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A Rapid, Sensitive Assay to Detect EGFR Mutation in Small Biopsy Specimens from Lung Cancer

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It has been demonstrated that lung cancers, specifically a subset of pulmonary adenocarcinomas, with epidermal growth factor receptor (EGFR) mutation are highly sensitive to EGFR-targeted drugs. Therefore, a rapid, sensitive assay for mutation detection using routine pathological specimens is demanded in clinical practice to predict the response. We therefore developed a new assay for detecting EGFR mutation using only a paraffin section of a small biopsy specimen. The method was very sensitive, detecting as few as 5% cancer cells in a background of normal cells, the results usually being obtained within 4 hours. Furthermore, it was accurate, as shown by the high concordance with reverse transcriptase-polymerase chain reaction-coupled direct sequencing (186 of 195, 95%). The practical application of this assay to 29 cases treated with gefitinib resulted in a high prediction rate: 10 of the 11 responders were shown to be positive for the mutation, and all patients with progressive disease were negative. In addition, a mutation at codon 790, conferring gefitinib resistance, was successfully analyzed in a similar manner. In conclusion, the assay is a rapid, sensitive method using paraffin sections of biopsy specimens without a tumor cell-enrichment procedure and is quite useful to select a treatment of choice in clinical practice. *(J Mol Diagn 2006, 8:335–341; DOI: 10.2353/jmoldx.2006.050104)*

During the last decade, small molecules that inhibit receptor protein kinase activity have been developed.[1] Gefitinib is one such drug that targets epidermal growth factor receptor (EGFR) kinase. The EGFR, also known as HER1 or ErbB, is a 170-kd receptor tyrosine kinase (TK) that dimerizes and phosphorylates several tyrosine residues on the binding of several specific ligands.[2,3] These phosphorylated tyrosines serve as binding sites for several signal transducers that initiate multiple signaling pathways, resulting in cell proliferation, migration and metastasis, evasion of apoptosis, or angiogenesis, through Ras-Raf-MEK-ERK, phosphatidylinositol-3 kinase-AKT, and PAK-JNKK-JNK pathways. EGFR is expressed in more than 80% of non-small-cell lung cancers (NSCLCs), in addition to a wide range of epithelial cancers. However, clinical trials have shown significant variability in response to gefitinib: 10 to 20% of patients respond to gefitinib treatment, and in some patients, the response is dramatic, whereas the remaining patients show no response. Although further analysis has revealed some prevalence in responders, no definite determinant of the response has been established.

Recently, it has been reported that EGFR somatic mutation can be identified in a subset of pulmonary adenocarcinomas and that tumors with EGFR mutations are highly sensitive to gefitinib.[4,5] This correlation has subsequently been confirmed by our group and others,[6–9] and thus the development of a rapid and sensitive assay to predict gefitinib response by means of the presence or absence of the mutation is demanded clinically. Paraffin sections are a convenient source for such an assay in practice, but most studies using immunohistochemistry failed to predict the response.[10–12]

In this study, we introduce a practical approach using a rapid screening assay of EGFR mutation to predict gefitinib response. This method uses only a single paraffin section of a small biopsy specimen and does not require a tumor cell-enrichment procedure. The result is usually obtained within 4 hours and can be applied to a large number of samples.

Materials and Methods

Patients and Tissues

A series of 195 NSCLCs, in which the mutational status of the EGFR-TK domain with both reverse transcriptase-polymerase chain reaction (RT-PCR)-coupled direct sequencing and the new assay presented here was accessible, was used for this study. Some of the mutational results by RT-PCR-coupled direct sequencing have been

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reported previously.[13] DNA for the new assay was prepared from a section of tissue microarray blotted with 0.6-mm tissue cores of the 195 cases. To examine a correlation with the clinical response evaluated according to the guidelines of Response Evaluation Criteria in Solid Tumors (RECIST), a paraffin section of each biopsy specimen was examined for EGFR mutation in 29 patients treated with gefitinib because of the failure of first or second line therapy. To analyze the codon 790 mutation, which has been reported in association with acquired resistance to gefitinib treatment, four tissues were examined. One, reported as a rare case, was shown to have T790M, independent of gefitinib treatment.[13,14] The other three presented with a recurrent tumor after gefitinib treatment, and the recurrent tumor and corresponding initial tumor tissue were examined. Appropriate approval was obtained from the institutional review committee in addition to written informed consent from the patients.

Mutation Assay by RT-PCR-Coupled Direct Sequencing

Frozen tissue from the tumor specimens was grossly dissected to pass as many tumor cells as possible into the extraction solution (at least 25% of tumor cell content), followed by the extraction of total RNA with an RNeasy kit (Qiagen, Valencia, CA). For RT-PCR-coupled direct sequencing, the EGFR tyrosine kinase domain (exon 18 to 24) was amplified, and then the products were directly sequenced with an ABI PRISM 310 Genetic Analyzer (Applied Biosystems, Foster City, CA). The primer set used was described previously.[13]

DNA Extraction from Paraffin-Embedded Tissues

Tumor cell-rich area in a hematoxylin and eosin-stained section was marked under a microscope, and tissues were scratched from the area of another deparaffinized unstained section. Pieces of the scratched tissue were incubated with 1× PCR buffer containing 100 μg/ml proteinase K for 1 hour at 54°C. After heat inactivation with 95°C for 3 minutes, the solution was directly used for template DNA for the assay.

EGFR Mutation Detection

To detect the point mutations at codons 858 and 790 of the EGFR gene, we used the cycleave PCR technique. This technique is based on a chimeric DNA-RNA-DNA probe labeled with a fluorescent dye and quencher at each end. The RNA sequence of the probes corresponds to that of the wild type and point mutation labeled with FMA and ROX, respectively. When mutant molecules are present in the sample and PCR-amplified DNA generates a complete hybrid with the RNA portion of the mutant probe, RNase-H digests the probe at the RNA-DNA heteroduplex into two pieces, leading to a significant increase in fluorescence intensity by separation of the fluorescent dye from the quencher. The intensity of the wild-type probe served as an internal control for the assay. This assay was performed using a cycleave PCR core kit (TAKARA, Co., Ltd., Ohtsu, Japan), and sequences of the primer set and the probes were as follows: PCR forward primer for L858R, 5′-AGGAACGTACTGGTGAAAAC-3′; PCR reverse primer for L858R, 5′-TCCCTGGTGTCAGGAAAATG-3′; wild-type probe for L858R, 5′ FAM-CCA *U* CCCAAAAT-Eclipse 3′; probe for L858R mutation, 5′ FAM-CCC*G*CCCAAAAT-Eclipse 3′; PCR forward primer for T790M, 5′-ATCTGCCTCACCTCCAC-3′; PCR reverse primer for T790M, 5′-CAATATTGTCTTTGTGTTC-3′; wild-type probe for T790M, 5′ FAM-TGC*G*TGATGAG-Eclipse 3′; probe for T790M mutation, 5′ FAM-TGC*A*TGATGAG-Eclipse 3′ (italics represent RNA). Fluorescent signals were quantified with a Smart Cycler system (SC-100; Cepheid, Sunnyvale, CA).

To detect the deletion in exon 19 of the EGFR gene, common fragment analysis was used. Sample DNA was amplified with an FAM-labeled primer set as follows: forward, 5′ FAM-TCACAATTGCCAGTTAACGTCT-3′, and reverse, 5′-CAGCAAAGCAGAAACTCACATC-3′. PCR products were electrophoresed on an ABI PRISM 310. When a deletion mutation was present, PCR amplified the shorter segment of DNA, creating a new peak in an electropherogram.

Sensitivity Assay

In the preliminary examination, we prepared a mutation-positive control DNA, which contained exactly one-half each of wild-type and mutant molecules. According to the mixture ratio, the mutation-positive control DNA was mixed up with normal DNA, the concentration of which was equal to that of the mutation-positive control DNA. Therefore, 5% of tumor cells corresponded to 2.5% of mutant molecules in background of wild-type molecule. Using these mixtures of DNA, we examined the sensitivity of the assays (deletion of exon 19 and point mutation of L858R and T790M).

Statistical Analysis

The χ^2 test and Fisher's exact test for independence compared incidences of EGFR mutation, using SYSTAT software (SYSTAT Software Inc., Richmond, CA). A P value below 0.05 was considered statistically significant.

Results

Sensitivity of the New Assay

It is known that mutations in the EGFR tyrosine kinase domain are restricted to four exons, and the results of previous reports[4,5,8,9,13,15] revealed that the deletion in exon 19 and the point mutation of codon 858 in exon 21 covers about 90% of cases with EGFR-TK mutation. We therefore established assays using fragment analysis for

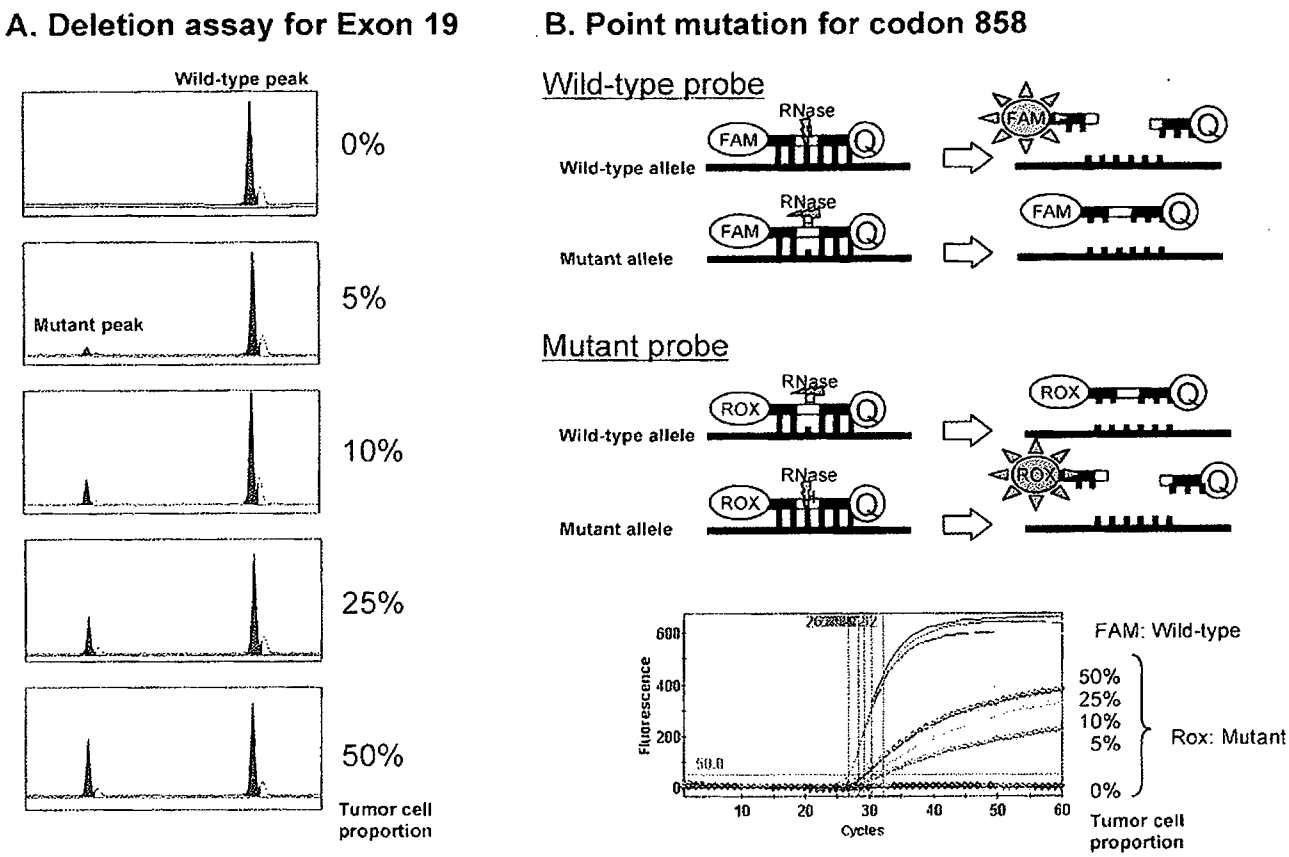

Figure 1. Sensitivity of the new assay. **A:** The sensitivity of the fragment analysis in the new assay. As few as 5% of tumor cells with the deletion could be detected. In the **top** of **B**, a brief explanation of the cycleave technology is displayed. Using this technique, as few as 5% of tumor cells with point mutation at codon 858 could be detected (**bottom** of **B**).

the deletion and cycleave real-time PCR for the point mutation of codon 858. The positive detection of mutated molecules makes this assay very sensitive, as shown in Figure 1. As few as ~5% of tumor cells could be detected in this assay.

Specificity of the New Assay and Concordance with Direct Sequencing

We evaluated the concordance of results between the new assay and conventional direct sequencing using 195 NSCLCs. The results are summarized in Table 1. Overall concordance was 186 of 195 (95%). When we excluded the seven evaluation cases, which were mutated in regions other than the targets of this assay, 99% of cases were concordant. In one case, mutation was only detected with the new assay, whereas one case was negative for mutation with the new assay but positive with direct sequencing. This disagreement resulted from the different tumor cell population in the samples examined. In the preliminary examination, at least 25% of tumor cells were required for detection of the gene mutation by direct sequencing (data not shown). Although tumor tissues in this analysis were dissected to contain more than 25% of tumor cells from most frozen sections, this case contained around 25% tumor cells, on the threshold of that detectable by the sequencing approach. In contrast, the paraffin section used for the new assay was rich in tumor cells. This difference in tumor cell content between frozen and paraffin sections may be the cause of the discrepancy. We confirmed this result by direct sequencing of the frozen section, using DNA microdissected with a laser capture microdissection system.

Practical Application for the Prediction of Gefitinib Response

To confirm whether the new assay is useful for the prediction of gefitinib response in clinical practice, we applied the assay to 29 gefitinib-treated cases whose response had been evaluated according to RECIST. A paraffin section of the large tumor tissue, which had been surgically resected a few years before relapse, was used in seven cases, whereas DNA was extracted from a paraffin section of transbronchial biopsy or computer tomography-assisted fine needle biopsy in 20 cases (Figure 2). Partial response was achieved in 11 cases; all but one were positive for the mutation, whereas five cases with progressive disease were negative with this assay (Table 2). EGFR mutation was detected in only 2 of 13 cases evaluated as stable disease. The correlation be-

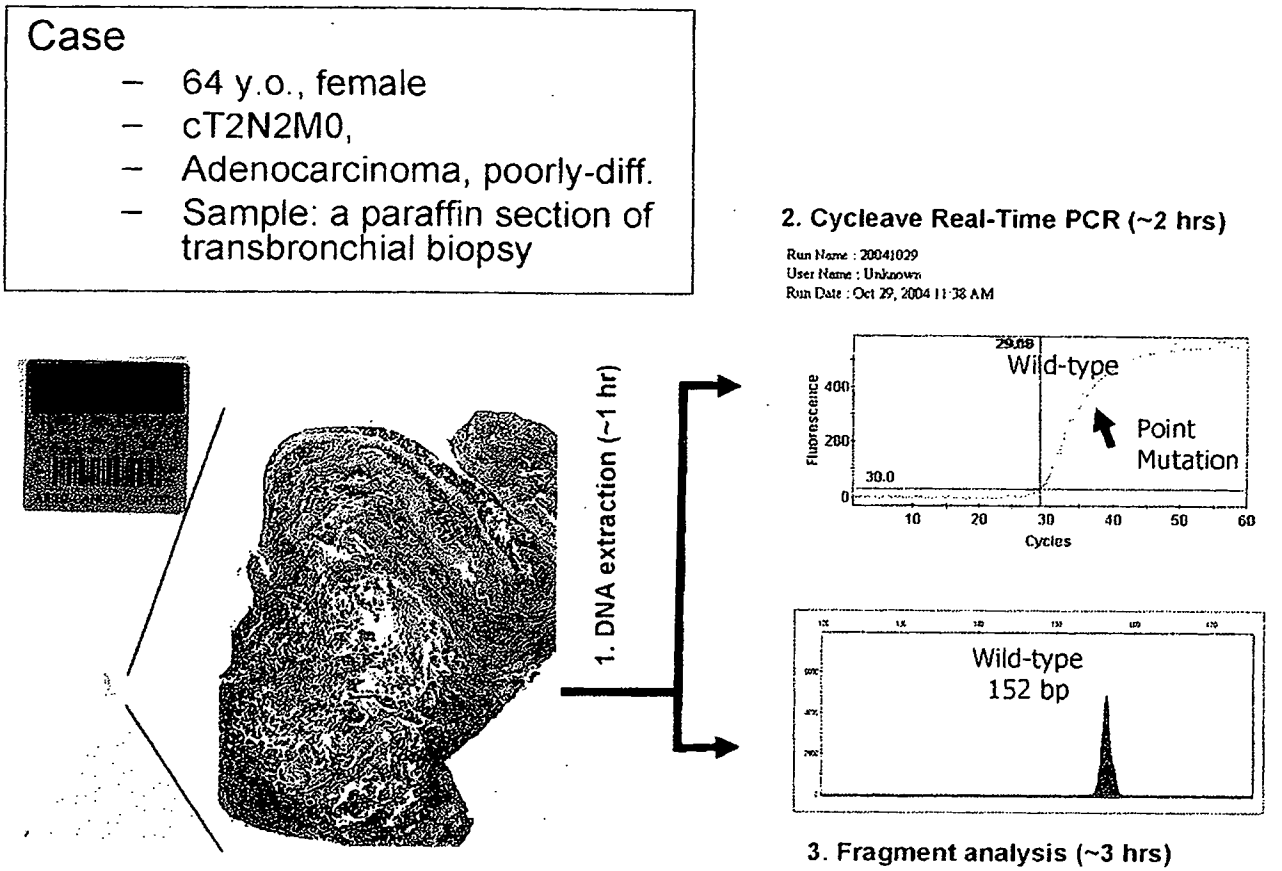

Figure 2. A representative result of the new assay. DNA was extracted from a paraffin section of the biopsy followed by simultaneous analysis using cycleave real-time PCR and fragment analysis. The entire procedure was completed within 4 hours. In this case, point mutation at codon 858 was detected, and the patient responded to gefitinib therapy.

tween EGFR mutation and gefitinib response was highly significant ($P = 0.0001$).

All of the 12 EGFR-mutated specimens were also examined by direct sequencing. In seven cases, identical results were obtained with both methods, whereas background noise prevented us from evaluating the results in the other five cases, all of which were small biopsy specimens. This may not indicate a lack of confirmation but rather suggests the superiority of this new assay, considering the good correlation of this result with clinical response and with the results obtained with direct sequencing using sufficient amounts of surgical tissue.

Detection of Mutation at Codon 790 Conferring Acquired Resistance to Gefitinib

Recently, it has been reported that a second mutation, at codon 790, was associated with acquired resistance to gefitinib.[16,17] On very rare occasions, the mutation was also detected independently of gefitinib treatment.[13,14] An assay for this mutation, using cycleave PCR, was similarly established (Table 3). In this assay, as few as 5% of tumor cells could be detected, as shown in Figure 3. A rare case, whose tumor was known to have T790M

Table 1. Comparison of Results between the Conventional and New Assays

	New assay		
Direct sequencing	Wild type	Mutation at codon 858	Deletion at exon 19
Wild type	116	1	0
Point mutation at codon 858	0	32	0
Deletion at exon 19	1	0	38
Point mutation at codon 719	3	0	0
Insertion at exon 20	3	0	0
Point mutation at codon 742	1	0	0

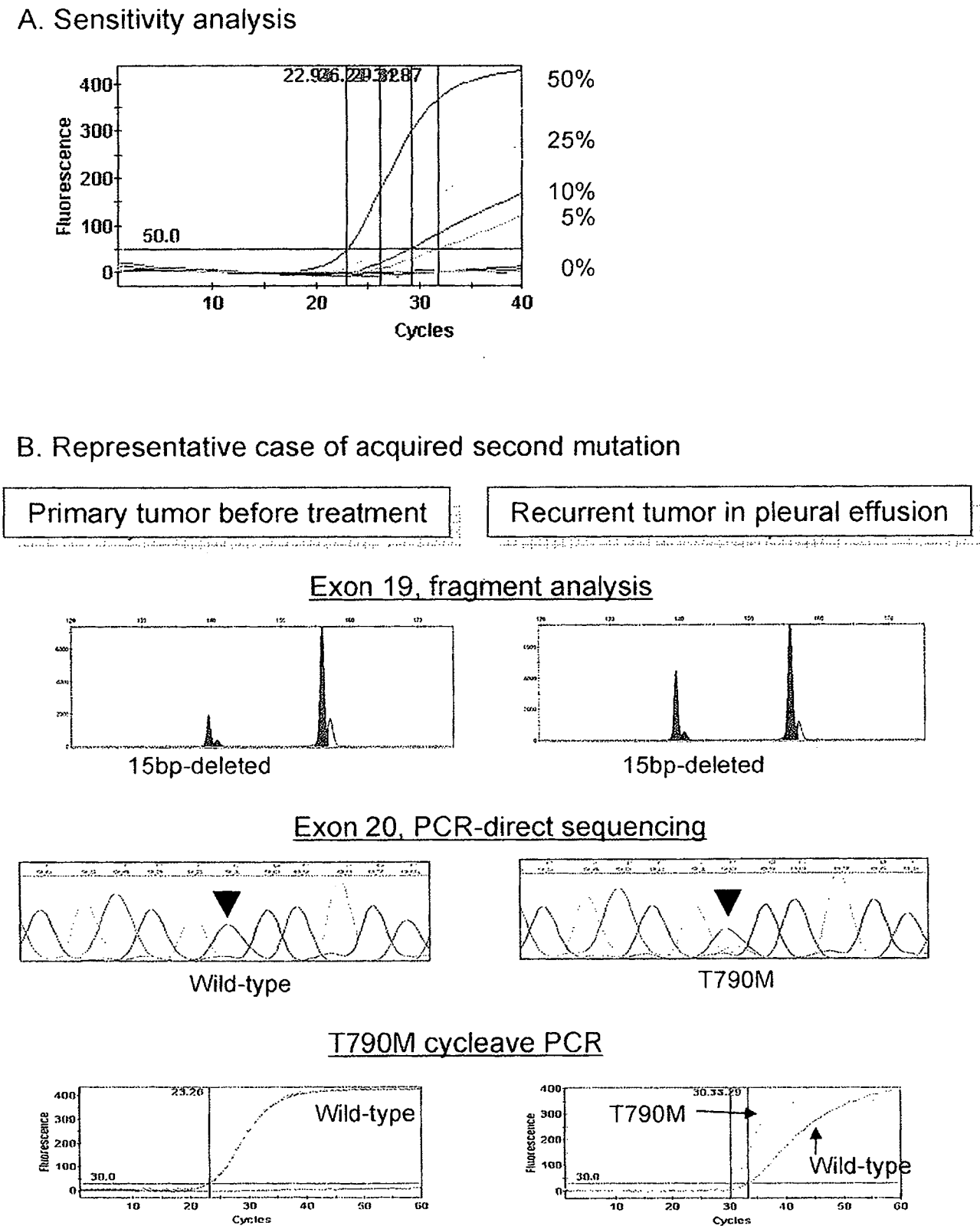

Figure 3. Detection of acquired mutation at codon 790. **A:** The sensitivity of this cycleave assay for T790M mutation. As few as 5% of tumor cells with T790M mutation could be detected. A representative result of acquired mutation at codon 790 after gefitinib treatment is displayed in **B** (Table 3, case 2). In contrast to the 15-bp deletion in exon 19 of the EGFR gene in both primary and recurrent tumors, T790M was detected only in the recurrent tumor, suggesting acquired mutation after gefitinib treatment. The result of the cycleave method was more obvious than that with direct sequencing.

Table 2. Practical Application of the New Assay

	Clinical response		
EGFR status	PD	NC	PR
Wild type	5	11	1
Mutated	0	2	10
Deletion in exon 19	0	2	5
Point mutation of codon 858	0	0	5

PD, progressive disease; NC, no change; PR, partial response.

mutation independently of gefitinib treatment,[16,17] was also positive in this assay. In one of the other three recurrent tumors, this assay clearly demonstrated the mutation (Figure 3), although it was often difficult to detect the mutated signal with direct sequencing of the PCR product.

Discussion

Paez et al[5] and Lynch et al[4] simultaneously published the result that somatic mutation of EGFR in lung adenocarcinoma predicts a clinical response to gefitinib. Erlotinib is another targeted small-molecule inhibitor of EGFR, and lung adenocarcinoma sensitive to erlotinib also harbored EGFR mutations. In addition, *in vitro* studies support the observation that EGFR mutations make tumor cells significantly sensitive to gefitinib[18] and erlotinib. This increased sensitivity may be explained by the "addiction to oncogene" hypothesis proposed by Weinstein.[19] Tumor cells with EGFR mutation are highly dependent on the activated EGFR pathway and are thus very susceptible to inhibition of this dependence. We have reported that patients with EGFR mutations survived longer than those without mutations after the initiation of gefitinib treatment.[7] Recently, failure to show a survival benefit in the IRESSA Survival Evaluation in Lung Cancer was announced. Gefitinib may not be effective enough to kill tumor cells that are not under a state of "addiction to EGFR mutation." Conversely, these findings suggest that selection of patients with EGFR-mutated tumors has the advantage of increasing the response rate of EGFR-targeted therapy. Furthermore, selection may also be efficient at preventing serious interstitial pneumonia occurring as a side effect.[20]

Although an assay using paraffin sections is very practical, immunohistochemical analysis of the tumors failed to predict the response. Currently, the microdissection of tumor cells and direct sequencing of PCR products is commonly used as a standard method. Regarding practical applications, the new assay reported here provides two benefits compared with the conventional method. First, microdissection is not necessary for the assay because a positive mutated signal makes this assay very sensitive. Second, this assay is rapid, does not require a purification step, and is usually completed within 4 hours: digestion with proteinase K for 1 hour, real-time PCR or regular PCR for 3 hours, and electrophoresis for 1 hour. In addition to paraffin sections, pleural effusion and specimens for fine needle aspiration cytology can be used. All three specimens of pleural effusion for the T790M cycleave assay were successfully analyzed, whereas direct sequencing occasionally resulted in an ambiguous result (Figure 3). The main targets for gefitinib or erlotinib therapy are recurrent and refractory tumors, and an assay using such specimens is therefore quite useful. However, the examination of limited regions of the EGFR gene appears to be a disadvantage of this study. Recent studies suggested that an insertion of exon 20 was shown to be resistant to EGFR inhibitors[25], whereas the gefitinib sensitivity of cells expressing the G719S mutant was significantly less than that of cells expressing the L858R mutant form[26]. Therefore, these results suggest that examination of the L858R mutation and deletion in exon 19 is reasonable, because these two mutations are likely to be a major target of the EGFR inhibitors.

A few approaches for the detection of EGFR mutation have been reported recently.[21–23] Comparing the assays, the advantage of the method presented here is its practical clinical use. Biopsy specimens frequently result in small, fragmented tissues containing only a few cancer cells. Using such biopsy specimens, the assay successfully demonstrated the EGFR mutations that correlate with gefitinib response, in contrast to failure of the direct sequencing of some biopsy specimens. Furthermore, the cycleave technique can be simultaneously applied for the detection of the K-ras mutation, which has been proposed to be an adverse prognostic marker for chemotherapy with erlotinib.[24]

In summary, we have introduced a new practical approach for the detection of EGFR mutations. This assay is very sensitive and useful for predicting gefitinib response. This rapid screening assay uses paraffin sections from biopsy without the need for a microdissection

Table 3. Detection of T790M Mutation Associated with Acquired Resistance to Gefitinib

Patient	Gefitinib treatment	Tissue examined	T790M mutation	Comments
Case 1*	No	Primary tumor	Yes	A rare case, harboring T790M mutation independent of gefitinib treatment
Case 2	Yes	Pleural effusion	Yes	15-bp deletion of exon 19 in the primary and recurrent cancers (Figure 3)
Case 3	Yes	Pleural effusion	No	9-bp deletion of exon 19 in the primary and recurrent cancers
Case 4	Yes	Pleural effusion	No	15-bp deletion of exon 19 in the primary and recurrent cancers

*The mutation of codon 790 in a primary cancer, which was demonstrated with RT-PCR direct sequencing, has been reported previously.

procedure and has significant advantages over other methods.

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AN EXTREMELY SOLID VARIANT OF ADENOID CYSTIC CARCINOMA ARISING IN THE LOWER TRACHEA

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Summary

A 54-year-old Japanese man consulted our hospital because he was diagnosed as having pneumoconiosis on a medical check up. Bronchoscopic examination showed a buldging endobronchial polypoid lesion in the right. main stem bronchus and partial polypectomy was performed. Histological examination showed that the tumor was composed of large solid sheets of medium sized tumor cells with moderate nuclear pleomorphism and lacked the characteristic cribriform or cylindromatous pattern. Small tubules or cystic spaces, which contained pale eosinophilic fluid or hyalinized stromas, were present within tumor sheets. Immunohistochemically, S-100 and smooth muscle actin were positive for tubular or peritubular areas. So a provisional pathologic diagnosis for polypectomy specimen was salivary gland-like carcinoma of low grade malignancy. The tumor was surgically resected. In a peripheral small area corresponding to 0.1% of tumor, a few cribriform nests containing basophilic mucoid materials were recognized. Taken together, the pathologic diagnosis was an extremely solid variant of adenoid cystic carcinoma arising in the lower trachea.

Key words : Adenoid cystic carcinoma, Solid variant, Trachea

Introduction

Adenoid cystic carcinoma (ACC) is the most common salivary gland-like tumor occurring in the lower respiratory tract and usually arises in the lower trachea, main stem bronchi or lobar bronchi[1]. ACC is classified into tubular, cribriform and solid histological subtype[2-4] and the presence of characteristic cribriform or cylindromatous growth pattern serves to confirm the correct pathologic diagnosis for ACC[5]. However, there are a few circumstances that may induce difficulties in the pathologic diagnosis by the lack of the distinctive cribriform or cylindromatous growth pattern. In the present case, we encounted ACC showing an extremely solid growth pattern with cribriform nests rarely seen in less than 0.1% of tumorous area and without cylindromatous pattern. We had great difficulty in establishing a pathologic diagnosis by preoperative polypectomy specimen that showed tumorous

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large solid cell sheets that entirely lacked cribriform or cylindromatous pattern histologically. We herein report a rare case of extremely solid variant of ACC arising in the lower trachea and discuss the differential pathologic diagnosis and the key to making an accurate diagnosis.

Case Report

A 64-year-old Japanese man consulted our hospital after he was diagnosed as having pneumoconiosis on a medical check up. On bronchoscopic examination, polypoid tumor at the anterior wall of right main bronchus adjacent to carina was incidentally revealed. Endoscopically, the tumor presented as a buldging endobronchial polypoid lesion with a smooth surface (Fig.1). Bronchoscopic partial polypectomy was performed and a provisional pathologic diagnosis was made as salivary gland-like carcinoma of low-grade malignancy. Clinically, metastases were not found in any other organs or lymph nodes. Laboratory tests including serum CEA, NSE and CYFRA were in the normal range. The tumor was completely resected at Osaka City General Hospital.

Fig. 1. Bronchial endoscopy showing a buldging endobronchial polypoid lesion with a smooth surface arising in the right main bronchus adjacent to the carina

Pathologic Findings

1 Polypectomy specimen: Polypectomy specimen showed that the tumor was composed of large solid sheets with occasional cystic spaces (Fig.2). Large solid cell sheets consisted of medium sized tumor cells with moderate nuclear pleomorphism and inconspicuous nucleoli. Numerous small tubules in variously sized and large cystic spaces, which contained pale eosinophilic fluid or hyalinized stroma, were recognized within the sheets (Fig.3). Vacuolated cells or spindle cells were sometimes seen. Mitoses ranged from 6 to 7 per 10 high-power fields. There were no hemorrhagic or necrotic areas. The tumor lacked the characteristic cribriform or cylindromatous pattern of conventional ACC and had little stroma other than intraluminal hyalinized structures. Immunohistochemically most tumor

Fig. 2. Large solid tumor cell sheets with occasional cystic spaces.

cells were positive for AE1/AE3, Cytokeratin 7 (CK7) and vimentin. Epithelial membrane antigen (EMA), smooth muscle actin (SMA) and S-100 were positive for tubules or peritubular areas. There was no reactivity with CEA, TTF-1, CK20, desmin, h-Caldesmon or GFAP. MIB-1 labeling index (MIB-1 LI) was 20%. From this polypectomy specimen, we made a provisional pathologic diagnosis of salivary gland-like carcinoma of low-grade malignancy.

Fig. 3. Numerous small tubules and large cystic spaces within the solid cell sheets.

II. Surgically resected specimen : The surgically resected specimen showed that the tumor was of lower tracheal origin and extended beyond the cartilage plate (Fig.4). In a limited peripheral area of tumor adjacent to the surrounding non-neoplastic tracheal epithelium, which corresponded to 0.1% of the tumor, a few cribriform nests with variable amounts of basophilic mucoid materials were present (Fig.5). Alcian blue-PAS double stain showed the histological presence of glands and pseudoglands in these cribriform nests. Taking findings together, we made a pathologic diagnosis of an extremely solid variant of ACC arising in the lower trachea. All resected lymph nodes were free of malignancy histologically.

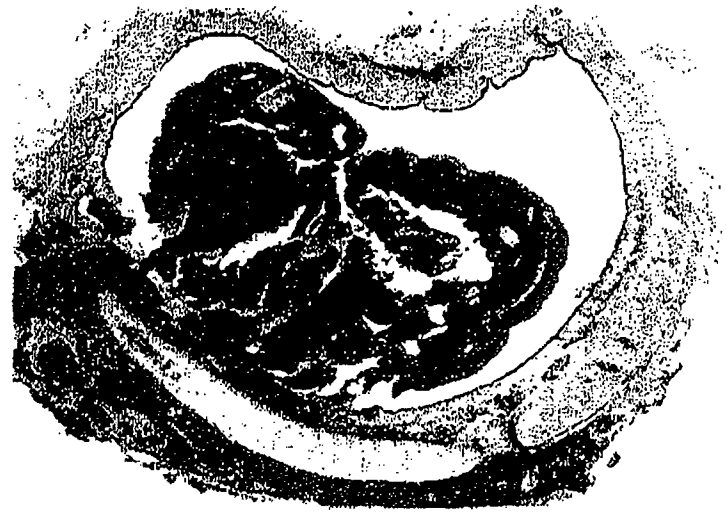

Fig. 4. Tumor extending beyond the cartilage plate of the lower trachea.

Discussion

Histologically, adenoid cystic carcinoma (ACC) was classified into tubular, cribriform and solid variants and the overall prognosis of ACC in relation to distant metastasis and survival is worst for the solid variant[2)3)4)]. The morphologic features of ACC are sufficiently distinctive in the majority of cases to permit adequate diagnosis on routine hematoxylin and eosin sections, particularly for the cribriform and tubular variants[5)]. The histological presence of characteristic cribriform or cylindromatous growth pattern serves to confirm the correct diagnosis. However, if these growth patterns are completely absent as in our polypectomy specimen, pathologists would have great difficulty in

making a pathologic diagnosis of ACC.

In the differential diagnosis of the extremely solid variant of ACC, epithelial-myoepithelial carcinoma, myoepithelial carcinoma, basal cell adenocarcinoma and solid-cribriform type of basal cell adenoma are possibilities. Epithelial-myoepithelial carcinoma shows a mixed pattern of glands lined by a dual layer of cells and solid sheets of either spindle cells or clear cells, and co-existence of the glandular and solid components in variable proportion. The inner layer of the glands stains for Cytokeratin and EMA, and the outer layer for S-100 and SMA[6]. However, in our case, clear cells were absent and AE1/AE3 was positive in most tumor cells. Myoepithelial carcinoma is composed largely of clear cells that display histological and immunohistochemical features of myoepithelial differentiation[7]. The polyp in this case showed occasional ductal structures lined by eosinophilic cells and immunohistochemical myoepithelial differentiation was recognized in ductal or periductal areas. Basal cell adenocarcinoma is essentially a caricature of basal cell adenoma and is composed of groups of basaloid cells arranged in solid, tubular, trabecular and membranous patterns[8]. However, in basal cell adenocarcinoma, pseudocysts occasionally seen in our case were rare. Solid-cribriform type of basal cell adenoma is an unusual example of basal cell adenoma[9]. In the solid-cribriform type of basal cell adenoma, infiltrative growth of the tumor seen in our case is absent. However, in the partial polypectomy specimen that was entirely composed of solid cell sheets like our case, diagnostic exclusion of the solid-cribriform type of basal cell adenoma was very difficult. In this case, immunohistochemical examination of MIB-1 was very useful because Nagao et al. reported that their basal cell adenoma cases showed Ki-67 (MIB-1) labeling index < 5%[10]. Based on their report, the MIB-1 LI 20% in our case would support ACC rather than basal cell adenoma.

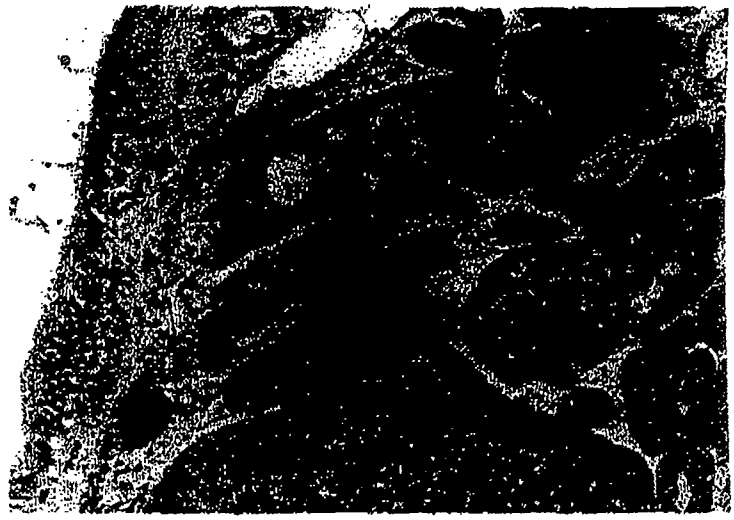

Fig. 5. A few cribriform nests containing basophilic mucoid materials.

In conclusion, the key to accurate diagnosis of the extremely solid variant of ACC was as follows : (1) recognition of dual tumor cell type ; (2) histological presence of myoepithelial differentiation; (3) extensive detection of the characteristic cribriform nests ; (4) high MIB-1 LI> 5% ; (5) knowledge of the extremely solid variant of ACC.

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Analysis of *Epidermal Growth Factor Receptor* Gene Mutation in Patients with Non–Small Cell Lung Cancer and Acquired Resistance to Gefitinib

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Abstract

Purpose: Non–small cell lung cancers carrying activating mutations in the gene for the epidermal growth factor receptor (EGFR) are highly sensitive to EGFR-specific tyrosine kinase inhibitors. However, most patients who initially respond subsequently experience disease progression while still on treatment. Part of this "acquired resistance" is attributable to a secondary mutation resulting in threonine to methionine at codon 790 (T790M) of EGFR.

Experimental Design: We sequenced exons 18 to 21 of the *EGFR* gene to look for secondary mutations in tumors with acquired resistance to gefitinib in 14 patients with adenocarcinomas. Subcloning or cycleave PCR was used in addition to normal sequencing to increase the sensitivity of the assay. We also looked for T790M in pretreatment samples from 52 patients who were treated with gefitinib. We also looked for secondary *KRAS* gene mutations because tumors with *KRAS* mutations are generally resistant to tyrosine kinase inhibitors.

Results: Seven of 14 tumors had a secondary T790M mutation. There were no other novel secondary mutations. We detected no T790M mutations in pretreatment specimens from available five tumors among these seven tumors. Patients with T790M tended to be women, never smokers, and carrying deletion mutations, but the T790M was not associated with the duration of gefitinib administration. None of the tumors had an acquired mutation in the *KRAS* gene.

Conclusions: A secondary T790M mutation of *EGFR* accounted for half the tumors with acquired resistance to gefitinib in Japanese patients. Other drug-resistant secondary mutations are uncommon in the *EGFR* gene.

Activating mutations in the gene for the epidermal growth factor receptor (EGFR) are present in a subset of pulmonary adenocarcinomas. Tumors with *EGFR* mutations are highly sensitive to gefitinib and erlotinib, small-molecule EGFR-specific tyrosine kinase inhibitors (1–3). These mutations occur in the tyrosine kinase domain of the *EGFR* gene. Deletion mutations in exon 19 and the substitution of leucine with arginine at codon 858 (L858R) account for ~90% of all these mutations (4). *EGFR* mutations are more prevalent in women, never smokers, patients of Asian ethnicity, and those with adenocarcinoma histology (4). These features are the same as those of patients whose tumors have elevated sensitivity to EGFR-specific tyrosine kinase inhibitors. The response rates of lung cancers with an *EGFR* mutation are as high as 80% (5). Responses are often dramatic, and several reports have shown that patients with *EGFR* mutations survive significantly longer after gefitinib treatment than patients without mutations (6). However, it is also common for patients to show disease progression after presenting with an initial marked response to EGFR-specific tyrosine kinase inhibitors. The mean duration of the initial response is about 3 to 7 months (7, 8).

Recently, it has been reported by two groups that a secondary threonine-to-methionine mutation at codon 790 (T790M) of the *EGFR* gene is related to the acquired resistance to gefitinib and erlotinib (9, 10). Crystal structure modeling has shown that residue T790 is located in the ATP-binding pocket of the catalytic region of EGFR, and it seems to be critical for the binding of erlotinib and gefitinib (9). Substitution of the threonine at codon 790 with a bulkier residue, such as methionine, would result in steric hindrance to the binding of these two drugs. A secondary T790M mutation has been identified in one tumor (9) and in three of six tumors (10) with acquired resistance to gefitinib.

Imatinib is a tyrosine kinase inhibitor specific for BCR-ABL, KIT, and platelet-derived growth factor A, which is used to treat

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chronic myelogenous leukemia (CML) and gastrointestinal stromal tumor. Analogous secondary mutations in the kinase domains of these genes are considered to constitute one of the mechanisms of acquired drug resistance (11–14). The structural similarity between ABL and EGFR tyrosine kinases is fairly high, and the most common mutation related to acquired resistance is a threonine-to-isoleucine mutation at codon 315 (T315I), corresponding to T790M in the *EGFR* gene (15). In CML, 20 to 30 other mutations of the *ABL* gene have been identified as responsible for acquired resistance to imatinib (12, 16–19), so secondary *EGFR* gene mutations other than T790M are possible (Fig. 1).

Secondary mutations of the *ABL* gene have also been detected in pretreatment samples from some CML patients, although the fraction of mutant cells was very low (16, 20). The existence of a similar mechanism is expected for non-small cell lung cancer. Furthermore, we and others have reported that the T790M mutation of the *EGFR* gene exists as a major mutation independently of gefitinib treatment, although instances are very rare (21, 22).

It has also been reported that *KRAS* mutations are associated with a lack of sensitivity to gefitinib and erlotinib (23, 24). Therefore, it is possible that acquired *KRAS* mutations are also associated with acquired resistance.

In this study, we looked for the T790M mutation and other secondary mutations of the *EGFR* gene in tumors from patients who showed disease progression after presenting with an initial response to EGFR-specific tyrosine kinase inhibitor treatment and in tumors before gefitinib treatment. We also looked for *KRAS* mutations in the same tumors.

Materials and Methods

Patients. Patients with non-small cell lung cancer who initially responded but subsequently experienced disease progression while on gefitinib treatment were defined as having "acquired resistance." A detailed definition of the effectiveness of gefitinib treatment was described in our previous study (25). Briefly, gefitinib treatment is judged to be effective when tumors show a decrease of at least a 30% in tumor diameter in imaging studies or when elevated carcinoembryonic antigen levels decrease to a level less than half the baseline level.

Fourteen tumor samples and 10 corresponding pretreatment tumor samples from eligible patients were obtained according to this definition at the time of diagnosis or treatment. The selection of patients depended only on whether a second tumor sample collected at the time of progression could be obtained. Appropriate approval from the institutional review board and the patients' written informed consent were obtained. Patient characteristics and details of the samples are shown in Table 1. All patients had adenocarcinomas, and the median duration of gefitinib treatment was 367 days (range, 69-921 days). We also analyzed the samples of 52 patients who had been treated with gefitinib for recurrent disease after they had undergone pulmonary resection. This cohort was part of our previous study, and their clinical details are described elsewhere (25).

Subcloning mutational analysis of the EGFR *gene.* Genomic DNA and total RNA (if possible) were extracted from each sample (Table 1). Exons 18 to 21 of the *EGFR* tyrosine kinase domain were amplified using PCR or reverse transcription-PCR (RT-PCR) methods. PCR for genomic DNA was done using AmpliTaq Gold (Applied Biosystems, Foster City, CA) and the following primers: exon 18, 5′-GAGGTGACCC-TTGTCTCTGTGT-3′ (forward) and 5′-CCCAAACACTCAGTGAAACAAA-3′ (reverse); exon 19, 5′-TGCCAGTTAACGTCTTCCTTCT-3′ (forward) and 5′-ATGTGGAGATGAGCAGGGTCTA-3′ (reverse); exon 20, 5′-TGAAACTC-AAGATCGCATTCAT-3′ (forward) and 5′-CATGGCAAACTCTTGCTATCC-3′

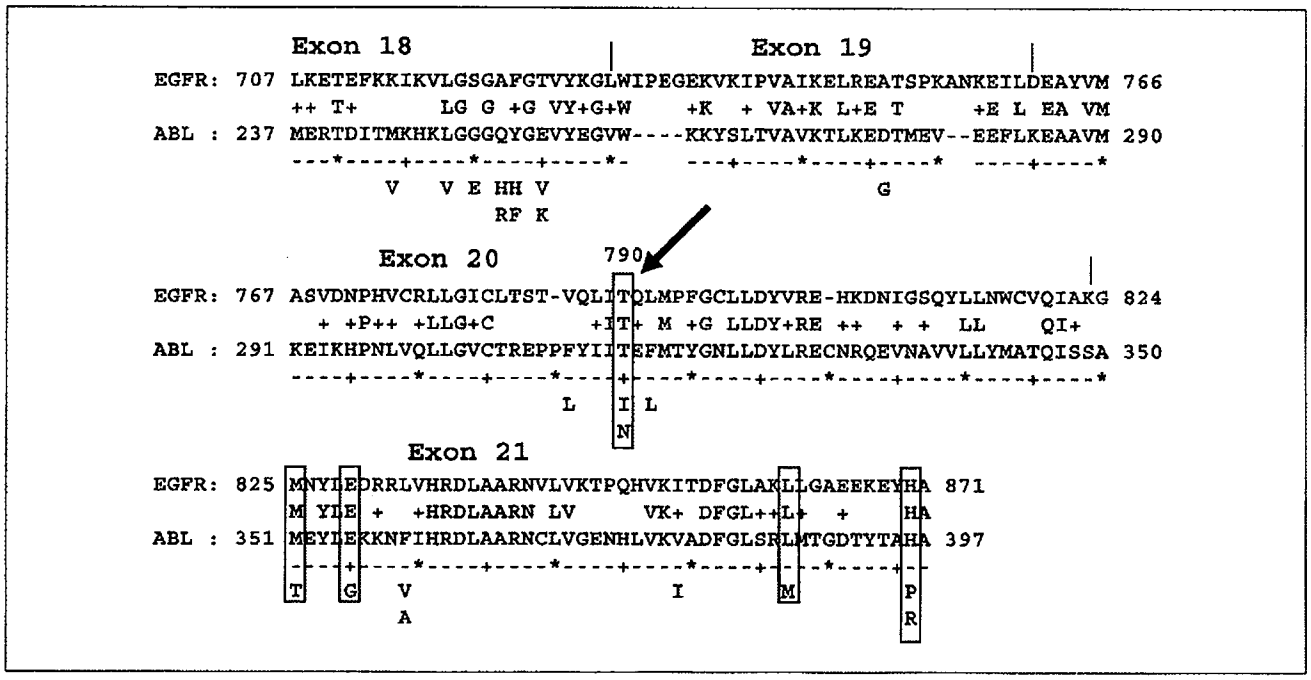

Fig. 1. Structural similarity between EGFR tyrosine kinase and ABL. This amino acid alignment was obtained using basic local alignment search tool, and both sequences were obtained from Genbank (accession nos.: EGFR, NM 005228; ABL, NM 005157). Top line, EGFR; bottom line, ABL. Vertical lines, boundaries between exons. Numbers at each end, codon numbers. Capital letters under the alignment, amino acid changes in ABL that have been reported as acquired imatinib resistance mutations. Square frames, qualifying codons as common codons in EGFR and ABL and as acquired resistance mutant codons in ABL. Arrow, location of codon 790 of EGFR and codon 315 of ABL.

Table 1. Patient characteristics and results of sequencing analysis

Patient no.	Sex	Smoking status	Prior treatment	Gefitinib response	Gefitinib treatment days	Analyzed specimen (state)	Nucleic acid	Activating mutation	T790M mutation	T790M (pre-gefitinib samples)
1	F	NS	S	E	642	LN (Fr)	RNA	Δ2	+	—
2	M	FS	S	E	368	PE (Al)	RNA	Δ3	–	—
3	M	NS	S	E	116	PE (Al)	RNA	Δ1	–	—
4	F	FS	CT	E	599	PE (CL)	RNA	Δ1	–	NA
5	F	NS	CRT	E	921	LU (Al)	RNA	Δ1	+	NA
6	F	NS	None	E	181	PE (Al)	RNA	Δ1	+	—
7	F	FS	CT	E	346	BO (Al)	RNA	Δ1	+	—
8	F	NS	S→CRT	E	623	LN (Al)	RNA	L858R	–	NA
9	M	FS	S	E	915	BR (Fr)	DNA	L858R*	–	—
10	M	FS	S→CRT	NE	69	PE (Al)	DNA	L858R	–	—
11	F	FS	None	E	560	LU (Fr)	RNA	L858R*	+	NA
12	F	NS	CT	E	239	PE (Al)	RNA	Δ1	+	—
13	F	NS	S	E	367	PE (Al)	RNA	L858R	–	—
14	F	NS	CRT	E	235	LN (Al)	RNA	Δ1	+	—

NOTE: Patients 1, 4, and 13 received gefitinib therapy twice. Pretreatment samples from patients 4, 5, 8, and 11 were not available. Patient 10 was defined as not evaluable according to our definition. However, this patient showed a 46% decrease in carcinoembryonic antigen and a marked reduction in pleural effusion on initial treatment before subsequent progression. Therefore, we regarded this case as eligible for this study.

Abbreviations: Al, alcohol fixed; BO, bone metastasis; BR, brain metastasis; CL, cell line; CRT, chemoradiotherapy; CT, chemotherapy; del, deletion; E, effective; F, female; Fr, frozen; FS, former smoker; ins, insertion; LN, lymph node; LU, lung tumor; M, male; NA, not available; NE, not evaluable; NS, never smoker; PE, pleural effusion; RT, radiotherapy; S, surgery; Δ1, del E746-A750; Δ2, del L747-P753 insS; Δ3, del L747-A750 insP.

*Patients 9 and 11 had another point mutation (L833V in patient 9 and R776H in patient 11).

(reverse); and exon 21, 5′-GAGCTTCTTCCCATGATGATCT-3′ (forward) and 5′-GAAAATGCTGGCTGACCTAAAG-3′ (reverse). The PCR conditions were as follows: 1 cycle of 95°C for 11 minutes, 45 cycles of 95°C for 30 seconds, 60°C for 30 seconds, and 72°C for 40 seconds followed by 1 cycle of 72°C for 4 minutes.

RT-PCR for RNA was done with primers 5′-AGCTTGTGGAGCCTCT-TACACC-3′ (forward 1) and 5′-TAAAATTGATTCCAATGCCATCC-3′ (reverse 1) in a one-step RT-PCR setup using Qiagen OneStep RT-PCR kits (Qiagen, Valencia, CA) as described previously (26). RT-PCR conditions were as follows: 1 cycle of 50°C for 30 minutes and 95°C for 15 minutes, 40 cycles of 94°C for 50 seconds, 62°C for 50 seconds, and 72°C for 1 minute followed by 1 cycle of 72°C for 10 minutes.

The PCR products were subcloned using TOPO TA Cloning kits (Invitrogen, Carlsbad, CA) according to the manufacturer's instructions. Each clone was then directly amplified with the same primers using AmpliTaq Gold and cycle sequenced using BigDye Terminator v3.1/1.1 cycle sequencing kits (Applied Biosystems). Subcloning PCR conditions were as follows: 1 cycle of 95°C for 11 minutes, 45 cycles of 95°C for 50 seconds, 62°C for 50 seconds, and 72°C for 70 seconds followed by 1 cycle of 72°C for 4 minutes.

The sequencing reaction products were electrophoresed using an ABI PRISM 3100 system (Applied Biosystems). Both forward and reverse sequences were analyzed with basic local alignment search tool, and the chromatograms were analyzed by manual review.

Cycleave real-time PCR assay. Details of the cycleave real-time PCR assay have been described previously (27). Briefly, genomic DNA was extracted, and exon 20 of the *EGFR* gene was amplified by real-time quantitative PCR assay on a SmartCycler (TaKaRa, Gifu, Japan) using Cycleave PCR Core kits (TaKaRa) with a T790M-specific cycling probe and a wild-type cycling probe. As few as ~5% of tumor cell molecules could be detected in this assay.

Mutational analysis of the KRAS *gene.* A RT-PCR direct sequence assay was done for RNA, and a cycleave real-time PCR assay was done for DNA. *KRAS* primers for PCR were 5′-GGCCTGCTGAAAATGACTGA-3′ (forward 1) and 5′-TCTTGCTAAGTCCTGAGCCTGTT-3′ (reverse 3). Codon 12 cycling probes and a wild-type cycling probe were used in cycleave real-time PCR assays. Direct sequencing was used to identify codon 12, 13, and 61 mutations.

Results

Detection of secondary mutations in the EGFR *gene or the* KRAS *gene.* For the analysis of secondary mutations, we first amplified exons 18 to 21 of the *EGFR* gene, which include the region homologous to the region of the *ABL* gene that contains all the secondary mutations thus far reported to be responsible for imatinib resistance in CML. All 14 tumors with acquired resistance had activating mutations of the *EGFR* gene, either deletion mutations, including codons 746 to 750 (nine patients), or L858R (five patients). Seven tumors had a secondary T790M mutation (Table 1; Fig. 2).

When we sequenced corresponding tumor samples that had been obtained before gefitinib treatment, the same activating mutations were always present, whereas T790M was not detected in any of the available pretreatment samples (samples for patients 4, 5, 8, and 11 were not available).

Mutant bands for T790M in the sample from patient 7 were as strong as the wild-type bands, and the mutant bands were stronger than the wild-type bands in patient 12 (Fig. 2). However, in most cases, the T790M mutant bands were weaker than the wild-type bands.

Two tumors had another point mutation as well as L858R (L833V in patient 9 and R776H in patient 11). L833 corresponds to F359 of ABL, where a secondary mutation to valine or alanine has been reported in CML (Fig. 1; ref. 12). However, the pretreatment sample of patient 9 revealed that L833V existed before treatment in the same ratio as the L858R band. The ratios of L833V and L858R bands were unchanged

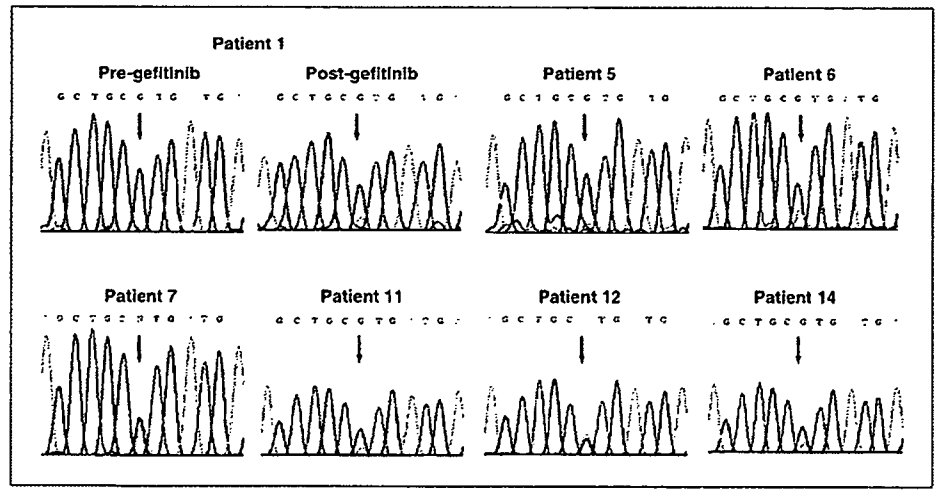

Fig. 2. Sequencing chromatograms for *EGFR* exon 20. Secondary T790M mutations were observed in seven patients. Antisense strands of each chromatogram. Arrows, small peaks of the C→T substitution at nucleotide 2,369 (G→A on the antisense strand), which results in the T790M mutation. This substitution was observed only in posttreatment samples. T790M mutant bands were clearly detected on sequencing chromatograms, except in that of patient 5; in this patient, it was unclear because of artifacts.

before and after gefitinib treatment. Although the T790M mutant band was weaker than the L858R mutant band in patient 11, the intensity of the R776H mutant band was the same as that of the L858R mutant band and both mutations were heterozygous. We considered these point mutations to be primary mutations and not associated with "acquired" resistance.

To increase the sensitivity for the detection of T790M and other possible secondary mutations in the tyrosine kinase domain, each PCR product was subcloned and multiple subclones were amplified and sequenced directly. All the T790M mutations found by sequencing the noncloned PCR products were confirmed by this subcloning method, but no new T790M mutations were detected even when >50 clones were analyzed in samples from patients 2 and 3 (Table 2). Furthermore, we detected no secondary mutations in exons 18 to 21 other than T790M.

The T790M mutations were either present in clones with activating (or sensitizing) mutations or in other clones without activating mutations (Table 2). In three tumors (of patients 1, 5, and 14), T790M was present only in clones with activating mutations, whereas in the remaining four tumors (patients 6, 7, 11, and 12), T790M was present in both clones with and without activating mutations. No tumor carried the T790M mutation only in the wild-type clones. However, four of five T790M mutations were in clones without activating mutations in the tumor of patient 6.

We also looked for mutations in codon 12 (and codons 13 and 61 in RNA samples) in the *KRAS* gene. However, none of the samples from the tumors studied had *KRAS* mutations.

Relationship between T790M mutation and clinical and genetic features. T790M mutations were more frequent in women (women, 7 of 10; men, 0 of 4), who had never smoked (never smoker, 5 of 8; previous smoker, 2 of 6), and with deletion mutations (deletion, 6 of 9; L858R, 1 of 5). There was no difference in the incidence of T790M in the presence or absence of prior chemotherapy (with, 4 of 8; without, 3 of 6; Table 1).

We also compared the duration of gefitinib treatment, which is considered to correlate roughly with the time to progression, with the presence or absence of T790M. However, the median treatment times were almost identical (tumors with T790M, 346 days; tumors without T790M, 368 days; Fig. 3).

Analysis of corresponding tumor tissues before gefitinib treatment in patient 1. To determine whether rare T790M

Table 2. Analysis of acquired mutation using the subcloning method

Patient no.	Activating mutation	Total clones	Activating mutant clones		Wild-type clones	
			With T790M	Without T790M	With T790M	Without T790M
1	Δ2	21	8	10	0	3
2	Δ3	54	0	52	0	2
3	Δ1	51	0	50	0	1
4	Δ1	21	0	13	0	8
5	Δ1	51	3	39	0	9
6	Δ1	47	1	17	4	25
7	Δ1	20	4	5	1	10
8	L858R	18	0	14	0	4
9	L858R	20	0	14	0	6
10	L858R	20	0	5	0	15
11	L858R	21	5	10	1	5
12	Δ1	23	11	9	1	2
13	L858R	21	0	8	0	13
14	Δ1	19	7	8	0	4

mutant clones existed before gefitinib treatment, we analyzed the corresponding tumor tissues of patient 1, whose tissue after gefitinib treatment had a secondary T790M mutation. Tumor tissue was obtained at the time of operation. PCR products from the tumor before gefitinib treatment were subcloned, and 103 subclones were amplified and sequenced directly. However, at this sensitivity, we detected no clone carrying the T790M mutation. Among 103 clones, 92 (89%) had activating deletion mutations, suggesting that the mutant allele was amplified before gefitinib treatment. The incidence of clones with deletional mutations was similar (18 of 21, 85%) in a cervical lymph node taken after gefitinib resistance had developed.

To further explore of possible association of T790M with metastatic spread, we looked for the T790M mutation in hilar and mediastinal lymph nodes with metastases dissected at the time of surgery. Genomic DNA was extracted from lymph nodes from four stations (aortopulmonary, ascending aorta, main bronchus, and intrapulmonary) and analyzed using cycleave real-time PCR. However, we detected no T790M mutations.

Analysis of tumors for T790M before gefitinib treatment in 52 patients who were treated with gefitinib. The possible presence of T790M at a low frequency in tumors before gefitinib treatment might affect the tumor response or the time to progression after gefitinib treatment. In a previous study, we sequenced exons 18 to 23 of the *EGFR* genes of 52 patients who had been treated with gefitinib for recurrent disease after they had undergone pulmonary resection. None of them had the T790M mutation. Here, we used a cycleave real-time PCR assay, which is more accurate analysis than normal sequence, to investigate whether rare T790M mutant cells were present. However, we detected no T790M mutations in these 52 tumors.

Discussion

We studied 14 tumors with acquired resistance to gefitinib for secondary mutations occurring in the *EGFR* tyrosine kinase domain. Seven of the 14 tumors had a secondary T790M mutation, an incidence consistent with those of previous studies (9, 10). Whereas clones with activating mutations (deletion or L858R) might well have been eliminated by selection pressure during gefitinib treatment, those clones were always present in tumors that developed acquired resistance. In most cases, clones with the T790M mutation were not predominant.

The T790M mutations occur more frequently in women who had never smoked and who had a deletion-type mutation. Time to progression did not differ between tumors that acquired secondary T790M mutations and those that did not. However, these tendencies require careful interpretation because of the number of samples was small.

In a previous report, Kobayashi et al. (9) showed that the T790M mutation was observed with either wild-type or deletion mutation sequences, whereas Pao et al. (10) showed that both the T790M and L858R mutations were in the same allele. Our data showed that three samples had the T790M mutation only in the clones with activating mutation and four samples had the T790M mutation in the clones with and without activating mutation, whereas the most of T790M mutation was in the clones with activating mutation, except for

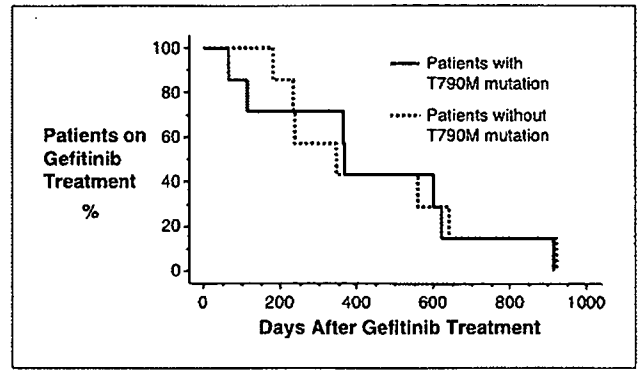

Fig. 3. Effect of theT790M mutation on the length of gefitinib treatment. The length of gefitinib treatment was considered to be roughly related to time to progression. Median treatment times were almost identical in both the presence and absence of theT790M mutation.

the samples of patient 6. It is possible that this could result from a PCR error or DNA repair error at the subcloning step. Bell et al. (28) have reported that artifactual PCR-generated allelic separation occurred with probability of ~30% in their analysis. However, it is also possible that the T790M mutation occurs in both alleles or that tumor heterogeneity exists.

In CML, 20 to 30 mutations in the *ABL* gene are responsible for acquired resistance to imatinib. Many types of mutations have been detected, and there are four distinguishable clusters (P-loop, T315, M351, and A-loop; ref. 29). Furthermore, secondary mutations in the ABL kinase domain are found in 50% to 90% of patients (29), many more than in patients with non-small cell lung cancer. We detected no novel mutations in the *EGFR* gene other than T790M. Two tumors had another point mutations together with L858R, L833V, or R776H. We considered these point mutations to be primary mutations and not associated with acquired resistance. However, these conclusions were based only on sequencing and subcloning methods, and we have no evidence of the functional effects of these mutations. There may be differences in the mechanisms of acquired resistance between non-small cell lung cancer and CML.

We previously reported that, in a series of 397 unselected patients with non-small cell lung cancer who had undergone surgery, 2 female patients with no history of smoking had L858R plus T790M mutations (21). Because these patients were not treated with gefitinib, T790M might well have conferred a growth advantage. These tumors were aggressive and later developed recurrent disease. One was treated with gefitinib but was refractory to treatment. A similar case was reported by another group (22). Inspired by this observation and because the secondary mutations related to imatinib resistance in CML were detected at low frequencies (0.01-0.9%) in pretreatment samples (16, 20), we attempted to detect minor clones with the T790M mutation in samples before gefitinib treatment. However, we could not detect the T790M mutation by assays that can detect mutant cells if there is about 1% to 5% at least. It remains unclear whether a more sensitive method would have detected rare clones with the T790M mutation in our samples.

Why tumors with T790M mutant cells acquire resistance to gefitinib despite the fact that mutant band for the T790M

mutation was almost always weaker than wild-type band remains unclear. It is possible that cells with the T790M mutation preexist at a very low frequency and gradually increase during gefitinib treatment by clonal selection as in cases of CML (16). It is also possible that amplification of the activating mutant allele occurs in resistant tumors and parts of them have the T790M mutation. Another possibility is that multiple coexisting mechanisms, including the T790M mutation, cause acquired resistance cooperatively or independently. A recent study suggested that increased internalization of ligand-bound EGFR is one of the mechanisms underlying acquired gefitinib resistance (30). It is also likely that *EGFR* gene amplification (31) by alteration of downstream molecules, such as AKT (32), might play a role in the acquisition of resistance to gefitinib.

Mutations in *KRAS* are associated with a lack of sensitivity to gefitinib and erlotinib (23). We looked for *KRAS* mutations because of the possibility that acquired *KRAS* mutations are associated with acquired resistance. There were no *KRAS* mutations in any tumor. The same finding has been reported in a previous study (10), suggesting that *KRAS* mutations are not associated with acquired resistance.

In conclusion, half of tumors with acquired resistance to gefitinib had secondary T790M mutations. No novel mutations in the *EGFR* gene were present in contrast to CML.

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Head and neck IMRT

Analysis of interfractional set-up errors and intrafractional organ motions during IMRT for head and neck tumors to define an appropriate planning target volume (PTV)- and planning organs at risk volume (PRV)-margins

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Abstract

Background and purpose: To analyze the interfractional set-up errors and intrafractional organ motions and to define appropriate planning target volume (PTV)- and planning organs at risk volume (PRV)-margins in intensity-modulated radiotherapy (IMRT) for head and neck tumors.

Patients and methods: Twenty-two patients with head and neck or brain tumors who were treated with IMRT were enrolled. The set-up errors were defined as the displacements of the coordinates of bony landmarks on the beam films from those on the simulation films. The organ motions were determined as the displacements of the coordinates of the landmarks on the images recorded every 3 min for 15 min on the X-ray simulator from those on the initial image.

Results: The standard deviations (SDs) of the systematic set-up errors (Σ-*INTER*) and organ motions (Σ-*intra*) distributed with a range of 0.7-1.3 and 0.2-0.8 mm, respectively. The average of the SDs of the random set-up errors (σ-*INTER*) and organ motions (σ-*intra*) ranged from 0.7 to 1.6 mm and from 0.3 to 0.6 mm, respectively. Appropriate PTV-margins and PRV-margins for all the landmarks ranged from 2.0 to 3.6 mm and from 1.8 to 2.4 mm, respectively.

Conclusions: We have adopted a PTV-margin of 5 mm and a PRV-margin of 3 mm for head and neck IMRT at our department.

Keywords: Set-up error; Organ motion; PTV-margin; PRV-margin; Head and neck IMRT

Intensity modulated radiotherapy (IMRT) has been applied to a variety of malignancies [2,12,15,27,32]. IMRT has been reported to have many advantages over conventional radiotherapy in delivering high doses to target volumes while sparing surrounding organs [4,9,19,23]. IMRT is especially effective in the treatment of head and neck tumors, since the clinical target volumes (CTV) are in contiguity with organs at risk (ORs) such as the salivary glands, brain stem and spinal cord. To make the most of the advantages of IMRT, the design of the planning target volume (PTV) and the planning organs at risk volume (PRV), is important process in the treatment planning. Inappropriate definitions of the PTV and PRV yield volumes receiving less than prescribed dose (cold spot) in the PTV or deliver intolerable doses to the ORs.

In the treatment of head and neck tumors, many authors have reported the set-up errors using various immobilizing devices [1,3,6,7,31]. However, little has been reported on the intrafractional organ motions during irradiation of head and neck tumors [20,22]. IMRT needs a long treatment time of 15-30 mm for a single fraction. Therefore, the organ motions of the head and neck tumors during the treatment with IMRT may attain substantial magnitude. Since, the effects of the set-up errors and the organ motions on the dose distribution are basically equal, both the errors should be taken into account for setting the PTV- and PRV-margins [17,26]. The aims of the present study are to analyze both the interfractional set-up errors and intrafractional organ motions in head and neck IMRT and to decide the appropriate PTV- and PRV-margins for head and neck IMRT at our department.

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Materials and methods

Interfractional set-up error analysis

Ten consecutive patients with head and neck tumors treated with IMRT were evaluated for analyses of the interfractional set-up errors. Primary sites were the nasopharynx (7), oropharynx (2), and paranasal sinus (1). Median age was 62 (range 42-81) years. All the patients were immobilized with a thermoplastic shell covering head, neck and shoulders (Uni-frame® form MED-TEC, Orange City, IA, USA), which was fixed to the treatment couch. To reduce the interfractional set-up errors, we have adopted a strict criterion for the patient positioning as follows. On the first treatment day, after finishing verification of the isocenter, we recorded the coordinates (x, y, z) of the couch position as the reference. On the following treatments, at the start of the patient positioning, the couch was set at the reference position. Since the shell was fixed to the couch, the position of the shell was the same position at the start of the positioning during entire course of the treatment. If the laser-based positioning, which was carried out in the isocenter plane by matching the longitudinal and lateral lasers and the set-up markers depicted by ink-soaked thin-wire on the shell, moved away the couch more than 1 mm along any direction from the reference position, we repeated the positioning until the movement of the couch was within 1 mm.

At our department, as one of the procedures for quality assurance (QA) of the IMRT, we took two orthogonal, anterior-posterior (AP) and lateral films, for verification of the isocenter [27]. The orthogonal films taken with the treatment beam (beam films) were referred to those taken on the table of the X-ray simulator (simulation films). If the isocenter in the beam films deviated 2 mm or more from that in the simulation films on visual inspection, the treatment couch was adjusted to the correct position. Verification of the isocenter was carried out every day for the first week of the IMRT and weekly thereafter. The QA procedure was performed a total of 85 times in 10 patients (7-10 times per patient). In four patients, no adjustment of the couch was carried out. In six patients, a total of fifteen adjustments of the couch were performed (once or twice per patient). Of the 170 beam films analyzed in the present study, 155 (91%) were taken without an adjustment of the couch. The interfractional set-up errors were analyzed by comparing a total of 170 beam films (85 AP and 85 lateral films) with 20 simulation films (10 AP and 10 lateral films) for the 10 patients. Since the magnitudes of the movement of head and neck tumors may vary according to the location of the tumors, the position of each of four visible bony landmarks relative to the isocenter was evaluated. The four landmarks included maxilla, mandible, skull base, and cervical vertebrae (Fig. 1). The simulation films were digitally stored in Somavision (Varian Assoc., Palo Alto, CA) equipped with the X-ray simulator (Ximatoron EX, Varian Assoc., Palo Alto, CA). The beam films digitally translated using a commercial scanner were also stored in Somavision. The software in Somavision can calculate the coordinates of

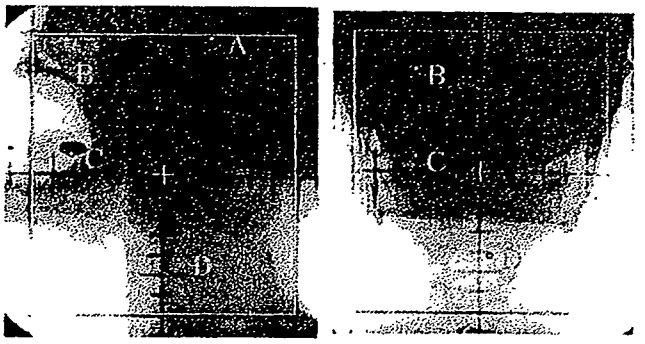

Fig. 1. Bony landmarks on simulation films; (A) skull base, (B) maxilla, (C) mandible, (D) cervical vertebrae. Each coordinate of the bony landmarks was calculated relative to the isocenter.

the four bony landmarks relative to the isocenter. Deviations of the coordinates of each landmark in the beam films from those in the simulation films were determined as the set-up errors for each bony landmark. The deviations in the lateral and cranio-caudal directions were measured using the AP films and those in the AP and cranio-caudal directions using the lateral films.

To calculate values or standard deviations (SDs) of systematic and random errors, we referred to the report by Rameijer et al. [21]. The systematic interfractional set-up error for a specific patient *Sp-INTER* is calculated as the mean of the set-up errors for that patient. The mean of the *Sp-INTER* values for all the patients in a given population is denoted by μ-*INTER*, whereas its SD is given by Σ-*INTER*. The random set-up error for a specific patient, σp-*INTER*, was calculated as the SD of the set-up errors from fraction to fraction. To characterize the random errors in a given population, an appropriate average is calculated by the root mean square of the σp-*INTER* values for all the patients, and is denoted by σ-*INTER*. The distribution of the interfractional set-up errors in a given population is characterized by the set (μ-*INTER*, Σ-*INTER*, σ-*INTER*).

Intrafractional organ motion analysis

In the analyses of the intrafractional organ motions, nine patients with head and neck tumors and three with brain tumors were evaluated. Primary sites were the nasopharynx (4), cervical esophagus (2), paranasal sinus (2), oral cavity (1), and malignant glioma (three). Median age was 62 (range 42-81) years. Since the electronic portal imaging device (EPID) or tracking system for radiopaque markers implanted into the tumors is not equipped with our radiotherapy treatment system, we adopted a practical and convenient method to assess the intrafractional organ motions in the present study. The method was as follows. First, on the X-ray simulator with the same table couch that our treatment system (Clinac-600C accelerator, Varian Assoc., Palo Alto, CA, USA) has, the patient was positioned and fixed with the same immobilizing device as used at the treatment. Second, for 15 min under the condition that the patient was immobilized on the X-ray simulator, AP and lateral images were digitally stored at 3 min intervals (6 times). Third, the coordinates of the same bony landmarks as analyzed for the