutation was analyzed with the method described previously, using an unstained paraffin section (8). This technique allows the detection of tumor cells constituting as little as 5% of a mixture of tumor cells with normal tissue using a single paraffin section. When frozen tissues were available, the mutational status of EGFR was accessed with standard reverse transcription-PCR coupled direct sequencing, as described previously (4), in addition to DNA-based analysis. In this assay, the mutational status of the L858R point mutation and the deletion of exon 19 were obtained when we examined paraffin sections, whereas direct sequencing using RNA revealed the mutational status of the whole tyrosine kinase domain.

Copy number analysis of EGFR. Gene amplification was analyzed by fluorescence in situ hybridization, using the LSI EGFR SpectrumOrange/CEP 7 SpectrumGreen probe (Vysis; Abbott Laboratories) according to the manufacturer’s protocol. Fluorescence in situ hybridization was done on serial paraffin sections in the same tissue areas as the gene dosage analysis. A more than 4-fold increase of EGFR gene signals relative to CEP7 signals was considered a gene amplification. The results were confirmed by TaqMan-based gene dosage analysis as described previously (9).

Statistical analysis. Fisher’s exact test for independence and unpaired t tests were used to show the correlation of clinicopathologic variables with EGFR mutation. P < 0.05 was considered statistically significant.

Results

SCLCs with EGFR mutation. Among 122 SCLCs examined (Table 1), we found EGFR mutations in five cases (4%). The mutations included L858R point mutations (three patients), a G719A point mutation (one patient), and a 15-bp deletion in exon 19 (one patient). Both frozen and paraffin tissues of 10 tumors, 2 of which harbored the above EGFR mutation, were available for analysis. They were examined using both reverse transcription-PCR coupled sequencing and assays for paraffin sections. The results were identical to those of the other analysis.

Clinicopathologic features of SCLCs with EGFR mutations. EGFR mutations were restricted to a very minor proportion (5 of 122; 4%) of SCLCs, and the clinicopathologic features of the patients with the mutation showed a trend similar to those of patients without the mutation. There were no significant differences in age, sex, and clinical stage at presentation. In contrast, accumulated smoking dose (pack-years) in patients with the mutation was much lower, and the difference was statistically significant (unpaired t test, P = 0.02). Indeed, three of the five patients with EGFR mutations were smokers with less than 40 pack-years. It is of note that one of the five patients was treated with gefitinib, and partial response was observed (case 2).

Morphologic features of SCLC with EGFR mutations. There are two subtypes of SCLC in the current WHO classification; thus, we examined whether the morphologic subtypes were associated with EGFR mutations. The combined subtype constituted a minor proportion (15 of 122, 12%) in this series, and three of them were positive for EGFR mutations (Table 1). Preferential mutation in the combined type were statistically significant (Fisher’s exact test, P < 0.01). In two cases of the combined subtype (cases 1 and 3), SCLC components consisted of only a part of the nodule, and adenocarcinoma components constituted the predominant part. The representative morphologic features are displayed in Fig. 1. The other combined subtype (case 5) showed a mixture of SCLC and adenocarcinoma components throughout the tumor.

EGFR amplification in SCLCs. We have recently reported that EGFR amplification occurs in association with EGFR mutation (9). We therefore examined the EGFR gene copy number in the five SCLCs with EGFR mutations. Four of them showed gene amplification (Table 2), and the signals of the EGFR gene were loosely clustered (Fig. 2), suggesting a high degree of amplification, as is the case in homogeneously staining region patterns. Notably, three cases of combined SCLC subtypes harbored EGFR amplifications only in the adenocarcinoma component, but not in the SCLC component (Fig. 2).

Discussion

SCLC is a distinct neoplasm in terms of clinical aggressiveness, despite its high response to both chemotherapy and irradiation therapy. This aggressive cancer does not confer to
thelung, and it can develop in organs other than the lung, all of which share distinctive pathologic and immunohistochemical features, irrespective of their site of origin. These extrapulmonary carcinomas are characterized by frequent admixture with conventional carcinoma of the originating organ, such as adenocarcinoma in gastrointestinal tumors, and squamous cell carcinoma in head and neck cancers. This is true in SCLC. Nicholson et al. reported that 28 of 100 surgically resected SCLCs had a histologic component of non–small cell lung cancers (10). In our study, \textit{EGFR} gene mutation was detected in 5 of 122 SCLCs. Because \textit{EGFR} mutation was quite specific for adenocarcinoma, it is suggested that SCLCs with \textit{EGFR} mutations are associated with adenocarcinoma. Indeed, three of the five combined SCLCs had an adenocarcinoma component but not a squamous cell carcinoma component.

It has been suggested that the amine-precursor uptake and decarboxylase cells described by Pearse in 1969 (11) are the putative original cells of small carcinoma. These cells were described as comprising a neuroendocrine system in many organs, and as having ultrastructural features shared by small cell carcinomas. However, this hypothesis cannot explain the existence of combined SCLC, which is an admixture of small cell carcinoma and conventional adenocarcinoma or squamous cell carcinoma. Therefore, a multipotential cancer stem cell capable of divergent differentiation has been suggested as a putative origin of small cell carcinoma. Alternatively, the SCLC component may arise as a consequence of undifferentiated transformation from conventional carcinoma. Case 2 in the present study supported the latter scenario, because SCLC is the only component that metastasized to the lymph nodes. Furthermore, the vast majority of lung cancers harboring \textit{EGFR} mutations are adenocarcinomas, supporting the idea that the adenocarcinomas existed prior to the development of SCLC in at least three of the cases of SCLC with \textit{EGFR} mutations.

However, the results of \textit{EGFR} amplification analyses support the former possibility. In three cases of combined subtype of SCLC with an \textit{EGFR} mutation, only the adenocarcinoma component, not the SCLC component, harbored the amplification. This is in contrast to the uniform detection of \textit{EGFR} mutations in both components. Because \textit{EGFR} mutations in SCLC are rather rare, it is unlikely that the two components are independent of their origin. Rather, it is believed that they originated from a common ancestor. Therefore, it is suggested that the mutation occurred before a point branching off to SCLC and adenocarcinoma components, whereas gene amplification was acquired after that point. Cases 3 and 5 may be considered to have followed this scenario. However, case 1 was inconsistent with it because SCLC emerged after the therapy.

In case 1, the initial adenocarcinoma harbored both \textit{EGFR} mutation and amplification. Subsequently, SCLC, which lacked...
gene amplification, developed after the chemotherapy and gefitinib therapy. It was unlikely that the amplification was removed from cancer cells due to therapy. We have recently reported heterogeneous distribution of EGFR amplification in lung adenocarcinoma (9), and thus we suggested that only a clone without amplification was selected, survived, and was subsequently transformed to SCLC. The reported SCLC with EGFR mutation followed this pattern of progression (2, 3, 12), and lack of EGFR expression in SCLC may be a clue to this phenomenon. Under heavy selection pressure by gefitinib therapy, only a clone which is independent of EGFR-driven growth signals has a chance to expand. Transformation to SCLC fulfills this condition because EGFR expression in the SCLC was at a very low or undetectable level (13–15). Indeed, the SCLC component lacked EGFR expression, in contrast to positive expression in the initial adenocarcinoma and adenocarcinoma components (data not shown). This may be another mechanism for tolerance to the EGFR tyrosine kinase inhibitor, in addition to secondary genetic alterations.

Clinically, it is noteworthy that a partial response was achieved in one of the patients with an EGFR mutation who was treated with gefitinib. Because EGFR expression is at a very low or undetectable level in SCLC, it would be expected that EGFR tyrosine kinase inhibitors are not effective against SCLC even if the EGFR is mutated. However, a similar marked reduction of such cancers by EGFR tyrosine kinase inhibitor treatment has also been reported (2, 3). EGFR tyrosine kinase inhibitors may be a treatment option for SCLC with EGFR mutations, and a mutation test may be helpful to select such patients in addition to clinical characteristics, including the light smoker and histologic combined subtypes.

In summary, we examined 122 SCLCs and found 5 (4%) of them harboring EGFR mutations. The SCLCs with EGFR mutations were seen in the light smoker and histologic combined subtypes. Because of the specific involvement of EGFR mutations in adenocarcinoma, it is suggested that the SCLCs may have developed from pre-existing adenocarcinomas. However, we have concluded that this development may...

Table 2. Clinicopathologic features of five SCLCs with EGFR mutations

<table>
<thead>
<tr>
<th>Case</th>
<th>Sex/Age (y)</th>
<th>Pack-years smoking</th>
<th>EGFR mutation</th>
<th>EGFR amplification</th>
<th>Stage</th>
<th>Sample and histologic subtype</th>
<th>Clinical course</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>F/36</td>
<td>0</td>
<td>L858R</td>
<td>Amplified (&gt;6)*</td>
<td>ED</td>
<td>Resected tumor; combined type (diagnosis of adenocarcinoma with a biopsy prior to surgery)</td>
<td>Stage IV adenocarcinoma was treated with CBDCA and PAC, followed by gefitinib, because of positive EGFR mutation with a biopsy specimen. Partial response was achieved but the tumor regrew. It was surgically resected, and histologically revealed to be combined small and adenocarcinoma.</td>
</tr>
<tr>
<td>2</td>
<td>M/81</td>
<td>40</td>
<td>G719A</td>
<td>Amplified (&gt;6)</td>
<td>ED</td>
<td>Biopsy specimen; conventional type</td>
<td>Stage IV SCLC was treated with gefitinib, because of the detection of G719A mutation using a lung biopsy specimen. A partial response was obtained.</td>
</tr>
<tr>
<td>3</td>
<td>M/69</td>
<td>30</td>
<td>L858R</td>
<td>Amplified (&gt;6)*</td>
<td>LD</td>
<td>Biopsy specimen, combined type</td>
<td>A biopsy specimen for lung cancer (cT1N0M0) was surgically removed, and subsequent pathologic examination revealed combined SCLC. Adjuvant chemotherapy (CDDP and CPT-11) were administered. The patient is alive without recurrence.</td>
</tr>
<tr>
<td>4</td>
<td>F/89</td>
<td>2.5</td>
<td>L858R</td>
<td>Low polysomy</td>
<td>LD</td>
<td>Biopsy specimen; conventional type</td>
<td>A biopsy specimen for lung cancer (cT1N0M0) was diagnosed as SCLC. The patient refused any therapy, and was not a part of follow-up.</td>
</tr>
<tr>
<td>5</td>
<td>M/65</td>
<td>67.5</td>
<td>Ex.19Del</td>
<td>Amplified (&gt;6)*</td>
<td>LD</td>
<td>Resected tumor; combined type (cytological diagnosis of SCLC prior to surgery)</td>
<td>cT1N1M0 cancer was treated with CDDP and TXT, followed by surgical resection of the tumor. Combined SCLC was revealed, and the patient was treated with adjuvant chemotherapy and irradiation. Three years later, SCLC recurred.</td>
</tr>
</tbody>
</table>

Abbreviations: F, female; M, male; LD, limited disease; ED, extended disease; CBDCA, carboplatin; PAC, paclitaxel; CDDP, cisplatin; CPT-11, irinotecan.

* Only in the adenocarcinoma component.
not be simply linear, considering the discordant distribution of EGFR amplification.

Acknowledgments

The authors thank Noriko Shibata for her excellent technical assistance with the molecular genetic experiments, Edwin L. Carty for English editing, and Hiroji Ishida and the members of the Department of Pathology, Aichi Cancer Center, for their assistance with the preparation of paraffin sections.
Epidermal Growth Factor Receptor Mutations in Small Cell Lung Cancer

Akiko Tatematsu, Junichi Shimizu, Yoshiko Murakami, et al.


Updated version
Access the most recent version of this article at:
http://clincancerres.aacrjournals.org/content/14/19/6092

Cited articles
This article cites 14 articles, 5 of which you can access for free at:
http://clincancerres.aacrjournals.org/content/14/19/6092.full.html#ref-list-1

Citing articles
This article has been cited by 8 HighWire-hosted articles. Access the articles at:
/content/14/19/6092.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.