significantly increased in PC-9 and PC-9/ZD2001R cells but not in PC-9/ZD2001 cells (Fig. 4A and B). According to the results of Akt phosphorylation, induction was inhibited by gefitinib in PC-9 and PC-9/ZD2001R cells but not in PC-9/ZD2001 cells. Wortmannin could inhibit induction in all three cell lines. Consistent with the results of protein expression, treatment with TNF-α increased the expression level of c-IAP1 and c-IAP2 mRNA in PC-9 and PC-9/ZD2001R cells in a dose-dependent manner (Fig. 5A and B). After treatment with 100 ng/mL TNF-α for 12 hours, the expression levels of both c-IAP1 and c-IAP2 mRNA were significantly increased in PC-9 cells (c-IAP1, 7.05 ± 0.62; c-IAP2, 18.22 ± 0.25) and PC-9/ZD2001R cells (c-IAP1, 7.02 ± 0.54; c-IAP2, 11.56 ± 0.75) but not in PC-9/ZD2001 cells (c-IAP1, 2.60 ± 0.58; c-IAP2, 2.83 ± 0.66). These observations suggest that TNF-α-induced apoptotic signaling is not inhibited by its own antiapoptotic effects, such as IAPs induction, owing to the weak effect of TNF-α-mediated signaling and the Akt/NF-κB pathway via EGFR in this gefitinib-resistant cell line.

Discussion

We have shown that the gefitinib-acquired resistant NSCLC cell line PC-9/ZD2001 acquired collateral sensitivity to the apoptotic effect of TNF-α. Because this collateral sensitivity was significantly diminished in the revertant PC-9/ZD2001R, it might be correlated with gefitinib resistance. As described before, PC-9/ZD2001 also acquired collateral sensitivities to some anticancer drugs, such as vinorelbine, paclitaxel, camptothecin, and 5-fluorouracil. However, this cell line did not show the collateral sensitivities to cisplatin, etoposide, mitomycin C, and cyclophosphamide.[5] Moreover, there was no difference of susceptibility to serum-starved condition between PC-9 and PC-9/ZD2001 (data not shown). From these observations, it can be concluded that the collateral sensitivities of the gefitinib-resistant cells are specific to some cell stresses and are not caused by the fragility of the cells. Because the same tendency of sensitivity was seen in the other resistant clones, PC-9/ZD2002 and PC-9/ZD2003, the acquired sensitivity to the anticancer drugs and TNF-α could be a general phenomenon even in the clinical gefitinib-resistant cells.

TNF-α activates not only apoptotic signaling but also antiapoptotic signaling via the Akt/NF-κB activation (22, 23). Activation of the downstream transcription factor NF-κB inhibits various types of apoptotic cell death by inducing apoptotic inhibitory proteins (22, 23), such as bcl-2 (24), bcl-xl (25), forkhead (26), and IAPs (10, 11, 27, 28). As described before, it is thought that the cytotoxic effect of TNF-α is determined by ratios between the apoptosis-inducing and the apoptosis-inhibiting effects (5–7, 12, 14, 15).

In parental PC-9 cells, TNF-α induced EGFR autophosphorylation and subsequent Akt/NF-κB pathway activation (Fig. 4A and B). This autophosphorylation was completely inhibited by a low concentration of gefitinib (10 nmol/L). From these observations, we think that TNF-α-induced Akt/NF-κB pathway activation occurs mainly through cross-talk from TNFR to EGFR in this cell line. Because the expression level of EGFR was significantly decreased in PC-9/ZD2001 as compared with the parental PC-9, the decline of the cross-talk signaling might partially diminish the TNF-α-induced activation of the Akt/NF-κB pathway. Our results are supported by those of an earlier study showing that resistance to the cytotoxic effect of TNF-α is associated with high expression of Her family receptors, such as EGFR (Her1), erbB2/Her2/neu, or Her3, in a panel of human tumor cell lines (29). However, the decreased EGFR signaling from the Akt/NF-κB pathway could not be fully explained by the lower EGFR expression in PC-9/ZD2001 because EGFR expression remained only partially restored in the revertant PC-9/ZD2001R cell line. In light of these observations, to clarify the mechanisms of collateral sensitivity to TNF-α in the gefitinib-resistant cells, we focused on the cross-talk signaling from TNFR to EGFR in PC-9, PC-9/ZD2001, and PC-9/ZD2001R cells.

Several recent articles have reported that TNFR mediates cross-talk signaling to EGFR through a ligand-dependent and -independent manner (16–19, 21, 23). Chan et al. (17) have reported that exposure of human mammary epithelial cells to TNF-α results in transactivation of EGFR through metalloprotease-dependent shedding of EGFR ligand(s). Hirota et al. (18) reported that EGFR transactivation by TNF-α is

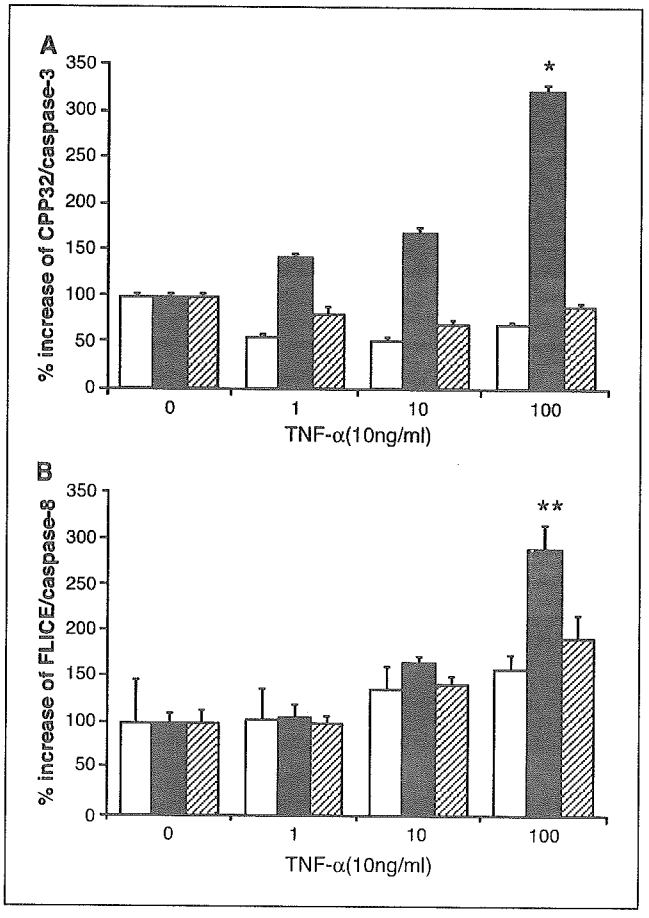

Fig. 3. TNF-α-mediated activation of CPP32/caspase-3 and FLICE/caspase-8 in PC-9, PC-9/ZD2001, and PC-9/ZD2001R cells. Activation of CPP32/caspase-3 and FLICE/caspase-8 was measured as described in Materials and Methods. The cells were exposed to the indicated concentrations of TNF-α for 12 hours; after which equivalent amounts of samples were reacted with the substrates DEVD-pNA and IETD-pNA. Absorbance was measured at 400 and 405 nm with a microtiter plate reader. *A*, CPP32/caspase-3. *B*, FLICE/caspase-8. TNF-α activated FLICE/caspase-8 in all three cell lines but activated CPP32/caspase-3 only in PC-9/ZD2001 cells. Data calculated as the percentage increase compared with respective untreated controls. Points, mean of three different experiments each done in triplicate; bars, SD. Open columns, PC-9; closed columns, PC-9/ZD2001; hatched columns, PC-9/ZD2001R. *, $P < 0.001$, PC-9 versus PC-9/ZD2001. **, $P = 0.02$, PC-9 versus PC-9/ZD2001.

regulated by means of redox-dependent mechanisms. The transactivation of EGFR was observed to occur quickly, after <30 minutes of exposure to TNF-α in PC-9 cells (Fig. 4A and B). No additional induction of ligands, EGF and transforming growth factor-α, were detected by ELISA in the culturing medium of the cells even after 6 hours of 100 ng/mL TNF-α exposure (data not shown). From these observations, we think that this activation could occur independently of ligands but not through TNF-α-mediated ligands synthesis or proteolytic releasing of preexisting ligands from the disrupted cells. Although TNF-α induced the same levels of EGFR autophosphorylation in all three cell lines, this EGFR activation is minimally transmitted to the downstream Akt/NF-κB pathway in the resistant PC-9/ZD2001 cells (Fig. 4A). Moreover, an inhibitory effect of gefitinib on TNF-α-induced Akt/NF-κB activation was not observed although wortmannin, a phosphatidylinositol 3-kinase inhibitor, completely inhibited this signaling in PC-9/ZD2001 cells (Fig. 4B). These results suggest that the weak effect of EGFR on Akt/NF-κB signaling could occur between EGFR and phosphatidylinositol 3-kinase in PC-9/ZD2001 cells.

Several articles reported that the sensitivity to gefitinib is regulated by active mutant EGFR (30, 31), by the expression level of phosphatase and tensin homologue/MMAC/TEP (32), and by levels of Akt phosphorylation (13, 33, 34). Because the gefitinib-hypersensitive PC-9 cells originally had 15-bp deletion mutation in exon 19 of EGFR, they were thought to have a gefitinib-sensitive active mutant EGFR (35); however, because we found no alteration of the EGFR mRNA sequence in PC-9/ZD2001 cells (data not shown), we conclude that this gefitinib-resistant cell line was a good model for acquired gefitinib resistance. In our previous study, EGFR signaling mediated by transforming growth factor-α, an EGFR ligand, could not activate the mitogen-activated protein signaling pathway but could partially activate the Akt signaling cascade in PC-9/ZD2001. In PC-9/ZD2001R cells, the association between EGFR and mitogen-activated protein kinase signaling was completely reconstituted. On the basis of this result, we conclude that the decrease of EGFR signaling to the mitogen-activated protein kinase signaling pathway might contribute to acquired gefitinib resistance.[5] In this study, TNF-α significantly induced EGFR autophosphorylation but subsequent activation of the Akt signaling cascade was little observed in PC-9/ZD2001 (Fig. 4A and B). This decreased EGFR signaling on Akt could be partially caused by the decrease in EGFR expression but we have

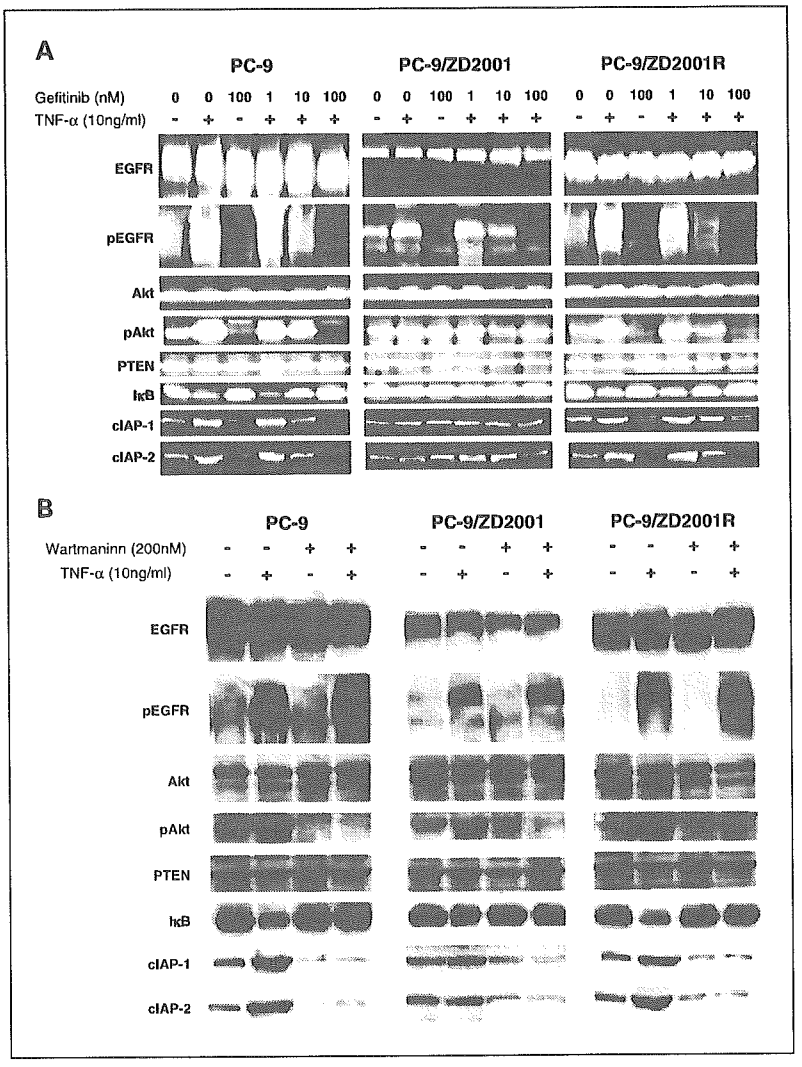

Fig. 4. Inhibitory effect of gefitinib on TNF-α-induced phosphorylation of Akt1 and degradation of IκB. Cells were treated with TNF-α with or without gefitinib (*A*) or wortmannin (*B*) simultaneously for 30 minutes at 37°C. Cell lysates were prepared and equivalent amounts of protein from each cell lysate were resolved with 10% SDS-PAGE, transferred to nitrocellulose membranes, and subjected to Western blotting with specific antibodies (as described in Materials and Methods). The EGFR and Akt1 membranes were stripped and reblotted with antibodies against phospho-EGFR (Tyr1045) and phospho-Akt, respectively. Expression of β-actin was used as internal control. Although treatment with TNF-α significantly phosphorylated EGFR in all three cell lines, downstream Akt/NF-κB activation was observed in PC-9 and PC-9/ZD2001R but weakly in PC-9/ZD2001. Gefitinib inhibited cross-talk signaling in PC-9 and PC-9/ZD2001R cells but not in PC-9/ZD2001 cells (*A*). A phosphatidylinositol 3-kinase inhibitor, wortmannin, completely inhibited this signaling in all three cell lines (*B*).

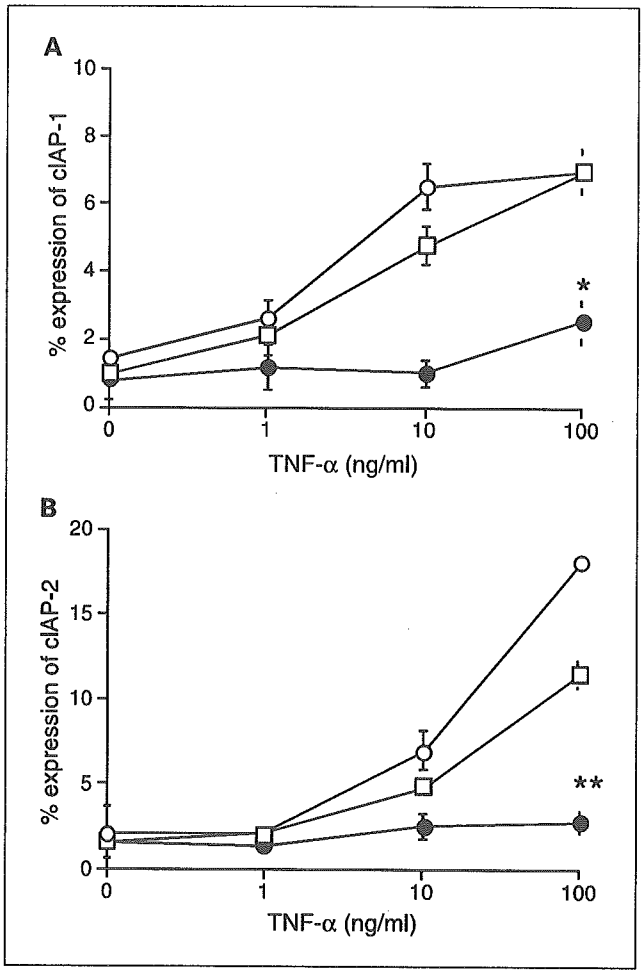

Fig. 5. TNF-α induced c-IAP1 and c-IAP2 mRNA expression in PC-9 and PC-9/ZD2001R cells but not in PC-9/ZD2001 cells. The cells were exposed to the indicated concentrations of TNF-α for 12 hours; after which mRNA was isolated with the guanidium isothiocyanate method. Induction of c-IAP1 (*A*) and c-IAP2 (*B*) mRNA was measured with a fluorescence-based real-time RT-PCR method using specific primer sets (as described in Materials and Methods). The expression levels of c-IAP1 and c-IAP2 mRNA were significantly and dose-dependently increased by exposure to TNF-α in PC-9 and PC-9/ZD2001R cells but this enhancement was rarely observed in PC-9/ZD2001 cells. Results expressed as the percentage of each cell line compared with the internal control, expression of β-actin mRNA. ○, PC-9; ●, PC-9/ZD2001; □, PC-9/ZD2001R. Points, mean of three different experiments; bars, SD. *, $P < 0.001$.

no data to explain the discrepancy between transforming growth factor-α-mediated and TNF-α-mediated EGFR signaling in this cell line. Nevertheless, TNF-α-mediated cross-talk signaling to EGFR, although ligand independent, seems to cause downstream activation in a different way from that caused through ligand-mediated direct EGFR activation. Akt/NF-κB signaling is also known to be downstream of other receptors, such as other Her family receptors (36), platelet-derived growth factor receptor (37), and IFN receptor (38). We previously confirmed the expression of other Her family receptors, Her2 and Her3, in PC-9 cells. Possibly, signaling of these receptors may be able to modulate the TNF-α-mediated cross-talk signaling and Akt/NF-κB signaling. Various aspects of TNF-α-induced cross-talk signaling to EGFR, such as EGFR heterodimer formation with other Her family receptors and downstream signaling specificity, require further investigation.

Human IAPs, c-IAP1 and c-IAP2, have been reported to block the apoptotic events caused by caspase-8 activation by directly combining with caspase-3 and caspase-7 and restraining them (10, 27). IAPs play a key role in the resistance to apoptotic effect of TNF-α superfamily of proteins (39) and various anticancer drugs (40, 41); for this reason, IAPs are considered promising targets in anticancer therapy (42, 43). To evaluate TNF-α-mediated antiapoptotic signaling, we measured IAP induction in these cell lines by means of Western blotting analysis and real-time RT-PCR. As might be expected, IAPs and their mRNAs were markedly induced by TNF-α in PC-9 and PC-9/ZD2001R cells but not in PC-9/ZD2001 cells (Fig. 5A and B). TNF-α-induced activation of caspase-3, but rarely of caspase-8, was significantly lower in PC-9 and PC-9/ZD2001R as compared with PC-9/ZD2001 (Fig. 3A and B). These results suggest that TNF-α precisely activates apoptotic signaling through caspase-8 in all three cell lines and that induction of IAPs blocks downstream signaling by inhibiting caspase-3 in PC-9 and PC-9/ZD2001R. In these cell lines, the induction of IAPs likely plays a key role in determining the sensitivity to TNF-α-mediated apoptosis among the antiapoptotic proteins that are induced by NF-κB-mediated transcription.

Several clinical studies of TNF-α as an anticancer treatment have been done, mainly in the 1970s; however, treatment with TNF-α was greatly limited by its side effects, particularly its toxicity to previously healthy organs (44–49). Recently, several new anticancer therapies using TNF-α have been developed, such as RGD-V29 (F4614) and TNF-erade (Biologic), in an attempt to reduce adverse effects (8, 9, 50, 51). We have shown that a NSCLC cell line with acquired resistance to gefitinib acquired collateral sensitivity to TNF-α. These data strongly suggest that treatment with TNF-α might be effective against tumors that have acquired resistance to gefitinib after long-term administration of this drug. Further analysis is required before clinical application.

In summary, the cross-talk signaling from TNFR to EGFR and subsequent IAP induction play important roles in the resistance to TNF-α-induced apoptosis in PC-9 cells. Because this signaling cascade is decreased in the gefitinib-resistant PC-9/ZD2001 cells, TNF-α did not activate the Akt/NF-κB cascade. This decrease of EGFR signaling to Akt/NF-κB pathway, which is related to gefitinib-acquired resistance, may contribute to the acquisition of hypersensitivity to TNF-α in this cell line.

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Standard Thoracic Radiotherapy With or Without Concurrent Daily Low-dose Carboplatin in Elderly Patients with Locally Advanced Non-small Cell Lung Cancer: a Phase III Trial of the Japan Clinical Oncology Group (JCOG9812)

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Background: The purpose of this study was to evaluate whether radiotherapy with carboplatin would result in longer survival than radiotherapy alone in elderly patients with unresectable stage III non-small cell lung cancer (NSCLC).
Methods: Eligible patients were 71 years of age or older with unresectable stage III NSCLC. Patients were randomly assigned to the radiotherapy alone (RT) arm, irradiation with 60 Gy; or the chemoradiotherapy (CRT) arm, the same radiotherapy and additional concurrent use of carboplatin 30 mg/m^2 per fraction up to the first 20 fractions.
Results: This study was terminated early when 46 patients were registered from November 1999 to February 2001. Four patients (one in the RT arm, three in the CRT arm) were considered to have died due to treatment-related causes. The JCOG Radiotherapy Committee assessed these treatment-related deaths (TRDs) and the compliance with radiotherapy in this trial. They found that 60% of the cases corresponded to protocol deviation and 7% were protocol violation in dose constraint to the normal lung, two of whom died due to radiation pneumonitis. As to the effectiveness for the 46 patients enrolled, the median survival time was 428 days [95% confidence interval (CI) = 212–680 days] in the RT arm versus 554 days (95% CI = 331 to not estimable) in the CRT arm.
Conclusions: Due to the early termination of this study, the effectiveness of concurrent use of carboplatin remains unclear. We re-planned and started a study with an active quality control program which was developed by the JCOG Radiotherapy Committee.

Key words: non-small cell lung cancer – elderly patients – carboplatin – chemoradiotherapy

INTRODUCTION

Lung cancer is the leading cause of cancer-related deaths in the USA, Europe and Japan. In Japan, the number of elderly is increasing dramatically. In 2001, the proportion of Japanese population older than 65 years was 18%; in other words, the number of people older than 65 years exceeded 22 million (1). Lung cancer death rates for men and women aged 75 or more have increased to ~531 and 138 per 100 000 population, respectively (1). To establish the effective treatment for the elderly with lung cancer has thus become of greater importance.

Until recently, the standard treatment for locally advanced non-small cell lung cancer (NSCLC) was radiotherapy alone. However, the 5-year survival rate of patients with stage III remained under 10% (2–4). To improve the survival rates, many clinical trials comparing radiotherapy with chemoradiotherapy have been conducted (5–11). A recent meta-analysis suggested that the combination of chemotherapy containing cisplatin (CDDP) and radiation could improve the survival rate compared with radiotherapy alone (12,13). However, it is still unclear whether the combined chemoradiotherapy is also suitable for elderly patients. This is partly because the elderly had been considered inappropriate as study patients.

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Almost all evidence available has thus been derived from subset analysis of trials for locally advanced NSCLC. A secondary analysis of RTOG 94-10 revealed a greater survival benefit for concurrent chemotherapy (14). Schild et al. reported no significant difference in tumor regression between younger and older patients in an NCCTG trial (15). Meanwhile, some reports on inoperable NSCLC patients indicate that chemoradiotherapy has survival benefit compared with radiotherapy, but this may not be applicable for those >70 years of age, for whom radiation alone could be most beneficial (16,17).

Therefore, we cannot treat the elderly in the same way as we can younger patients: first, as elderly patients have poorer prognosis than younger patients, they may think that their quality of life is more important than risking radical treatment. Secondly, the elderly tend to be vulnerable to intensive care and toxicities of treatment drugs (18–21). Less toxic therapy may be more effective for the elderly with NSCLC.

Some clinical trials, in which the elderly were not included, showed some efficacy of carboplatin (CBDCA), an analog of CDDP, having no nephrotoxicity, neurotoxicity or ototoxicity and being much less emesis-provoking than CDDP (22–24). Additionally, some investigators found the same radiosensitizing properties of CBDCA (25–28) as also found for CDDP. Therefore, we hypothesized CBDCA to be more acceptable in the treatment of elderly patients. A phase II study has reported the use of radiotherapy and concurrent low-dose daily CBDCA in elderly patients with locally advanced NSCLC (29). For stage III patients, the median survival time (MST) was 15.1 months. Given an MST of ~10 months by radiation alone (5,6,8,9,11,17), this combined chemoradiotherapy seemed promising. Here we performed a randomized study to determine whether this combined chemoradiotherapy has an impact on survival in elderly patients with unresectable locally advanced NSCLC compared with radiotherapy alone.

PATIENTS AND METHODS

PATIENTS

Eligibility criteria for this study were as follows: age ≥71 years; a histologically confirmed non-small cell carcinoma; unresectable disease; stage IIIA except T3N1M0 and IIIB which does not have disease extended to any contralateral hilar nodes or any supraclavicular nodes, atelectasis of the entire lung or malignant pleural effusions; measurable disease; a required radiation field of less than one half of one lung; no previous chemotherapy or radiotherapy; an Eastern Cooperative Oncology Group (ECOG) performance status (PS) of 0–2; PaO_2 ≥70 torr, white blood cell count ≥4000/μl, hemoglobin level ≥9.5 g/dl, platelet count ≥100 000/μl, serum bilirubin level ≤1.5 mg/dl, serum aspartate aminotransferase (AST) and alanine aminotransferase (ALT) ≤ twice the upper limit of normal, and serum creatinine level ≤ the upper limit of normal; a life expectancy of at least 3 months; and written informed consent. Exclusion criteria included patients with active infection, interstitial pneumonia or active lung fibrosis, chronic obstructive pulmonary disease (COPD) or uncontrolled heart disease, an active synchronous cancer, or a metachronous cancer within three disease-free years.

Staging was performed by chest radiograph in two directions, computed tomography (CT) scan or magnetic resonance imaging (MRI) of the head, CT scan of the chest, CT scan or ultrasound of the abdomen, and bone scintigraphy.

TREATMENT

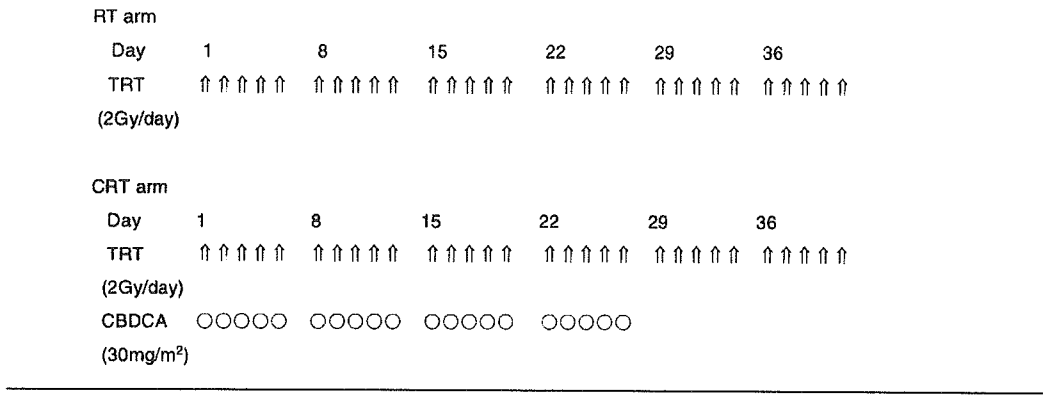
Patients were randomly assigned to the radiotherapy (RT) arm or the chemoradiotherapy (CRT) arm, by the minimization method of balancing PS (0 or 1 versus 2), stage (IIIA versus IIIB) and institution. The RT consisted of 60 Gy in 30 fractions over 6 weeks. In the CRT arm, patients received the same radiotherapy as in the RT arm and concurrent intravenous administration of CBDCA 30 mg/m^2 (30 min infusion) 1 h before every radiation treatment up to the first 20 fractions (Fig. 1).

Radiotherapy was delivered with megavoltage (6–10 MeV photons) equipment using anterior/posterior opposed fields up to 40 Gy including the primary tumor, the metastatic lymph nodes and the regional node. A booster dose of 20 Gy was given to the primary tumor and the metastatic lymph nodes for a total dose of 60 Gy using bilateral oblique fields. The clinical target volume (CTV) for the primary tumor was defined as the gross tumor volume (GTV) plus 1 cm taking account of subclinical extension. CTV and GTV for the metastatic nodes (>1 cm in shortest dimension) were the same. Regional nodes excluding contra-lateral hilar and supraclavicular nodes were included in the CTV; however, lower mediastinal nodes were included only if the primary tumor was located in the lower lobe of the lung. The planning target volumes for the primary tumor, the metastatic lymph nodes and regional nodes were determined as CTVs plus 0.5–1.0 cm margins laterally and 1.0–2.0 cm margins cranio-caudally taking account of set up variations and internal organ motion. Lung heterogeneity corrections were not used.

The criteria for stopping the treatment are pulmonary toxicities, which include the National Cancer Institute-Common Toxicity Criteria (NCI-CTC; version 2.0) grade 2 respiratory distress and <60 torr PaO_2, other than hematopoietic toxicities (leukopenia, neutropenia and thrombocytopenia) or gastrointestinal toxicities (dysphagia).

EVALUATION

To assess the rate of tumor response and toxicity, all patients received a complete blood cell count; blood chemistry, including AST, ALT, lactate dehydrogenase, bilirubin, serum creatinine, blood urea nitrogen, total protein, serum albumin, serum electrolytes and calcium; and weekly chest X-rays during the treatment period. Best overall response was evaluated as tumor response by mono- or bi-dimensional measurement in accordance with the World Health Organization (WHO) criteria (30), and toxicity was evaluated in accordance with the NCI-CTC (version 2.0).



RT, radiotherapy; CRT, chemotherapy; TRT, thoracic radiotherapy; CBDCA, carboplatin.

Figure 1. Treatment schema.

Study Design and Statistical Analysis

This trial was a multi-center randomized phase III study. The study protocol was approved by the JCOG Clinical Trials Review Committee and the institutional review board of each participating institution before the initiation of the study.

The primary end-point was overall survival, which was defined as the interval from randomization to death from any cause. Secondary end-points were response rate, which was the proportion of the patients evaluated as having a complete reponse (CR) or partial response (PR) in best overall response out of all eligible patients; progression-free survival (PFS) defined as the interval from randomization to the diagnosis of progression or death from any cause; sites of progression; and toxicity. The estimate of survival time was performed by the Kaplan–Meier method (31). The trial was designed to have an 80% power to detect 5 months difference in MST (10 months in the RT arm and 15 months in the CRT arm) with a one-sided alpha of 0.05 by log rank test (32). The planned sample size was 190 patients by Shoenfeld and Richter's methods (33) with 1.5 years follow-up after 3 years accrual.

In-house interim monitoring is performed by the JCOG Data Center to ensure data submission, patient eligibility, protocol compliance, safety and on-schedule study progress. The monitoring reports are submitted and reviewed by the JCOG Data and Safety Monitoring Committee (DSMC) twice yearly.

An expedited report was required by the JCOG DSMC to allow rapid identification of any life-threatening adverse events or unexpected toxicities according to the JCOG toxicity reporting system based on the ICH-E2A guidelines.

RESULTS

From November 1999 to February 2001, 46 patients were enrolled in this study: 23 in the RT arm and 23 in the CRT arm. Four treatment-related deaths (TRDs) had been reported, however, before the forty-sixth patient were assigned. Therefore, we suspended the registration and checked the details of all randomized patients to assess the safety of treatment regimens. As a result, it was revealed that three of these deaths were due to pneumonitis. The JCOG DSMC advised consultation with the JCOG Radiotherapy Committee (RC) about the radiotherapy compliance in all patients. The JCOG RC collected each patient's irradiation planning data retrospectively and found poor protocol compliance which was related to TRD. Consequently, we decided to terminate this trial in August 2001 following the recommendation of the JCOG DSMC.

PATIENTS CHARACTERISITICS

Patient characteristics are listed in Table 1. No specific characteristics of patients were found in the elderly patients with locally advanced NSCLC compared with younger patiests and the two treatment arms were well balanced with respect to age and stage.

Toxicity of Treatment

Both hematological and non-hematological toxicities during the treatment and follow-up period were assessed. Table 2 summarizes the hematological toxicity. Patients receiving CBDCA suffered from leukocytopenia, neutropenia and thrombocytopenia more than patients receiving RT alone. There was no grade 4 hematological toxicity in the RT arm. Two (8.7%) and four (17.4%) patients in the CRT arm experienced grade 4 leukocytopenia and neutropenia, respectively.

Non-hematological toxicity observed in this study is listed in Table 3. None of the patients developed grade 3 esophagitis in either treatment arm. In the RT arm, other grade 3/4 toxicities were edema, fatigue, dyspnea and pneumonitis in one patient each. In the CRT arm, other grade 3/4 toxicities were neutropenic fever, dyspnea and pneumonitis. Grade 3/4 (RTOG/EORTC Radiation Toxicity Score) of late lung toxicity was observed in two patients in the RT arm and four patients in the CRT arm. Four TRDs were observed in this study. Three of

Table 1. Patient characteristics

Characteristics	RT arm	CRT arm
No. of eligible patients	23	23
Age (years)		
Median	77	77
Range	72–84	71–83
Male/female	19/4	16/7
Type of tumor		
Adenocarcinoma	6	11
Squamous cell	16	11
Large cell	1	1
PS (ECOG)		
0	3	9
1	19	13
2	1	1
Stage of disease		
IIIA	11	12
IIIB	12	11
Weight loss		
<10%	21	23
≥10%	2	0

RT, radiotherapy; CRT, chemoradiotherapy; PS, performance status.

Table 2. Hematological toxicity

	RT arm (n = 23)					CRT arm (n = 23)				
Grade	1	2	3	4	%grade 4	1	2	3	4	%grade 4
Leukocytes	10	2	2	0	0	3	7	11	2	8.7
Neutrophils	4	3	0	0	0	2	8	6	4	17.4
Hemoglobin	5	3	0	0	0	5	8	3	0	0
Platelets	2	0	2	0	0	4	5	8	0	0

RT, radiotherapy; CRT, chemoradiotherapy.

these patients were thought to have died as a result of pneumonitis. The details of these cases are follows. Case 1: a 78-year-old man had stage IIIA (T3N2) squamous cell carcinoma. He was treated with RT alone and died of pneumonitis at 28 days after therapy. Case 2: a 79-year-old man had stage IIIB (T4N2) adenocarcinoma. He was treated with CBDCA + RT and died of bacterial pneumonia at 37 days after therapy and had been taking steroid hormone due to radiation pneumonitis. Case 3: a 73-year-old man had stage IIIA (T3N2) squamous cell carcinoma. He was treated with CBDCA + RT and died of pneumonitis at 80 days after therapy. Case 4: a 80-year-old man had stage IIIB (T4N2) squamous cell carcinoma. He was treated with CBDCA + RT and died of pneumonitis at 54 days after therapy. Thus, three out of four TRDs were in the CRT arm and one was in the RT arm.

Table 3. Non-hematological toxicity

	RT arm (n = 23)					CRT arm (n = 23)				
Grade	1	2	3	4	% grade 4	1	2	3	4	% grade 4
Edema	0	0	0	1	4.5	0	0	0	0	0
Fatigue	1	0	0	1	4.5	7	1	0	0	0
Fever	3	0	0	0	0	1	1	0	0	0
Esophagitis	13	2	0	0	0	10	2	0	0	0
Nausea	0	0	0	–	–	2	2	0	–	–
Vomiting	0	0	0	0	0	1	0	0	0	0
Febrile neutropenia	–	–	0	0	0	–	–	1	0	0
Cough	3	1	0	–	–	6	0	0	–	–
Dyspnea	–	0	0	1	4.5	–	2	1	0	0
Pneumonitis	1	0	0	–	4.5	1	0	1	0	0
Creatinine	1	0	0	0	0	0	0	0	0	0
Hyponatremia	7	–	0	0	0	5	–	1	0	0
Heart	0	0	0	0	0	0	1	0	0	0
Lung	8	4	2	0	0	9	6	1	3	13.0

RT, radiotherapy; CRT, chemoradiotherapy.

Protocol Compliance

In the RT arm, 22 (95.6%) patients received full treatment doses. In the CRT arm, 20 (87.0%) patients completed the treatment. As to the administration of CBDCA, there were few protocol deviations.

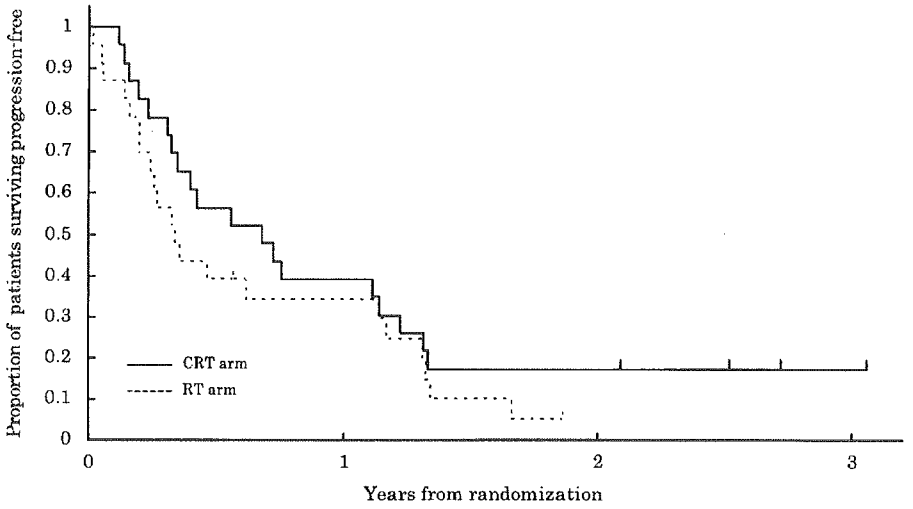
Three of the patients discontinued the protocol treatment: one was due to grade 2 eruption, one was due to cerebral infarction and one was due to insufficient recovery from leukopenia. One patient in the RT arm did not start the treatment due to local progression (Table 4).

Quality Assurance of Radiotherapy

We evaluated the quality of radiotherapy retrospectively based on the collected radiation therapy planning data. The data of 45 patients were reviewed and evaluated for the analysis. Details of this analysis have been reported by Ishikura et al. (34); three cases were revealed to be protocol violation due to normal lung volume constraint defined in the protocol. Unacceptable protocol deviations were identified as follows; 17, 15 and 31 cases on field border placement for the primary tumor, the metastatic lymph nodes and the elective nodal irradiation, respectively. Overall, 27 of 45 cases (60%) had at least one unacceptable deviation. Most cases judged to have protocol violation were primarily due to a smaller radiation field. Only 18 cases (40%) were judged to be protocol compliant.

Response and Survival

The tumor response in each arm is listed in Table 5. No patients achieved a CR in either arm. Of the 23 patients in the RT arm, 12 [52.2%, 95% confidence interval (CI) = 30.6–73.2%] achieved PR and six (26.1%) had stable disease. Of the



RT, radiotherapy; CRT, chemoradiotherapy.

Figure 2. Progression-free survival for patients treated with radiation alone or radiation with concurrent daily CBDCA.

Table 4. Protocol compliance

Pattern	RT arm (n = 23)	CRT arm (n = 23)
Complete protocol treatment	22	20
Progression/relapse*	1	0
Adverse events		
Cerebral infarction	0	1
Eruption	0	1
Leukopenia	0	1
Patient refusal	0	0
Death on protocol	0	0
Other	0	0

*Before starting the radiotherapy.
RT, radiotherapy; CRT, chemoradiotherapy.

Table 5. Response to treatment

Response	RT arm (n = 23)	CRT arm (n = 23)
Complete response	0 (0)	0 (0)
Partial response	12 (52.2)	11 (47.8)
Stable disease	6 (26.1)	7 (30.4)
Progression	4 (17.4)	4 (17.4)
Not evaluable	1 (4.4)	1 (4.4)
Objective response	52.2%	47.8%

RT, radiotherapy; CRT, chemoradiotherapy.

23 patients in the CRT arm, 11 (47.8%, 95% CI = 26.8–69.4%) achieved PR and seven (30.4%) had stable disease.

Seventeen (73.9%) patients in the RT arm and 15 (65.2%) patients in the CRT arm had died at the time of analysis. The median progression-free survival time was 122 days (95% CI = 88–413 days) on the RT arm versus 248 days (95% CI = 127–416 days) on the CRT arm (Fig. 2.). The MST was 428 days (95% CI = 212–680 days) on the RT arm versus 554 days (95% CI = 331 to not estimable) on the CRT arm (Fig. 3.). The 1-year survival rate was 60.9% (95% CI = 40.9–80.8%) on the RT arm versus 65.2% (95% CI = 45.8–84.7%) on the CRT arm.

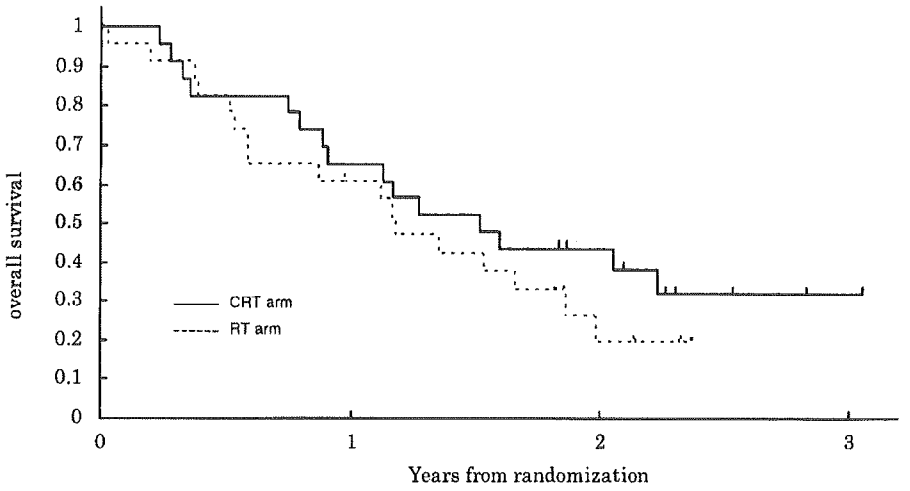
Pattern of Progression/Relapse

The first site of disease progression or relapse is listed in Table 6. Sixteen patients in the RT arm and 13 patients in the CRT arm had relapsed or had disease progression at the time of analysis. Eight patients (out of 16, 50.0%) in the RT arm and seven patients (out of 13, 53.8%) in the CRT arm had relapse or disease progression within the radiation field whether relapse outside the radiation field occurred or not.

DISCUSSION

We conducted this randomized controlled trial to determine whether chemoradiotherapy was superior to radiotherapy alone with respect to overall survival of elderly patients with locally advanced NSCLC. The study was terminated early when 24% of the planned sample size was accrued because of a high proportion of TRDs due to radiation pneumonitis and protocol violation.

Pulmonary toxicities including radiation pneumonitis and fibrosis caused by radiation therapy are, in general, common but not severe. In this study, however, the risk of TRD was 8.7% (four out of 46) and was much higher than in other trials. For instance, Ohe et al. (35) retrospectively analyzed the incidence of TRDs in the treatment of thoracic radiotherapy and/or chemotherapy for patients with locally advanced NSCLC, and reported that seven of 448 patients (1.6%)



RT, radiotherapy; CRT, chemoradiotherapy.

Figure 3. Overall survival for patients treated with radiation alone or radiation with concurrent daily CBDCA.

Table 6. First site of disease progression

	RT arm ($n = 23$)	CRT arm ($n = 23$)
Local	8	5
Distant	8	6
Local + distant	0	2

RT, radiotherapy; CRT, chemoradiotherapy.

died of radiation-induced pneumonitis. The high proportion of pulmonary toxicities in our trial may be due partly to the high age of the patients. Schild et al. (15) reported that they found 6% of elderly (older than 75 years) with NSCLC had grade 4 pneumonitis whereas this was the case in only 1% of younger patients ($P = 0.02$). It was controversial that the four TRDs out of 46 was sufficient reason to terminate the on-going trial; however, we thought it was serious that half of the TRDs (two out of four) were judged to be associated with protocol violation concerning the radiation field, which was to be less than half of one lung. Because the JCOG had not yet established the quality control/assurance system for radiotherapy before this trial, we concluded that we would not be able to control the risk of radiation pnuemonitis due to protocol deviation if we continued this study. What was an issue in this study was not only the high TRD rate, but also the poor protocol compliance of RT. The reasons for the poor protocol compliance are limited participation of radiation oncologists during protocol development, limited educational resources for attending radiation oncologists and no quality control program. Although the retrospective systematic review of radiation planning and protocol compliance of radiotherapy was the first experience in the JCOG, both the Lung Cancer Study Group and the entire JCOG had become aware of the importance of a quality control system for radiotherapy. The JCOG Executive Committee decided to establish the Radiation Therapy Quality Assurance Center (RTQAC) within the JCOG Data Center under the supervision of the JCOG Radiotherapy Committee. The RTQAC started the prospective quality control and quality assurance (QC/QA) program in September 2002 with a new activated phase III study for limited disease of small cell lung cancer, JCOG0202. Up to 2004, the QC/QA program has been expanded to the other group studies, such as esophageal cancer study, breast cancer study, prostate cancer study and brain tumor study. In addition, the JCOG Executive Committee mandates the QC/QA program by the RTQAC for all JCOG trials when protocol treatment includes radiation therapy.

The clinical question raised in this trial has not been answered. The data from the 46 patients enrolled were not considered to be conclusive because of the small sample size. No remarkable difference was found between the arms in terms of safety and efficacy such as tumor response, PFS and overall survival. We considered that it still remained an important clinical question to be investigated whether the daily low-dose CBDCA plus radiotherapy was effective or not. Therefore, we re-planned and started a new phase III trial (JCOG0301), in which the prospective QC/QA program by the RTQAC is added to the identical design to this JCOG9812. The protocol involves initial review of radiation planning and final review of the actual radiation record for all randomized patients. The JCOG0301 was activated in September 2003, and we have achieved very good protocol compliance upto now.

Acknowledgments

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Epidermal growth factor receptor gene mutation in non-small cell lung cancer using highly sensitive and fast TaqMan PCR assay

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KEYWORDS
EGFR mutation;
Gefitinib;
Molecular targeted therapy;
Non-small cell lung cancer;
TaqMan PCR assay

Summary Epidermal growth factor receptor (*EGFR*) gene mutations have been found in a subset of non-small cell lung cancer (NSCLC) with good clinical response to gefitinib therapy. A quick and sensitive method with large throughput is required to utilize the information to determine whether the molecular targeted therapy should be applied for the particular NSCLC patients. Using probes for the 13 different mutations including 11 that have already been reported, we have genotyped the *EGFR* mutation status in 94 NSCLC patients using the TaqMan PCR assay. We have also genotyped the *EGFR* mutations status in additional 182 NSCLC patients, as well as 63 gastric, 95 esophagus and 70 colon carcinoma patients. In 94 NSCLC samples, the result of the TaqMan PCR assay perfectly matched with that of the sequencing excluding one patient. In one sample in which no *EGFR* mutation was detected by direct sequencing, the TaqMan PCR assay detected a mutation. This patient was a gefitinib responder. In a serial dilution study, the assay could detect a mutant sample diluted in 1/10 with a wild-type sample. Of 182 NSCLC samples, 46 mutations were detected. *EGFR* mutation was significantly correlated with gender,

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smoking status, pathological subtypes, and differentiation of lung cancers. There was no mutation detected by the TaqMan PCR assay in gastric, esophagus and colon carcinomas. TaqMan PCR assay is a rapid and sensitive method of detection of *EGFR* mutations with high throughput, and may be useful to determine whether gefitinib should be offered for the treatment of NSCLC patients. The TaqMan PCR assay can offer us a complementary and confirmative test.

1. Introduction

Lung cancer is the deadliest cancer in many developed countries. Gefitinib (Iressa®, Astra Zeneca, London, UK), an inhibitor of the epidermal growth factor receptor (*EGFR*) tyrosine kinase, has been approved in Japan and the United States for the treatment of non-small cell lung cancer (NSCLC). Recently, erlotinib (Tarceva®, Roche, Basel, Switzerland), another inhibitor of *EGFR* tyrosine kinase, has been approved in the United States and Switzerland for the treatment of NSCLC. Gefitinib caused significant tumor shrinkage in 27.5% of Japanese NSCLC patients but in only 10.4% of Caucasian population [1–4]. Unfortunately, the addition of gefitinib to the traditional chemotherapy did not add any benefit to the patient survival [3], although overexpression of EGFR protein was seen in relatively high frequencies [5]. We and others have shown that the somatic mutation in tyrosine kinase (TK) domain of *EGFR* is associated with sensitivity of NSCLC to gefitinib [6–8]. Gefitinib targets the ATP-binding cleft with the TK domain and the reported mutations are either deletion or single amino acid substitutions in exon 18, 19, or 21 clustered around the ATP-binding pocket of the TK domain.

In vitro, *EGFR* mutations have been reported to confer enhanced tyrosine kinase activity in response to epidermal growth factor (EGF) and increased sensitivity to inhibition by gefitinib [6,7,9,10]. Thus, it is highly likely that *EGFR* mutation is a critical determinant of the patient's response to gefitinib. To determine the *EGFR* gene status may bring important information whether gefitinib is a therapeutic option for the NSCLC patient. If we can avoid unnecessary prescription of gefitinib in patients who are in fact non-responders, we will avoid fatal side effects of the drug and significantly reduce the health care cost. Fluorescent dye-based genotyping technology using the 5′ nuclease assay (TaqMan PCR assay) was developed as a large-scale and highly sensitive method in SNP scoring [11–16]. For SNP genotyping, one pair of TaqMan probes and one pair of PCR primers are used. Two TaqMan probes differ at the polymorphic site, with one probe complementary to the wild-type allele and the other to the variant allele. Recently, this method is being applied for genotyping of insertion/deletion polymorphism as a simple and cost-effective method [17].

We applied this genotyping technique with TaqMan probe to detect *EGFR* somatic mutations. Probes were designed according to the 13 different *EGFR* mutations including 11 that have already been reported. We show in this paper that this method is sensitive enough to detect the mutation in samples contaminated with 9-fold excess of wild-type samples. It is also fast and could be applied in large-scale screening.

2. Materials and methods

2.1. Patients and genomic DNA

NSCLC tissues were obtained by surgical excision between 1997 and 1999 from 67 patients at Nagoya City University Hospital in Japan. NSCLC tissues were also obtained from 27 patients at National Hospital Organization, Kinki-Chuo Chest Medical Center who were subsequently treated with gefitinib. Of 27 gefitinib treated samples, six transbronchial biopsy samples were obtained. These 94 samples were sequenced and also analyzed using TaqMan PCR assay. We have also analyzed additional 182 recent NSCLC cases, as well as 63 gastric, 95 esophagus and 70 colon carcinomas, operated between 2000 and 2003 at Nagoya City University Hospital using TaqMan PCR assay. The research was approved by the Institutional Review Board of each hospital. All the patients consented to the use of their tissues for the present analysis. The tissues were placed in liquid nitrogen immediately after resection or fixed by formalin and paraffin embedded. Genomic DNA was extracted using Wizard SV Genomic DNA Purification System (Promega) according to the manufacturer's instructions.

2.2. Genomic DNA PCR and DNA sequencing

All of 27 samples from National Hospital Organization, Kinki-Chuo Chest Medical Center were amplified by PCR reaction for genotyping analysis.

The primers for amplification of exon18, exon19, exon20, and exon21 were designed as previously described [7]. The reaction mixtures were contained with 1 μl of template DNA, 2 μl of 10× LA PCR Buffer II, 2 μl of 25 mM $MgCl_2$, 3.2 μl of 2.5 mM dNTP mixture, 0.4 μl of each primer (250 μM), 0.5 μl of TaKaRa LA Taq (5 U/μl), 10 μl of ddH_2O in a volume of 20 μl. Thermal cycling conditions were as follows: initial denaturation at 94 °C for 5 min; followed by 30 cycles of 94 °C for 30 s; 64 °C for 30 s; and 72 °C for 1 min. The final extension was for 5 min at 72 °C. The PCR products were sequenced by ABI PRISM 3100 Genetic Analyzer® and analyzed by ABI PRISM SeqScape Software Version 2.1.1®.

2.3. Genotyping by the TaqMan PCR assay

The primers and TaqMan® MGB probes were designed with Primer Express 2.0 software (Applied Biosystems). The sequences of the allele-specific probes and primers used in the TaqMan PCR assay are shown in Table 1. TaqMan PCR and genotyping analysis were performed on Applied Biosystems 7500 Real Time PCR System (Applied Biosystems) in the manufacture's instructions. The reaction mixtures were amplified in 1 μl of genomic DNA (10 ng/μl) or 1 μl of 100-fold diluted PCR products, 5 μl of 2× TaqMan® Universal Master Mix (Applied Biosystems), 0.5 μl of 20× primer/probe mix (each final concentration of primer and probe is 9 μM and 2 μM), 3.5 μl of ddH_2O in a volume of 10 μl. PCR cycling conditions were as follows: one cycle at 95 °C for 10 min; and 40 cycle at 95 °C for 15 s and 58 °C for 1 min. The results were analyzed on Applied Biosystems 7500 Real Time PCR System using allelic discrimination assay program.

2.4. *EGFR* DNA amplification

The *EGFR* gene amplification was analyzed for 27 gefitinib treated patients by quantitative real-time PCR, performed on a PRISM 7500 sequence detector (Applied Biosystems) by using a QuantiTect SYBR Green kit (Qiagen Inc., Valencia, CA). We have quantified each tumor DNA by comparing the target locus to the reference *Line-1*, a repetitive element for which copy numbers per haploid genome are similar among all of the human normal and neoplastic cells. Quantification is based on standard curves from a serial dilution of human normal genomic DNA. The relative *EGFR* copy number level was also normalized to normal human genomic DNA as calibrator. Copy number change of *EGFR* gene relative to the *Line-1* and the calibrator were determined by using the formula $(T_{EGFR}/T_{Line\text{-}1})/(C_{EGFR}/C_{Line\text{-}1})$, where T_{EGFR} and $T_{Line\text{-}1}$ are quantity from tumor DNA by using *EGFR* and *Line-1*, and C_{EGFR} and $C_{Line\text{-}1}$ are quantity from calibrator by using *EGFR* and *Line-1*. PCRs for each primer set were performed in at least triplicate, and means were reported. Conditions for quantitative PCR reaction were as follows: one cycle of 50 °C for 2 min; one cycle of 95 °C for 15 min; 40 cycles of 95 °C for 15 s; 56 °C for 30 s; and 72 °C for 34 s. At the end of the PCR reaction, samples were subjected to a melting analysis to confirm specificity of the amplicon. Primers for *EGFR* gene were designed by using Primers 3[12] to span a 100–150 bp non-repetitive region at exon 28 and were synthesized by Invitrogen (Carlsbad, CA). Primer sequences for *EGFR* gene used in this study are as follows: forward, CCACCAAATTAGCCTGGACA; and reverse, CGCGACCCTTAGGTATTCTG. *EGFR* amplification (increased *EGFR* copy number) was defined as more than five copies.

2.5. Statistical analysis

For comparisons of proportions, the Fisher's Exact test was used. The two-sided significance level was at $P < 0.05$. We did all analyses using a Stat View (version 5, SAS Institute Inc., Cary, NC) software.

3. Results

3.1. Genotyping by genomic DNA sequencing

We have already published the *EGFR* genomic DNA sequencing data of 67 NSCLC samples [7,18]. Seventeen cases had a mutated allele and there were six different mutations. Other groups have also reported additional somatic mutations in the same region of the *EGFR* gene [6,8]. We first sequenced some additional samples to find previously unknown mutations. Twenty-seven NSCLC tumor samples from National Hospital Organization, Kinki-Chuo Chest Medical Center were subjected to conventional genomic DNA sequencing in exon 18, 19, 20, and 21. Nine of 27 cases (33.3%) had a mutation. Of these nine cases, two were novel mutations. One patient carried a 24 nucleotide in-frame deletion (2239–2262), removing amino-acid 747 through 754, and three nucleotides insertion at 2270, adding one asparagine (delL747–K754&insK757NK) as shown in Fig. 1A and B. This region overlaps with the other deletion mutations reported previously [6,7]. Another tumor had two mutations: one amino acid substitution in the exon 21: leucine–proline at codon 838 (L838P) (Fig. 1C); and a deletion

Table 1 Sequence of the mutation specific TaqMan probes and PCR primers

Mutation no.	Probe name	Nucleotide	Amino acid	Primer sequence (forward)	TaqMan probe	Primer sequence (reverse)
	WT1				VIC–ATTAAGAGAAGCAACATCT	
1	Del 1a	2235–2249del	E746–A750del		FAM–CGCTATCAAAACATCT	
2	Del 1b	2236–2250del			FAM–CTATCAAGACATCTCC	
3	Del 2	2254–2277del	S752–I759del		FAM–AGAAGCAACACTCGAT	
	WT2			CCCAGAAGGTGAGAAAGTTAAAATTC	VIC–CGAAAGCCAACAAG	CCCACACAGCAAAGCAGAAA
4	Del 3	2239–2247del, 2248G > C	L747–E749del, A750P		FAM–CAAGGAACCAACATC	
5	Del 4	2240–2257del	L747–S752del, P753S		FAM–AAGGAATCGAAAGCC	
6	Del 5	2238–2255del, 2237A > T	L747–S752del, E746V		FAM–CAAGGTTCCGAAAGC	
7	Del 6	2240–2251del	L747–A750del, T747S		FAM–TCAAGGAATCATCTCC	
	WT3				VIC–AAGTGCTGGGCTCC	
8	G719C	2155G > T	G719C	TGAGGATCTTGAAGGAAACTGAATTC	FAM–AAAGTGCTGTGCTCC	TGCCAGGGACCTTACCTTATACA
9	G719S	2155G > A	G719S		FAM–AAAGTGCTGTGCTCC	
	WT4				VIC–TTGGGCTGGCCAAA	
10	L858R	2573T > G	L858R	CCGCAGCATGTCAAGATCAC	FAM–TTGGGCGGGCCAA	TCCTTCTGCATGGTATTCTTTCTCT
	WT5				VIC–CCAAACTGCTGGGTG	
11	L861Q	2582T > A	L861Q		FAM–CCAAACAGCTGGGTG	
	WT6				VIC–ATTAAGAGAAGCAACATCT	
12	Novel Del	2239–2262del	L747–K754del	CCCAGAAGGTGAGAAAGTTAAAATTC	FAM–CTATCAAGGAAGCCAACAA–MGB	CCCACACAGCAAAGCAGAAA
12	Novel Ins	2265–2267 InsCAA	N756Ins		FAM–CCAACAACAAGGAAAT–MGB	
	WT7			GGAGGACCGTCGCTTGGT	VIC–CGCGACCTGGCAG–MGB	CCCAAAATCTGTGATCTTGACATG
13	L838P	2513T > C	L838P		FAM–CGCGACCCGGCAG–MGB	

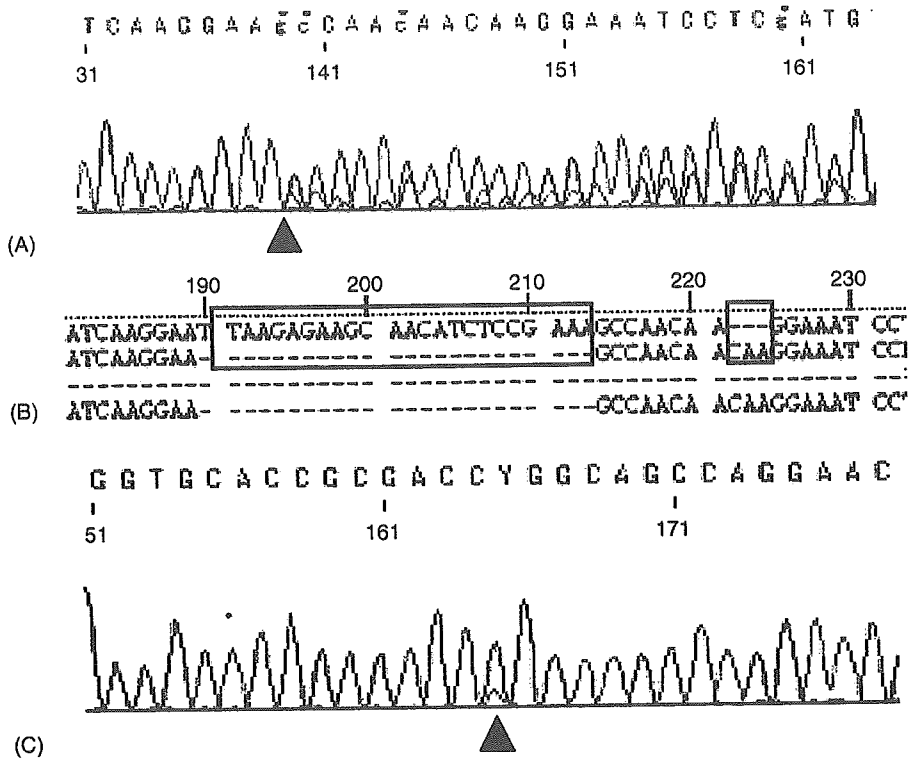

Fig. 1 (A) Data from direct sequencing showing a novel 24 nucleotide in-frame deletion (2239–2262), removing amino-acid 747–754 (arrow head: deletion start). (B) Nucleotide sequence of the novel insertion–deletion mutant as aligned with the wild-type sequence. Three nucleotides (CAA) are inserted at the position 2270 in the exon 19, adding one asparagine (delL747–K754&insK757NK) (box: insertion–deletion sequence, first line: wild-type sequence; second line: mutation type sequence). (C) DNA sequencing of case #6. The other mutation found in case #6. Amino acid substitution: leucine to proline at codon 838 (L838P) due to T–C substitution at position 2513 in exon 21 (arrow head: mutation point).

mutation (Del 5). The substituted amino acid is conserved among all the erbB family members. We designed TaqMan probes for these two novel mutations as described below. We have not determined whether these nine genomic abnormalities found in this cohort are somatic or genomic.

3.2. Analysis using TaqMan PCR assay

Next, we subjected these 94 NSCLC samples to TaqMan PCR assay. To detect all of these mutations specifically, we designed 13 sets of specific TaqMan probes. They targeted 11 previously reported mutations and the two novel mutations that were identified in this paper (Table 1). Each probe has been shown to anneal only to the correct sequence. Using this analysis, 27 cases were detected to have a mutation. In all of the cases except case #1, the results of TaqMan PCR were in complete agreement with the genomic DNA sequencing data (Table 2). Typical results of the TaqMan PCR assay and their corresponding DNA sequence data are shown in Fig. 2. In Table 2, cases #1 to #9 were responders for gefitinib (partial response), and cases #10 to #27 were non-responders.

Case #1 was determined to have a mutation carrying amino acid substitution in exon 21 (L858R) by the TaqMan PCR assay (Fig. 3A). The genomic DNA sequencing could not detect the mutation (Fig. 3B). As the PCR assay has suggested that the sample had a significant contamination with wild-type DNA, we did a serial dilution experiment to determine the relative content of the mutated alleles in this tumor. The standard curve was configured using a titration by 10% steps with the control synthetic oligos harboring the mutant sequence (Fig. 3C), and the approximation curve was calculated (Fig. 3D). In reference to this data, the data for the case #1 suggested that this tumor contained 11% mutated allele and 89% normal allele. The first sequence data was rechecked and a very small peak was found to be present which was compatible with a substitution of G for T at nucleotide 2573 (L858R) (Fig. 3B). The heterogeneous tumor cells or contamination with wild-type DNA from the normal tissue was suspected. The genomic DNA of case #1 was newly

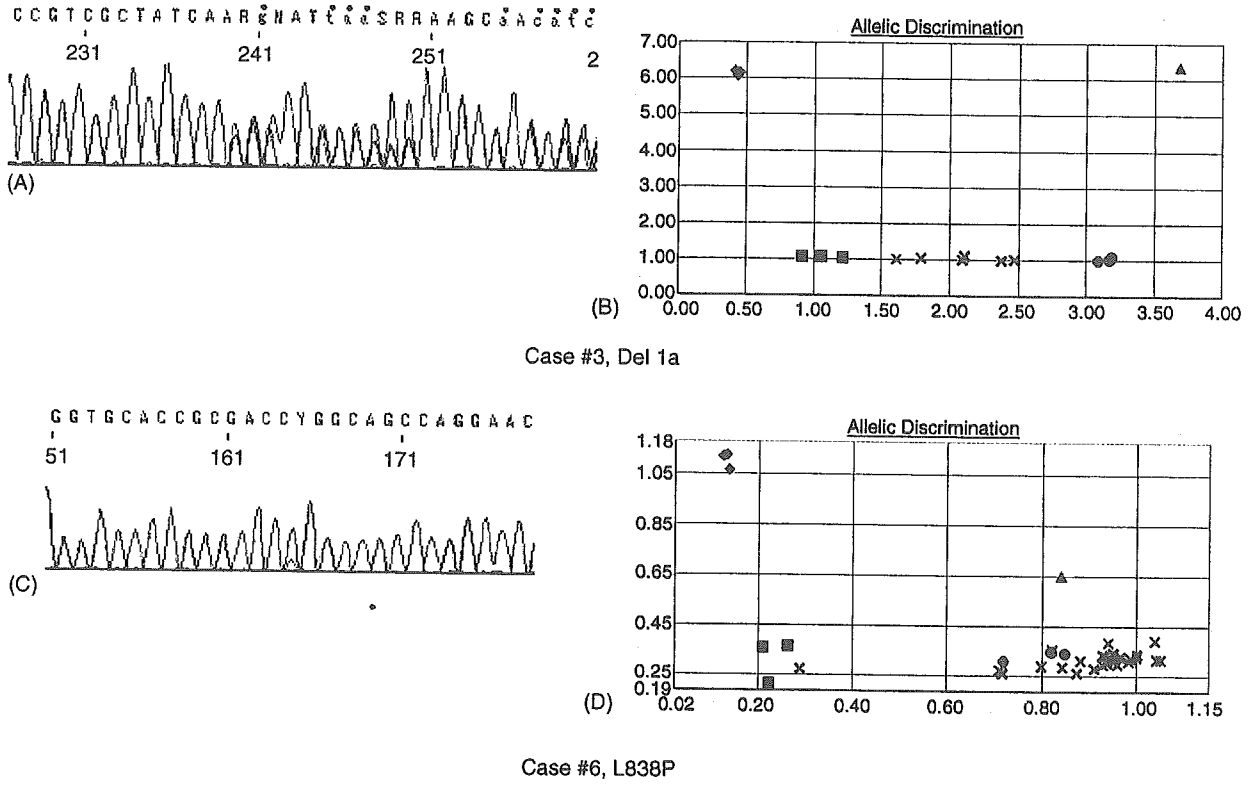

Fig. 2 In the TaqMan PCR assay, triangles indicate the samples with the somatic mutations. Diamonds indicate the mutation controls (artificial template oligo). Circles indicate the wild-type controls (artificial template oligo). Crosses indicate samples that turned out to be wild type. Squares indicate controls without DNA template. Both abscissa and ordinate are fluorescent intensity of each dye. Samples with mutation appear deviated from the abscissa. Heterozygous samples appear deviated from both abscissa and ordinate and are plotted roughly at 45° if the sample contained mutation and wild-type alleles at 1:1 ration. (A) Genotyping by DNA sequencing (case #3, Del 1a). (B) Genotyping by TaqMan PCR assay (case #3, Del 1a). (C) Genotyping by DNA sequencing (case #6, L838P). (D) Genotyping by TaqMan PCR assay (case #6, L838P).

prepared and sequenced again. The sequence data now showed a clear peak of the mutated allele (Fig. 3E). A repeat TaqMan PCR assay of the newly prepared DNA now revealed a proportion of 35% tumor DNA and 65% wild-type DNA (Fig. 3C). In nine gefitinib responders, six patients (66.7%) had *EGFR* mutation from TaqMan PCR assay. Of 27 gefitinib treated samples, six trans-bronchial biopsy samples were also evaluated by TaqMan PCR assay. In these six samples, the result from biopsy samples analysis perfectly matched with that of the surgical removed samples.

3.3. Analysis of *EGFR* DNA copy number

The *EGFR* gene amplification of 27 samples from patients who were treated with gefitinib at National Hospital Organization, Kinki-Chuo Chest Medical Center, was analyzed by quantitative real-time PCR. Four of 27 cases were found to have *EGFR* DNA amplifications (*EGFR* copy number >5) (Table 2). In these four cases, two had *EGFR* mutation. The two cases showed a clinical response to gefitinib. In the 10 cases with *EGFR* mutation in this cohort, only two had *EGFR* amplification. The *EGFR* amplification did not correlate with *EGFR* mutation status ($p = 0.6125$). The *EGFR* amplification did not correlate with any of the clinicopathological factors. There was not any statistically significantly correlation between *EGFR* amplification and overall survival (data not shown).

3.4. *EGFR* mutation status in the additional 182 NCSLC samples

In addition to the 67 cases we have already reported and 27 cases we have sequenced in this paper, we genotyped additional 182 recently operated NSCLCs for *EGFR* mutations using TaqMan PCR assay. Forty-six mutations were detected (25.3%):

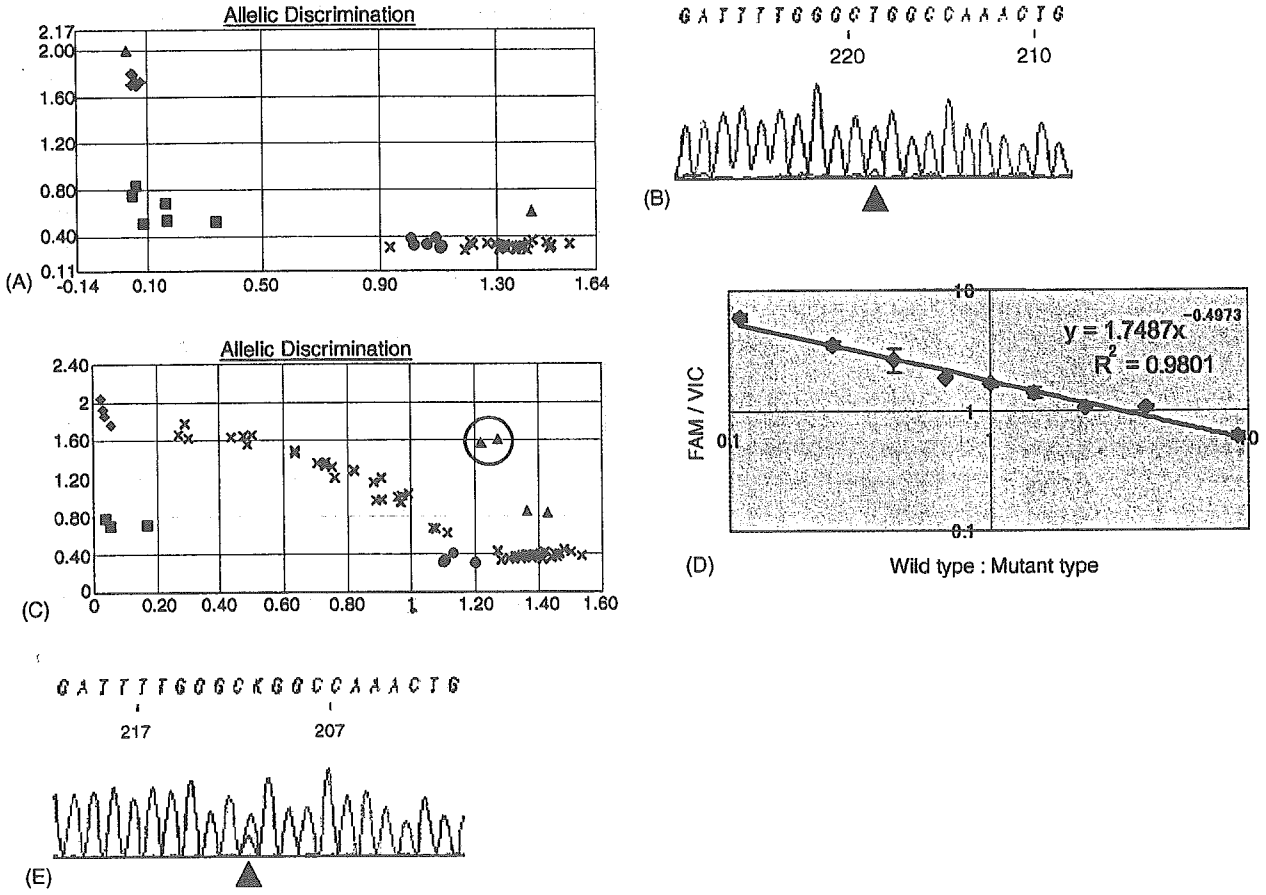

Fig. 3 (A) TaqMan analysis of case #1. Case #1 appeared to have mutation carrying amino acid substitution in exon 21 (L858R) by TaqMan PCR assay. The triangle deviating about 10% from the abscissa is the sample. (B) DNA sequencing of case #1. The first screening data by genomic DNA sequencing of case #1 shows a barely identifiable mutation peak representing a G for T at nucleotide 2573 (arrow head: mutation point). (C) TaqMan PCR assay of titrated samples. The standard curve was configured using a titration by 10% steps of the control synthetic oligos harboring mutated sequence by TaqMan PCR assay. The sample of case #1 is indicated as closed triangles which deviate about 10% from the abscissa. This showed that this tumor contained the mutated allele at the proportion of 11%. Closed triangles in the circle indicate the genomic DNA of case #1 that was newly prepared that was calculated as 35% of total DNA fraction. (D) The approximation curve calculated from the data in Fig. 3C. The *x*-axis indicates the wild type/mutant type ratio, and *y*-axis indicates FAM/VIC which is the degree of deviation from the *x*-axis relative to the 100% mutation control ($y = 1.7487x^{-0.4973}$, $R^2 = 0.9801$). (E) DNA sequencing of the case #1 that has been newly prepared. The sequence showed a clear peak of mutated allele that was substituted G—T at position 2573 (arrow head: mutation point).

20 patients had the L858R mutation; 22 had the deletion mutation in exon 19; two had the G719C mutation; and two patients had the L861Q mutation. Relationship between the *EGFR* mutation and clinical—pathologic factors in additional 182 NSCLC patients is shown in Table 3. Among those with *EGFR* mutation, 17/127 (13.4%) were male and 29/55 (52.7%) were female; 27/46 (58.7%) were never-smokers and 12/113 (10.6%) were ever-smokers; 45/97 (46.4%) were adenocarcinoma and 1/85 (1.2%) was non-adenocarcinoma; 35/80 (43.8%) were well differentiated and 11/85 (12.9%) were moderately or poorly differentiated. The mutation status were significantly correlated with gender (women versus men, $p < 0.0001$), smoking status (never-smokers versus ever-smokers, $p < 0.0001$), pathological subtypes (adenocarcinoma versus non-adenocarcinoma, $p < 0.0001$), and differentiation (well versus moderately or poorly, $p < 0.0001$). In 46 patients with *EGFR* mutations, 43 genomic DNA from matched normal lung tissues were available and were showed to be wild type by TaqMan PCR assay, suggesting that these mutations were somatic. There was no mutation detected by the TaqMan PCR assay in gastric, esophagus and colon carcinomas.

Table 2 Mutation status of the *EGFR* gene and *EGFR* copy number in 27 Gefitinib treated samples

Sample no.	Sequence	TaqMan	Copy number
1	WT	L858R	2.41
2	Del/Ins	Del/Ins	2.78
3	Del 1a	Del 1a	1.6
4	Del 1b	Del 1b	2.19
5	WT	WT	2.1
6	Del 5/L838P	Del 5/L838P	5.97
7	WT	WT	2.03
8	WT	WT	2.08
9	Del 3	Del 3	1.52
10	WT	WT	1.83
11	WT	WT	3.94
12	G719S	G719S	2.79
13	WT	WT	1.14
14	WT	WT	1.67
15	WT	WT	3.13
16	Del 1b	Del 1b	2.31
17	WT	WT	1.35
18	WT	WT	1.15
19	WT	WT	1.42
20	WT	WT	2.34
21	Del 1b	Del 1b	1.28
22	WT	WT	2.26
23	WT	WT	6.79
24	L858R	L858R	9.74
25	WT	WT	5.08
26	WT	WT	1.47
27	WT	WT	1.16

Case #1 to #9: responders; case #10 to #27: non-responders. *EGFR* amplification (increased *EGFR* copy number) was defined as more than five copies.

4. Discussion

Gefitinib was developed as an inhibitor of *EGFR* tyrosine kinase that is often over-expressed in many cancers. It showed a promising effect on a few cancers in phase I trial [1]. Subsequently, however, in phase II randomized trials in which the drug was used in combination with other traditional chemotherapy, the effect was marginal in patients with NSCLC [7]. Last year, our group and others have reported identification of genetic mutations in the *EGFR* kinase domain [6,7]. The mutation was seen in a subset of NSCLC with a good response to gefitinib. These reports triggered further studies on the *EGFR* mutation and the tumor's response to gefitinib and erlotinib [6–8]. All the groups identified recurrent mutations in the same region around the ATP binding pocket in *EGFR* tyrosine kinase domain. In vitro studies have reported that the kinase activity of *EGFR* or the sensitivity to gefitinib showed a strong association with *EGFR* gene mutation [7,9]. In our analysis, 6/9 (66.7%) gefitinib-responders had *EGFR* mutations. Thus, some of gefitinib-responders might have other mechanism besides *EGFR* mutations.

In this paper, we were unable to show any differences in *EGFR* amplification between tumors carrying the wild-type *EGFR* sequence and tumors carrying the mutant *EGFR* sequence, which is not surprising as it has been convincingly shown that *EGFR* mutation and not expression levels is responsible for the clinical response to *EGFR* tyrosine kinase inhibitors [6,7,19]. Hirsch et al. [20] reported that *EGFR* gene copy number correlated with EGFR protein expression, but not with prognosis in a cohort of patients not treated with gefitinib. Cappuzzo et al. [21] reported that high *EGFR* gene copy number was associated with better survival. However, there was not any statistically significantly correlation between *EGFR* amplification and overall survival in our analysis. Further study will be needed to delineate the relationships among *EGFR* mutation, *EGFR* gene copy number, *EGFR* mRNA expression, and gefitinib sensitivity.

Over the past three decades, the incidence of lung adenocarcinoma has increased worldwide. Most individuals with lung adenocarcinoma, especially women, are nonsmokers, a population that is sensitive to gefitinib. Reported risk factors for the development of lung adenocarcinoma include cigarette smoking, exposure to cooking fumes, air pollution, second-hand smoke, asbestos, and radon; nutritional status; genetic susceptibility; immunologic dysfunction; tuberculosis infection; asthma; and human papilloma virus [22]. In our analysis of recently operated 182 cases, most of the *EGFR* mutations were present in adenocarcinomas except one case. Mutations were more prevalent in females than in males and in nonsmokers than in smokers, confirming and extending the results of previous reports [6,8,9,23]. More recently, it has been reported that all of adenocarcinomas carrying *EGFR* mutations were well to moderately differentiated [24]. These data were comparable with those obtained in our analysis.

In this report, we used the TaqMan PCR assay based on allele specific probe. This method combines the amplification and detection step, and does not require any post-PCR processing. This makes the TaqMan PCR assay easy-to-use and allows high throughput operation. Furthermore, this method was highly sensitive to detect *EGFR* mutations. One gefitinib responded case with a base-substitution mutation could be detected by the TaqMan PCR assay, although it was undetectable at the first conventional genomic sequencing. When the mutated allele consisted only about 10% of total

Table 3 Relationship between the *EGFR* mutation and clinical–pathologic factors

Factors	Patients with *EGFR* mutation	Patients without *EGFR* mutation	*p*-Value
Gender			
Male	17 (13.4%)	110	<0.0001
Female	29 (52.7%)	26	
Age			
≦64	26 (31.7%)	56	0.0868
>64	20 (20%)	80	
Smoking status			
Never-smokers	27 (58.7%)	19	<0.0001
Ever-smokers	12 (10.6%)	101	
Lymph node metastasis			
N0	34 (27.9%)	88	0.3625
N+	12 (20.7%)	46	
Differentiation			
Well	35 (43.8%)	45	<0.0001
Moderately/or poorly	11 (12.9%)	74	
Pathological subtypes			
Adeno	45 (46.4%)	52	<0.0001
Non-adeno	1 (1.2%)	84	
Stage			
I	33 (31.1%)	73	0.0555
II–IV	13 (17.6%)	61	

N+: lymph node metastasis positive; Adeno: adenocarcinoma.

genomic DNA content, it was not detected by the sequencing. It is alleged that the detection limit in genomic sequencing is about 25% content in general. Because, in the clinical settings, it is not always possible to obtain samples carrying containing homogeneous tumor cells, this highly sensitive method is preferable to the conventional sequencing. Previous reports might underestimate the *EGFR* mutations. The present method can be most effectively used with 5–10 ng of DNA but can analyze as few as 1 ng of tumor DNA. To investigate the correlation between *EGFR* mutations and the response to drugs, large-scale statistical analysis is needed. In these clinical research areas, we believe that this TaqMan PCR assay with high throughput is one of the powerful tools.

In trade off to its accuracy, this method is effective only to the mutations that are already known. The probes cannot be designed to the sequences of unknown mutations. Thus, we must take into account that there is always at a false negative risk in TaqMan PCR assay. However, with the high pace of research [23–25], most of the mutations in *EGFR* gene will be identified in a few years. The good news is the presence of predominant mutations (L858R and exon 19 deletions) which comprise 75–90% of all the *EGFR* mutations. The TaqMan PCR assay presented in this paper can offer us a complementary and confirmative test with sequencing. In our 94 sequenced samples, 24/27 (88.9%) were these predominant mutations. With highly significant correlation between the clinical response to gefitinib (and erlotinib) and *EGFR* mutation, many future clinical trials may first need *EGFR* mutation data using high throughput assays like the one described in this paper.

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