

Cytoplasmic expression of estrogen receptor β may predict poor outcome of EGFR-TKI therapy in metastatic lung adenocarcinoma

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Abstract. There is growing evidence that estrogen receptors (ER) are expressed in lung cancer cells, and are able to interact with the epidermal growth factor receptor (EGFR) signaling pathway. However, data on the association between cytoplasmic ER expression and the response to EGFR-tyrosine kinase inhibitors (TKI) treatment are limited. The aim of the present study was to investigate the associations between ER α /ER β expression and EGFR mutational status and response to TKI treatment in metastatic lung adenocarcinoma. A retrospective study of 126 consecutive patients with lung adenocarcinoma who were diagnosed with stage IV disease and had received EGFR-TKI treatment was conducted. ER expression was detected by immunohistochemistry. EGFR and GTPase KRas (KRAS) mutational statuses were evaluated by denaturing high performance liquid chromatography and PCR-restriction fragment length polymorphism, respectively. In the overall cohort of 126 lung adenocarcinoma samples analyzed, ER α expression in the nucleus of tumor cells was identified in 17 (18.9%) patients, whereas ER β expression was identified in the nucleus (22/126, 17.5%) and cytoplasm (17/126, 13.5%). The nuclear expression of ER β was positively associated with the degree of tumor differentiation ($P=0.010$). EGFR-sensitizing mutations were significantly associated with improved objective response rates (ORR), disease control rates (DCR), median progression-free survival (mPFS) and median overall survival (mOS) ($P<0.001$; $P<0.001$; $P=0.003$; and $P=0.026$, respectively). Patients with cytoplasmic ER β expression exhibited

non-significant poorer ORR, DCR, mPFS and mOS compared with patients without cytoplasmic ER β expression ($P=0.082$; $P=0.106$; $P=0.084$; and $P=0.119$, respectively). However, the significant decrease of ORR, DCR and mPFS was observed in patients with coexisting cytoplasmic ER β expression and EGFR-sensitizing mutations ($P=0.030$; $P=0.009$; and $P=0.018$, respectively) in comparison with the subgroup with EGFR sensitizing mutations but negative expression of cytoplasmic ER β . A trend towards shorter mOS was also observed in patients with coexisting cytoplasmic ER β expression and EGFR-sensitizing mutations ($P=0.071$). No KRAS mutations were identified in patients with cytoplasmic ER β expression. Subsequent to adjusting for sex, smoking status and EGFR mutation status, the Cox regression analysis indicated that cytoplasmic expression of ER β was a negative independent predictor for mPFS in the whole patient cohort (HR=1.870; 95% confidence interval 1.058-3.305; $P=0.031$). Cytoplasmic ER β expression was negatively correlated with the efficacy of EGFR-TKI treatment for metastatic lung adenocarcinoma, particularly for patients with coexisting cytoplasmic ER β expression and EGFR-sensitizing mutations. Cytoplasmic ER β may be a promising marker to predict the outcome of EGFR-TKI treatment.

Introduction

Lung cancer is the leading cause of cancer-associated mortality globally (1). Despite recent improvements in its management, the prognosis of patients with lung cancer remains poor. Although smoking is the predominant risk factor for lung cancer, a gradual increase of incidence in the adenocarcinoma subtype has been identified despite a decrease in the size of the smoking population (2). Therefore, etiological factors other than smoking may also serve a role in the development of lung adenocarcinoma.

It has been demonstrated that hormone replacement therapy may increase the risk of mortality for patients with lung cancer, whereas anti-estrogen therapy may reduce the risk of mortality (3-5). Previous laboratory and clinical studies have provided evidence suggesting that estrogen stimulates the proliferation of lung carcinoma cells and tumor growth through estrogen receptor (ER)-mediated signaling (6-8). A

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total of 2 forms of ERs have been identified, ER α and ER β , which are the products of 2 separate genes (9). ER α and ER β are expressed in non-small cell lung cancer (NSCLC) cell lines and tumor tissues, particularly adenocarcinoma (10).

Epidermal growth factor receptor (EGFR) gene mutational status is the most commonly-used biomarker for EGFR-tyrosine kinase inhibitor (TKI) therapy selection. Certain clinical characteristics, including Asian ethnicity, female sex, adenocarcinoma subtype and non-smoking status were predictive of good responses to therapy (11). Several studies have demonstrated that estrogen may trans-activate growth factor signaling pathways, including the EGFR pathway (6,12). ER protein expression is upregulated in response to gefitinib, an EGFR-TKI, and EGFR expression is upregulated in response to ER antagonists (13,14). The ER-EGFR signaling axis appears to be reciprocal, with ER signaling promoting the activation of EGFR, and EGFR signaling promoting the activation of ER (15). Therefore, the ER-EGFR signaling pathway may affect the efficacy of EGFR-TKI treatment. The aim of the present study was to examine the frequency of ER expression and to explore its association with clinicopathological factors, including EGFR mutation status, clinical responses to EGFR-TKI and patient prognosis.

Materials and methods

Patients and tissue specimens. Between January 2011 and July 2016, tissues from 126 consecutive patients with lung cancer with a pathological diagnosis of adenocarcinoma admitted to the Department of Medical Oncology at Peking University International Hospital (Beijing, China) and Beijing Cancer Hospital (Beijing, China) were retrieved by a fine needle aspiration biopsy and reviewed. All patients were diagnosed as stage IV according to the 7th edition of the TNM classification for lung tumors (16) and received EGFR-TKI therapy (250 mg gefitinib or 150 mg erlotinib orally once a day) until disease progression, intolerable toxicity or patient refusal. Inclusion criteria of the present study include a diagnosis of adenocarcinoma, stage IV disease and the patient was receiving EGFR-TKI treatment. Exclusion criteria included indeterminacy of EGFR mutational status and a low treatment compliance. Tumor responses were evaluated according to the Response Evaluation Criteria in Solid Tumors, version 1.1 (17). The present study was approved by the Institutional Ethic Committee of Beijing Cancer Hospital and Peking University International Hospital. Informed consent from the patients or their families was obtained prior to initiation of the study.

Immunohistochemistry. Tissue sections (4- μ m thick sections) obtained from the paraffin-embedded specimens were prepared on glass slides. The paraffin-embedded tissue blocks were sectioned (thickness 4 μ m) using a microtome and incubated in a 40°C water bath. The sections were transferred onto glass slides for immunohistochemistry. The samples were incubated in an oven for 2 h at 60°C. The sections were subsequently deparaffinized in xylene followed by a graded series of alcohol washes (100% ethyl alcohol for 5 min twice, 90, 80 and 70% for 5 min respectively) at room temperature.

The sections were placed in 0.1 mol/l citrate buffer (pH 6.0) and incubated in a pressure cooker for 3 min at 125°C

for antigen retrieval, then treated with 3% H₂O₂ for 5 min at room temperature. Samples were incubated with the following primary antibodies at room temperature for 30 min. A rabbit monoclonal antibody SP1 (cat. no. MA5-14501; Lab Vision Corporation, Fremont, CA, USA) against ER α at a dilution of 1:50 and mouse monoclonal antibody 14C8 (cat. no. ab288; Abcam, Cambridge, UK) against ER β at a dilution of 1:100 were used. A two-step polymer-horseradish peroxidase method (Dako; Agilent Technologies, Inc., Santa Clara, CA, USA) was used for detection. Positive controls for ER α and ER β were obtained from breast cancer cases from the Department of Breast Surgery of Peking University International Hospital in December 2016. Negative controls were performed as array sections without the primary antibody. Cytoplasm or nucleus staining intensity and pattern were evaluated using a scale from 0 to 3+: 0, completely negative; 1+, faint positivity; 2+, moderate positivity; 3+, strong positivity. Samples were scored as positive when >10% of tumor cells exhibited specific, positive staining in the nucleus or cytoplasm with at least 1+ staining. The immunohistochemistry analysis was performed independently by 2 pathologists (from the Department of Pathology, Peking University International Hospital and Beijing Cancer Hospital, Beijing, China), a light microscope at x200 magnification, in 10 randomly selected field of view was used.

EGFR and GTPase KRas (KRAS) mutation. Genomic DNA was extracted from paraffin-embedded biopsy tissues using the E.Z.N.A.[®] formalin-fixed paraffin-embedded (FFPE) DNA kit (Omega Bio-Tek, Inc., Norcross, GA, USA). EGFR-sensitizing mutations (in exon 19del746-750 and 21L858R) were detected by denaturing high performance liquid chromatography and KRAS mutations (codon 12 and 13 in exon 1) by polymerase chain reaction-restriction fragment length polymorphism. The detailed methods and procedures have been described in our previous studies (18,19).

Statistical analysis. All statistical analyses were performed with SPSS software (version 16.0; SPSS, Inc., Chicago, IL, USA). All data are expressed as the mean \pm standard deviation. The association between patient characteristics and ER expression and also clinical characteristics were analyzed using Pearson's χ^2 test or the Fisher's exact test. The time-to-event variables, for example overall survival (OS), progression-free survival (PFS), median OS (mOS) and median PFS (mPFS) were calculated using a Kaplan-Meier estimation. Comparisons between different groups were performed using log-rank tests. The Spearman's rank correlation was used to estimate the correlation between immunohistochemistry markers. Cox proportional hazards regression analysis was used to examine the effects of EGFR mutations, expression of ER β and clinical variables on survival rates. $P < 0.05$ (two-sided) was considered to indicate a statistically significant difference. The 95% confidence intervals (CIs) for odds ratios and frequencies were calculated as exact CIs.

Results

Clinical variables. The clinicopathological characteristics of patients are summarized in Table I. The 126 patients comprised

Table I. Patient cohort characteristics.

Characteristics	Frequency (%)	EGFR mutation (%)	ER α (%) (n=90)	Cyto-ER β (%)	Nuclear-ER β (%)
Sex					
Female	70 (55.6)	38 (54.3)	11 (22.0)	7 (10.0)	10 (14.3)
Male	56 (44.4)	26 (46.4)	6 (15.0)	10 (17.9)	12 (21.4)
Age, years					
≥ 60	76 (60.3)	33 (43.4)	14 (23.7)	11 (14.5)	13 (17.1)
<60	50 (39.7)	31 (62.0) ^a	3 (9.7)	6 (12.0)	9 (18.0)
Smoking status					
Ever or current	40 (31.7)	17 (42.5)	5 (15.6)	7 (17.5)	8 (20.0)
Never or light	86 (68.3)	47 (54.7)	12 (20.7)	10 (11.6)	14 (16.3)
Differentiation					
Undifferentiated + poor	30 (23.8)	15 (50.0)	4/22 (18.2)	4 (13.3)	1 (3.3)
Moderate	58 (46.0)	35 (60.3)	6/40 (15.0)	6 (10.3)	10 (17.2)
Well	34 (27.0)	12 (35.3)	6/28 (21.4)	7 (20.6)	11 (32.4) ^a
Unknown	4 (3.2)	2 (50.0)			
ORR					
CR + PR	46 (36.5)	34 (73.9)	6 (20.0)	3 (6.5)	9 (19.6)
SD + PD	80 (63.5)	30 (37.5) ^b	11 (18.3)	14 (17.5)	13 (16.2)
DCR					
CR + PR + SD	91 (72.2)	58 (63.7)	9 (14.8)	9 (9.9)	16 (17.6)
PD	35 (27.8)	6 (17.1) ^b	8 (27.6)	8 (22.9)	6 (17.1)

ORR, objective response rate; DCR, disease control rate; ER, estrogen receptor; EGFR, epidermal growth factor receptor; Cyto-ER β , cytoplasmic ER β . ^aP<0.05.

56 males and 70 females, with a median age of 62 years (range, 31-81 years). There were 76 patients aged >60 years, and the majority of patients were never/light smokers (defined as patients who had smoked less than 100 cigarettes in their lifetime) (86/126, 68.3%). All patients had tissue sample assessable for EGFR mutation and ER β expression detection, whereas only 90 samples were assessable for ER α detection as cancer tissues were obtained by fine needle aspiration biopsy, therefore a large amount was not collected. All patients received EGFR-TKI therapy, with 46 patients receiving EGFR-TKI treatment as first-line therapy.

ERs expression in lung adenocarcinoma. ER α was only expressed in the nucleus, whereas ER β staining was detected in the cytoplasm and nucleus. A total of 18.9% (17/90) lung tumors were positive for nuclear ER α expression, 17.5% (22/126) cases were positive for nuclear ER β expression, 13.5% (17/126) exhibited positive staining for cytoplasmic ER β expression and 3.2% (4/126) cases exhibited positive nuclear and cytoplasmic ER β staining. There was no statistically significant difference in ERs protein expression associated with sex, age or smoking status. However, the nuclear expression of ER β was positively correlated with the degree of tumor differentiation ($\chi^2=9.127$; P=0.010). No significant associations between the expression levels of the different ERs were identified in the cohort of the present study. Fig. 1 demonstrates representative immunohistochemical staining of ER α in the nucleus and ER β in the nucleus and cytoplasm in NSCLC cells.

Association between EGFR-sensitizing mutations and ERs expression. EGFR-sensitizing mutations were detected in 50.8% (64/126) patients, including 31 with exon19 alone, 29 with exon21 alone and 4 double mutations. The expression levels of any of the ERs were not significantly different between mutant and wild-type EGFR groups.

Biomarker-associated clinical outcomes. All patients who received EGFR-TKI treatment were evaluated for tumor response according to the Response Evaluation Criteria in Solid Tumors (version 1.1) (17). A total of 46 (36.5%) patients experienced partial response (PR), 45 (35.7%) exhibited stable disease (SD), and 35 (27.8%) exhibited progressive disease (PD). No complete response (CR) was observed in the cohort of the present study. In the overall cohort, the ORR was 36.5% (46/126) and the DCR was 72.2% (91/126). The mPFS was 7.5 months. The mOS was 22.5 months. As expected, patients with EGFR-sensitizing mutations exhibited a significantly increased ORR (53.1 vs. 19.4%; P<0.001), DCR (90.6 vs. 53.2%; P<0.001) and longer mPFS survival (10.7 vs. 2.1 months; P=0.003; Fig. 2A) compared with the wild-type patients. It was also identified that the presence of EGFR-sensitizing mutations was associated with an improved prognosis (35.4 vs. 25.9 months; $\chi^2=4.968$; P=0.026; Fig. 2B). Several previous studies have demonstrated that patients with advanced NSCLC with EGFR exon 19 del746-750 exhibited a longer mPFS following treatment with gefitinib or erlotinib compared

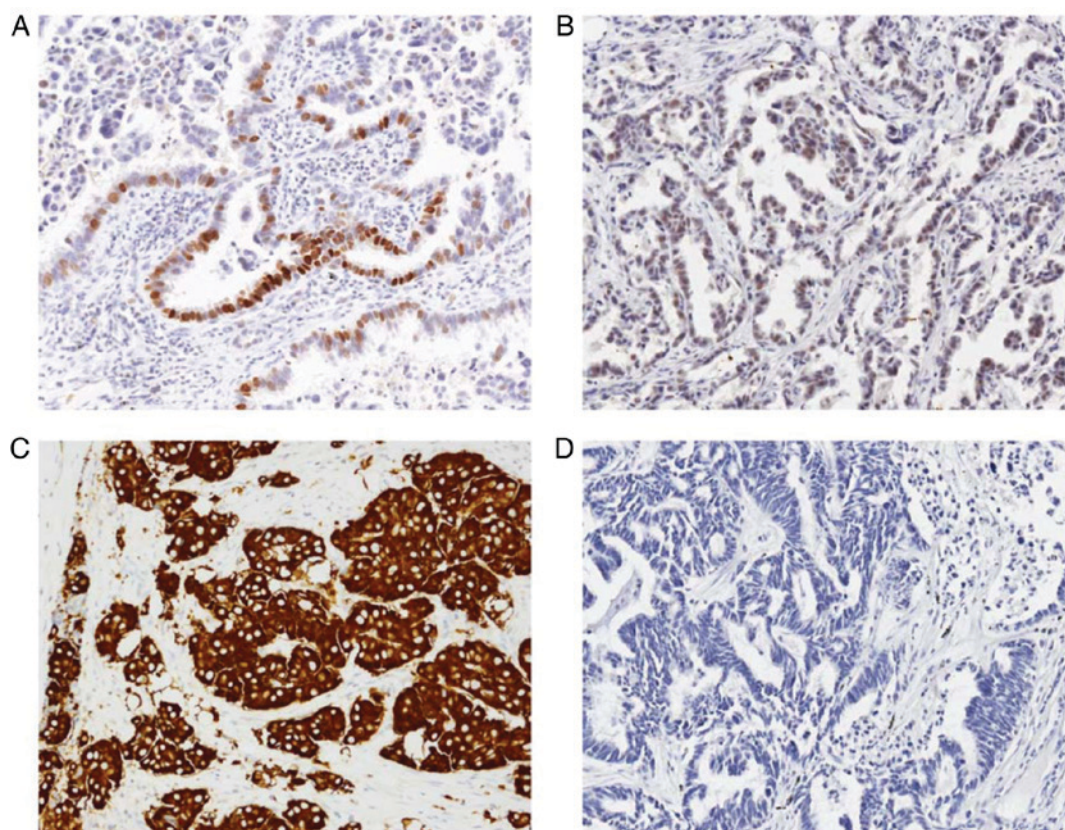


Figure 1. Representative immunohistochemical staining of ER α and ER β in lung adenocarcinoma tissue. All images were captured at magnification, x200. (A) positive nuclear ER α staining, (B) positive nuclear ER β staining, (C) positive cytoplasmic ER β staining, and (D) negative control. ER estrogen receptor.

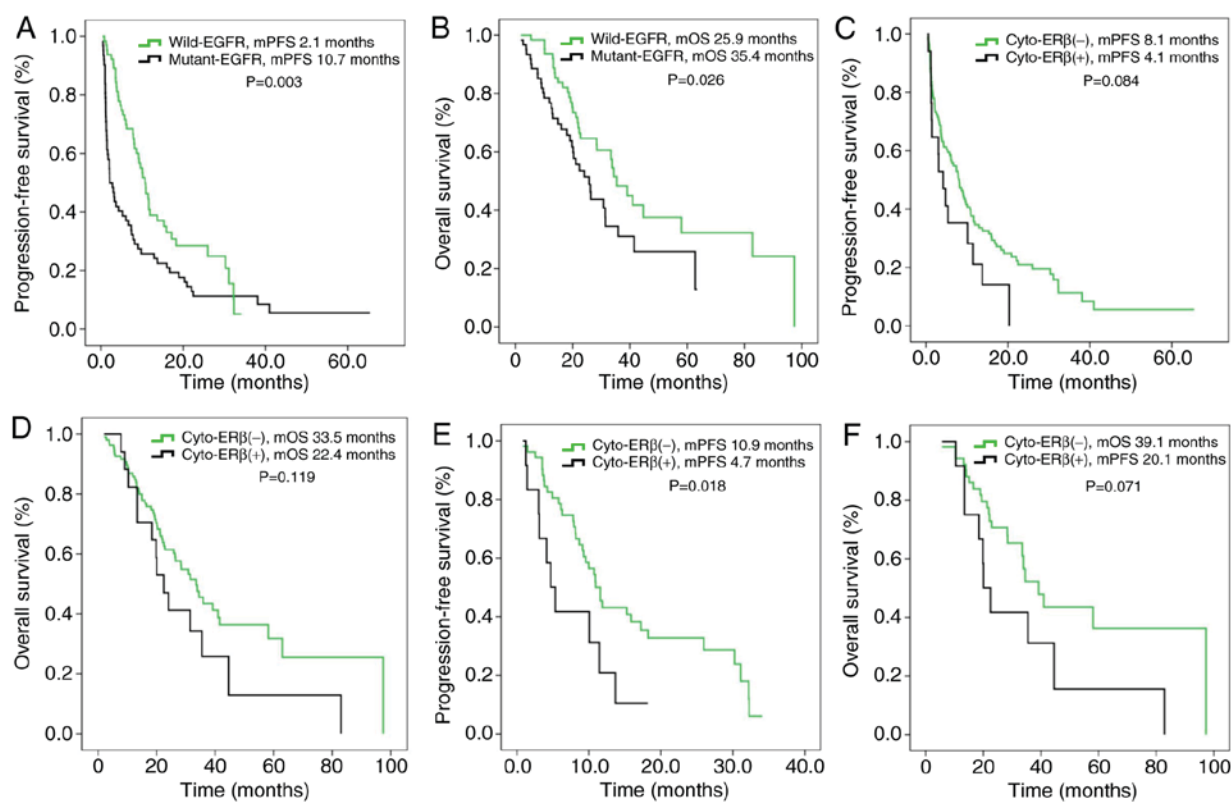


Figure 2. Kaplan-Meier curves stratified by EGFR mutation and cytoplasmic ER β expression. (A) PFS according to EGFR mutation status. (B) OS according to EGFR mutation status. (C) PFS according to cytoplasmic ER β expression in all patients. (D) OS according to cytoplasmic ER β expression in all patients. (E) PFS of patients with EGFR-sensitizing mutations according to cytoplasmic ER β expression. (F) OS of patients with EGFR-sensitizing mutations according to cytoplasmic ER β expression. EGFR, epidermal growth factor receptor; ER, estrogen receptor; PFS, progression-free survival; mPFS, median PFS; OS, overall survival; mOS, median OS.

Table II. Univariate analysis of PFS in all patients.

Characteristics	mPFS, months	95% CI	χ^2	P-value
Sex				
Male	4.7	0.429-8.904	4.375	0.036
Female	9.7	6.061-13.339		
Age, years				
≥60	7.9	5.420-10.314	0.653	0.419
<60	5.8	1.251-10.282		
Smoking status				
Ever or current	5.3	0.876-9.657	1.214	0.271
Never or light	8.2	4.869-11.531		
EGFR mutation				
Mutant	10.7	8.400-13.000	8.735	0.003
Wild-type	2.1	0.728-3.472		
Nuclear-ER α				
Positive	6.2	0.000-13.180	0.690	0.406
Negative	7.8	4.420-11.114		
Cyto-ER β				
Positive	4.1	1.859-6.341	2.988	0.084
Negative	8.1	5.707-10.493		
Nuclear-ER β				
Positive	7.3	3.584-11.016	0.954	0.329
Negative	7.8	4.771-10.762		

ER, estrogen receptor; EGFR, epidermal growth factor receptor; 95% CI, 95% confidence interval; Cyto-ER β , cytoplasmic-ER β ; mPFS, median progression-free survival.

with those with exon 21 L858R mutation (20,21). However, this significant difference was not observed in the cohort of the present study (11.6 vs. 10.1 months; $P=0.325$), which consistent with the results from Sequist *et al* (22). Table II summarizes the association between clinicopathological characteristics, ER expression and PFS in all patients.

In the present study, no significant association between tumor response or mPFS and the expression of nuclear ER α or nuclear ER β was observed. A trend toward a decreased tumor response rate was observed in patients with cytoplasmic expression of ER β when compared with cases without cytoplasmic expression (ORR, 17.6 vs. 39.4%, $P=0.082$; DCR, 52.9 vs. 75.2%, $P=0.106$). Similarly, patients with cytoplasmic ER β expression exhibited a poorer PFS (4.1 vs. 8.1 months; $\chi^2=2.988$; $P=0.084$; Fig. 2C) and exhibited a trend toward a poorer mOS (22.4 vs. 33.5 months; $\chi^2=2.428$; $P=0.119$; Fig. 2D) following EGFR-TKI treatment compared with those without cytoplasmic ER β expression, although this did not reach a statistical significance. In light of the predictive value of EGFR-sensitizing mutations in EGFR-TKI treatment, the associations between cytoplasmic ER β expression and clinical response and mPFS following EGFR-TKI treatment categorized by EGFR mutations were analyzed. No significant difference was observed in clinical response and mPFS in patients with wild-type EGFR genotypes, regardless

of whether cytoplasmic ER β was expressed or not. However, in the subgroup with EGFR-sensitizing mutations, patients with cytoplasmic ER β expression exhibited a significantly decreased ORR (25.0 vs. 59.6%; $\chi^2=4.691$; $P=0.030$) and DCR (66.7 vs. 96.2%; $\chi^2=6.809$; $P=0.009$), and exhibited a poorer mPFS (4.7 vs. 10.9 months; $\chi^2=5.602$; $P=0.018$; Fig. 2E) compared to patients without cytoplasmic ER β expression. It was also identified that patients with coexisting cytoplasmic ER β expression and EGFR sensitizing mutations tended to exhibit a shorter median OS, but the difference was not significant (20.1 vs. 39.1 months; $P=0.071$; Fig. 2F). In the Cox regression analysis adjusted for sex, smoking status and EGFR mutation status, the results indicated that cytoplasmic expression of ER β was an independent negative predictor for PFS in the whole group (Hazard ratio=1.870; 95% CI, 1.058-3.305; $P=0.031$; Table III). In order to exclude the effect on clinical response of EGFR-TKI treatment and survival by KRAS mutation, KRAS mutations were detected and no mutant KRAS was observed in any patients with cytoplasmic ER β expression. No significant difference was observed in OS between patients according to nuclear ER α or nuclear ER β expression.

Discussion

Although the lungs were not previously considered as a target organ for sex steroids, increasing evidence clearly indicates the importance of estrogen signaling in the initiation and progression of lung cancer (7). In addition, the cross-talk between ER and EGFR signaling pathways has been confirmed (15), but there have been few studies examining the association between ER expression and response to EGFR-TKI treatment in metastatic lung adenocarcinoma.

The frequency of ER α and β expression in NSCLC has been demonstrated to be inconsistent in previous studies (23-26). ER α expression cannot be detected in lung cancer using antibodies commonly used in breast tumors including clone number 6F11 or 1D5, which target full-length or the N terminus of ER α , respectively, due to the existence of ER α variants (26). Previous studies examining ER α immunohistochemical expression in FFPE NSCLC specimens using 6 different antibodies have identified in frequencies ranging from 0-38% for nuclear ER α expression and from 0-73% for cytoplasmic expression. In the present study, an ER α positive rate of 18.9% was identified using a monoclonal antibody against the COOH terminus of ER α , but all staining occurred in the nucleus alone. Unlike ER α expression in the present study, ER β has been demonstrated to be expressed in the nucleus and cytoplasm of cancerous cells (27), and the expression level in lung cancer tissues is significantly increased compared with normal lung tissues (28). Consistent with Skov *et al* (27), ER β expression was also observed in the nucleus and cytoplasm in lung tumors, and the positive rates were 17.5 and 13.5%, respectively. The distribution of ER β was more widespread compared with ER α in the immunohistochemical analysis of the present study. The positive rate of cytoplasmic ER β expression was similar (13.5 vs. 10.0%), but the nuclear expression of ER β was decreased in the present study (17.5 vs. 69.0%), compared with that of Skov *et al* (27). The reason for these conflicting results on the expression frequency and localization of ERs between different studies in lung cancer may be

Table III. Results of the multivariate analysis Cox proportional hazards model for progression-free survival.

Characteristics	Wald	HR	95% confidence interval	P-value
Cyto-ER β	4.640	1.870	1.058-3.305	0.031
Sex	4.334	0.575	0.342-0.968	0.037
EGFR mutation	11.925	0.487	0.324-0.733	0.001
Smoking status	0.137	0.902	0.524-1.554	0.711

Wald, Wald statistic for logistic regression algorithms; HR, hazard ratio; ER, estrogen receptor; EGFR, epidermal growth factor receptor; cyto-ER β , cytoplasmic-ER β .

due to lack of standardization of multiple aspects, including the antibodies used, interpretation of the staining and differences in the study population.

Differences in sex are an important characteristic of ER expression in lung cancer, which has been identified in several previous studies (29,30). ER α expression was exhibited in a significantly higher proportion of female patients compared with male patients (31), while the positive rate for ER β expression was increased in males (26). A trend toward a higher percentage of men exhibiting positive cytoplasmic ER β expression when compared with women [10 of 56 (17.9%) males vs. 7 of 70 (10.0%) females] was observed in the present study, which was similar to a study performed by Toh *et al* (30). In the present study, there were no significant associations between sex and the expression of ER α , or nuclear or cytoplasmic ER β . ER β expression has been demonstrated to be positively correlated with the degree of lung cancer differentiation (32), and a positive association between nuclear ER β expression and tumor differentiation was also observed in the present study. This suggests that ER β expression may, to a certain extent, reflect the degree of malignancy and therefore may be used as a predictor of prognosis.

A Japanese study investigating surgically-resected adenocarcinoma revealed a high expression frequency of ER α and ER β among 447 patients, and the authors identified a significantly positive correlation between strong nuclear expression of ER β and EGFR mutations (33). Similarly, Raso *et al* (34) also demonstrated that EGFR mutant adenocarcinoma exhibited a significantly increased expression of nuclear ER α and ER β compared with wild-type tumors. However, inconsistent with these studies, Deng *et al* (35) suggested that the percentage of samples with detectable expression of ER β was increased in patients with wild-type EGFR compared with a mutant EGFR group. The EGFR mutational status was available for all patients in the present study, but no significant association between EGFR mutations and expression of any ER was observed.

ER α and cytoplasmic ER β expression has been demonstrated to exhibit a significant association with poor outcome in patients with NSCLC (28,36), whereas nuclear ER β expression has been indicated to be a favorable prognostic factor (37), although only occasionally for male patients or patients with EGFR mutations (6,33). In the present study, a trend toward a poorer mOS was noted in patients with cytoplasmic expression of ER β ; however, the survival difference was non-significant, regardless of whole group or subgroups categorized by EGFR

mutational status or sex. Similarly, no significant difference of OS was identified in terms of nuclear ER α or nuclear ER β expression, regardless of sex or EGFR mutational status.

Previous studies have suggested a cross-talk between EGFR and the ER signaling pathway in the development of lung cancer (12,38-40). Estrogen depletion induced by endocrine therapy may activate EGFR signaling pathway, while ER β expression was increased following EGFR-TKI treatment in NSCLC cells (13). Therefore, expression of ERs may affect the outcome of EGFR-TKI treatment in NSCLC. In the cohort of the present study, an inverse correlation between cytoplasmic estrogen receptor β expression and clinical response of EGFR-TKI treatment was observed; however, the difference was not significant. Based on the predictive value of EGFR-sensitizing mutations in EGFR-TKI treatment, the association between cytoplasmic ER β expression and clinical response to EGFR-TKI therapy categorized by EGFR mutational status was analyzed and it was observed that patients with cytoplasmic ER β expression exhibited significantly decreased ORR, DCR and a poorer PFS compared with cases without cytoplasmic ER β expression in the mutant EGFR subgroup. Strong nuclear ER β expression has been demonstrated to predict a good clinical response and prolonged PFS of EGFR-TKI treatment for patients with lung adenocarcinoma (41), but this conclusion was not reached in the present study. Due to the controversial results on survival indicated by these studies (41-43), the present study analyzed the combined effect of positive cytoplasmic ER β staining/negative nuclear ER β staining compared with negative cytoplasmic ER β staining/positive nuclear ER β staining on survival, and did not identify a significant difference between these two groups. The present study suggests that cytoplasmic signal transduction may serve a more important role compared with nuclear signal transduction of ER β in lung cancer. To the best of our knowledge, the present study is the first to describe the association between cytoplasmic ER β expression and clinical responses of EGFR-TKI treatment in metastatic lung adenocarcinoma. Unfavorable clinical response rates and PFS were identified in patients with EGFR mutations and patients with metastasis with coexisting cytoplasmic ER β expression, but the reason remains unclear. The primary inclusion criteria of the present study were as follows: Adenocarcinoma diagnosis, stage IV and previous EGFR-TKI treatment. There have been a small number of previous studies including all these three criteria concomitantly (41-43). Therefore, there was discrepancy of cohort selection between our study and previous studies.

Nose *et al* (41) demonstrated that a strong expression of nuclear ER β was able to predict an improved clinical response and longer PFS following treatment with EGFR-TKI for lung adenocarcinoma; however, these data referred to the nuclear expression, and did not consider the clinical implications of cytoplasmic ER β , which was different to the protocols of the present study. The predictive discrepancy between these two studies additionally strengthened the concept of a distinct function between cytoplasmic and nuclear ER β . Increasing evidence indicated that ER β , but not ER α , served the predominant role in the initiation and development of lung cancer (6,44). ER β protein was detected in the cytoplasm of NSCLC cells, suggesting that the cytoplasmic component of ER β may be biologically significant (45). The cytoplasmic ER β compartment has not usually been considered or measured with nuclear staining together in previous studies, and therefore the clinical significance of cytoplasmic ER β staining may have been underestimated. Nuclear ER β was considered to serve an important role in tumor suppression in breast cancer, but increasing evidence has indicated that cytoplasmic ER β serves the opposite role in cancer cells (38,39). Similar with that in breast cancer, the clinical significance of ER β was also suggested to be diverse due to ER β localization in lung cancer cells through genomic, non-genomic and mitochondrial mechanisms (38-40,46). The estrogen-ER β complex binds to the nuclear estrogen response elements of target genes to stimulate gene transcription. The non-genomic mechanisms of ER β by which estrogen regulate cell functions are membrane-initiated, or 'pre-genomic' signaling pathways involving the activation of intracellular protein kinases, including phosphatidylinositol-3-kinase (PI3K), mitogen-activated protein kinase (MAPK) and c-Jun N-terminal kinase, which are considered common downstream substrates of EGFR signaling and usually occur in the cytoplasm (47,48). Estrogen may stimulate rapid activation of MAPK, PI3K, Proto-oncogene tyrosine-protein kinase Src and protein kinase B kinases that are associated with subsequent stimulation of cell proliferation, angiogenesis and tumor metastasis in NSCLC through the cytoplasmic ER-mediated signaling pathway (38-40). ER β present in cytoplasm was demonstrated to fail to translocate to the nucleus in the presence of estrogen in lung cancer cells, instead functioning through non-genomic mechanisms (49), which involved bidirectional crosstalk with growth factor receptor pathways, in particular the EGFR pathway (6,12). This ER-EGFR signaling axis appears to be reciprocal: ER signaling promotes the activation of EGFR, while EGFR signaling promotes the activation of ER (6,12). Therefore, the ER signaling pathway may affect the effect of EGFR-TKI therapy. These data also suggest that ER β demonstrates oncogenic features. The present study additionally indicated that the non-genomic ER β pathway in lung cancer also has important clinical significance. Based on the interaction between ER and the EGFR signaling pathway, anti-estrogen combined with anti-EGFR treatment may be a potential therapeutic option. Our previous results demonstrating an association between these 2 pathways additionally strengthened the possibility of combined therapy for a selected group of patients (42). Laboratory studies have indicated an robust synergistic effect on tumor growth when the two inhibitors were simultaneously used *in vitro* and *in vivo* in an NSCLC model (6,42). A phase I study designed to assess the safety and

tolerability of gefitinib combined with fulvestrant in 22 postmenopausal female patients with lung cancer demonstrated that the combination of these drugs was well-tolerated and exhibited anti-tumor activity in patients with stage IIIB/IV NSCLC (50). A phase II trial of erlotinib or erlotinib + fulvestrant in previously-treated patients with advanced NSCLC suggested that the clinical benefit rate was significantly increased among patients treated with the combination regimen (51). Two phase II clinical trials (trail nos. NCT 00100854 and NCT 01556191; clinicaltrials.gov) are currently ongoing to explore their effects on advanced NSCLC, mostly in a second-line setting and combined with the EGFR-TKI. Therefore, anti-estrogen therapy may be a novel strategy to reverse the resistance to EGFR-TKI treatment for patients harboring cytoplasmic ER β in metastatic lung adenocarcinoma.

However, due to the limitation of the small size sample and cohort selection in the present study, a larger cohort will be required to examine and validate the predictive value of these markers.

In summary, the results of the present study indicate that ER α and β were frequently expressed in metastatic lung adenocarcinoma, and that cytoplasmic ER β expression was identified to be a negative predictor for clinical response of EGFR-TKI treatment in patients with EGFR mutations. The ER and EGFR pathways together may contribute to the progression of lung cancer, and ER antagonists may become an alternative treatment for patients with acquired resistance to EGFR inhibitors.

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Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Authors' contributions

JL designed the project and was responsible for conducting the study. XD and LL performed the histological examination of the tumors samples and were major contributors in writing the manuscript. CT contributed to data analysis and interpretation. CM, WX, XWe, ZG, TZ, YF, LZ, XWa and LL were responsible for the acquisition of data. All authors read and approved the final manuscript.

Ethics approval and consent to participate

The study was approved by the Ethical Review Board of Peking University International Hospital (Beijing, China). Informed consent from the patients or their families was

obtained prior to initiation of the study. Ethical approval and informed consent was also obtained for the use of the breast cancer samples as controls.

Consent for publication

Identifying data, including names, initials, date of birth or hospital numbers, images or statements were not included in the manuscript. Informed consent for publication was obtained prior to initiation of the study.

Competing interests

The authors declare that they have no competing interests.

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