Prognostic and Therapeutic Implications of Aromatase Expression in Lung Adenocarcinomas with EGFR mutations

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The proportion of females among lung cancer patients with no smoking history is reportedly increasing, which implies that female hormones may affect the development of lung cancer. We examined mRNA expression of aromatase (CYP19A1), a possible intrinsic estrogen-synthetase, in patients with primary lung adenocarcinoma, and assessed its correlation with clinicopathologic factors including EGFR mutation status and prognosis. High aromatase gene expression was associated with poor outcomes. The prognostic significance of aromatase expression was also demonstrated in females, never-smokers, and patients with EGFR mutations, whereas such significance was not observed in their counterparts. In vitro analysis showed an antitumor effect of aromatase inhibitor in a lung adenocarcinoma cell line with an EGFR mutation and high aromatase expression. Our findings suggest aromatase is a possible therapeutic target in lung adenocarcinomas with EGFR mutations.
Abstract

Purpose: Lung adenocarcinomas among never-smokers are more common in females than in males; this implies that gender-dependent hormones promote smoking-unrelated lung adenocarcinoma. We therefore investigated mRNA expression of aromatase, an intrinsic estrogen synthetase, in lung adenocarcinoma and assessed its correlation to clinicopathological factors, including EGFR mutations and post-surgical prognosis.

Experimental Design: Aromatase mRNA expression in primary tumor samples from 110 lung adenocarcinoma patients was evaluated with qRT-PCR. Inhibitory effects of the aromatase inhibitor exemestane were assessed in lung adenocarcinoma cell lines (11-18 and HCC4006) that have EGFR mutations, separately and combined with EGFR tyrosine kinase inhibitor erlotinib.

Results: Aromatase gene expression was not correlated with patients’ clinicopathologic factors, including EGFR mutation status. High aromatase expression was associated with poor prognosis, for both recurrence-free survival (P = 0.004) and overall survival (P = 0.003). Additionally, the prognostic significance of aromatase expression was limited to females, never-smokers, and patients with EGFR mutations, but not in their counterparts. HCC4006, which has a low aromatase mRNA expression level, was not sensitive to exemestane, either alone or combined
with erlotinib. In contrast, growth of 11-18 cells, which have high aromatase expression, was significantly inhibited by exemestane, both alone and combined with erlotinib.

**Conclusions:** Aromatase is a candidate prognostic factor in patients with lung adenocarcinoma, especially in those with *EGFR* mutations, and may also be a beneficial therapeutic target in those patients.
Introduction

Worldwide, lung cancer is the leading cause of cancer death in males, and the second leading cause of cancer death in females (1). Although tobacco smoking is the predominant risk factor for lung cancer, approximately 25% of lung cancer cases are not attributable to tobacco use (2). The proportion of never-smokers among patients with non-small-cell lung cancer (NSCLC) has significantly increased for decades. NSCLC in never-smokers is more frequent in females and the adenocarcinoma cell type, and has a better prognosis compared to NSCLC in ever smokers (3, 4). Furthermore, frequencies of oncogenic drivers, such as mutations in KRAS or epidermal growth factor receptor (EGFR), or echinoderm microtubule-associated protein-like 4 (EML4)-anaplastic lymphoma kinase (ALK) fusion are different between lung cancers in never-smokers and those in smokers (5–7). These striking differences in epidemiological, clinical and molecular characteristics suggest that lung cancers associated with smoking and those unassociated with smoking are separate entities (2, 3).

The higher proportion of females among patients with lung cancer who have never smoked suggests a possible role for gender-dependent hormones in lung cancer development. Estrogen reportedly affects differentiation and maturation of the normal lungs (8) and stimulates lung
tumor growth in both laboratory-based (9–12) and clinical studies (13–16). Epidemiological studies also have suggested that endogenous and exogenous estrogen affect development of lung cancer (17). A post-hoc analysis of a randomized controlled trial in postmenopausal women showed that hormone replacement therapy (HRT) may increase the risk of death from lung cancer (18). A prospective cohort study confirmed dose-dependent increase in lung cancer risk among women who received HRT (19). A decreased incidence of lung cancer was observed in breast cancer patients treated with an aromatase inhibitor, exemestane, after tamoxifen therapy compared with patients who continued tamoxifen therapy (20). These data strongly support an important effect of female hormones in lung cancer development.

Aromatase (CYP19A1) is a cytochrome P-450 enzyme that converts androstenedione and testosterone to estrone and estradiol, respectively, and supports breast and endometrial cancer growth via autocrine and paracrine stimulation (21, 22). In not only gonadal tissue, but also in lung tissue, estrogen is synthesized mainly by aromatase (12, 23). Treatment with aromatase inhibitor has been found to suppress growth in lung cancer cell lines and mice tumor xenografts (12). In early-stage lung cancer, high aromatase expression reportedly correlates with poor
prognosis in women aged ≥ 65 years (13). These studies suggest that aromatase affects lung
cancer development, although the precise pathway is unclear.

After somatic EGFR mutations were discovered in NSCLC, many studies found higher mutation
frequencies in East Asians, women, never-smokers, and adenocarcinomas (5, 6). The prevalence
of EGFR mutation among female patients implies interactions between female hormones and
EGFR mutations. Interactions between estrogen receptor (ER) and EGFR pathways have been
extensively investigated in vitro (10, 11, 24, 25) and in tumor specimens (14, 15, 26, 27), but the
influence of aromatase on EGFR-dependent growth is not clear.

We studied expression and prognostic significance of aromatase, with regard to EGFR mutation
status, in patients with primary lung adenocarcinoma. We also examined growth inhibition by
aromatase inhibitor combined with EGFR tyrosine kinase inhibitor (TKI) on lung cancer cell
lines with EGFR mutations.
Materials and Methods

Human tissue samples

Primary tumor and corresponding non-neoplastic lung specimens were collected from 110 consecutive patients who underwent complete resections (R0) for primary lung adenocarcinoma from April 2007 to March 2011 at the Department of Surgery and Science, Kyushu University Hospital (Fukuoka, Japan), for whom surgical specimens were available and EGFR mutation status were determined (Table 1). This study included 44 men and 66 women, with a mean age of 67.7 years (range: 37–85 years) at surgical resection. Almost all of the women were postmenopausal. Histological tumor diagnoses were based on hematoxylin and eosin-stained preparations, using the WHO 2004 classification (28). Pathologic staging was performed according to the 7th edition of the TMN Classification of Malignant Tumours (29). EGFR mutation tests used the peptide nucleic acid-locked nucleic acid (PNA-LNA, Mitsubishi Chemical Medience, Tokyo, Japan) polymerase chain reaction (PCR) clamp method (30) with formalin-fixed paraffin-embedded sections of surgical specimens. No patient was treated with chemotherapy or radiotherapy prior to surgery. Thirty-nine (35.5%) patients received postoperative chemotherapy: 21 received oral tegafur and uracil, 17 were enrolled into a clinical
trial for the postoperative adjuvant chemotherapy (S-1 or cisplatin–S-1), and 1 received paclitaxel. A routine check-up with a physical examination, blood cell counts, serum chemistry, serum tumor markers including carcinoembryonic antigen and cytokeratin fragment 19, and chest X-rays were performed on an outpatient basis four times a year for the first 3 years, and thereafter twice annually. Computed tomography was performed twice a year for the first 3 years, and thereafter at least annually. Brain magnetic resonance imaging, and bone scintigram or fluorodeoxyglucose positron-emission tomography were performed annually. This study was approved by the Kyushu University Institutional Review Board for Clinical Research (no. 24-173).

Tumor samples and corresponding non-neoplastic lung tissues (most distant from tumor) were obtained immediately after resection, frozen in liquid nitrogen and stored at −80°C.

**Cells and reagents**

We obtained 21 lung adenocarcinoma cell lines and the breast cancer line MCF-7. A549, LK87, PC-9, and 11-18 cell lines were the kind gift of Dr. M. Takeshita. HCC4006 cell line was the kind gift of Dr. Adi F. Gazdar, and was confirmed by identification of the rare EGFR deletion mutation (del L747_E749, A750P) in this cell line (31). The ACC-LC-319 cell line was a kind gift from
Dr. T. Hida. Total RNAs from other cell lines were extracted in previous analyses (32, 33) or were the kind gifts of Dr. K. Tomizawa and Dr. T. Mitsudomi.

Driver mutations of the cell lines were KRAS mutations: A549, ACC-LC-94, H23, H358, H2009, LK87, and SK-LU1; EGFR mutations: H3255, HCC827, HCC4006, PC-9 and 11-18; MET mutation: H596; MET amplifications: ACC-LC-319 and H1993; Ros fusion: HCC78; HER2 mutation: H1781; EML4/ALK fusion, H2228; unknown: HCC193, SK-LC-3 and VMRC-LCD.

Cells were maintained in RPMI 1640 medium (Life Technologies, Tokyo, Japan) containing 10% fetal bovine serum (Life Technologies, Tokyo, Japan), 100 IU/ml penicillin, and 100 μg/ml streptomycin. The cells were maintained in a humidified atmosphere of 5% CO₂ in air at 37 °C.

EGFR-TKI erlotinib and aromatase inhibitor exemestane were purchased from Selleck Chemicals and LKT Laboratories, respectively.

**RNA extraction and quantitative RT-PCR**

The aromatase mRNA expression levels were evaluated by quantitative RT-PCR. Total RNA was extracted from resected lung tissues and cell lines using ISOGEN (Nippon Gene, Tokyo, Japan) according to the manufacturer’s protocol. cDNA was synthesized using a SuperScript™ III
First-Strand Synthesis SuperMix (Invitrogen, Carlsbad, CA) according to the manufacturer’s protocol. Quantitative PCR amplification was performed using Applied Biosystems StepOnePlus™ real-time PCR system (Life Technologies, Tokyo, Japan). TaqMan gene expression assay (Applied Biosystems, Tokyo, Japan) for CYP19A1 (Hs00903413_m1) was used and β-actin (Hs99999903_m1) was used as an internal control. The BD™ qPCR total RNA human reference (Clontech Laboratories, Inc., Palo Alto, CA), corresponding to a standardized mixture of total RNAs from a collection of adult human tissues, was used as a standard for quantitation. Relative aromatase mRNA expression levels of each sample (tissue and cell line) were standardized to those of β-actin and calculated relative to that of the total RNA human reference. Each sample was tested with triplicate measurements, and the mean value of the triplicate measurements was defined as a final value. We divided adenocarcinoma patients into two groups based on the expression level of aromatase compared with human reference; high aromatase expression was defined as being above the human reference expression, whereas low expression was defined as being below it.
Cell Proliferation Assay

HCC4006, 11-18, H358, H2228 and ACC-LC-319 cells (5 × 10^3) were plated into each well of 96-well flat-bottomed plates and grown in phenol red-free RPMI 1640 (Life Technologies, Tokyo, Japan) containing 10% dextran-coated charcoal-stripped fetal bovine serum (Biological Industries, Kibbutz Beit Haemek, Israel). Twenty-four hours later, dimethyl sulfoxide (DMSO), erlotinib, exemestane, or a combination of these drugs was added to achieve the indicated drug concentration, and cells were incubated for an additional 72 hours. The viability of drug-treated cells was determined by a WST-8 method using Cell Count Reagent SF (Nacalai Tesque, Kyoto, Japan) according to the manufacturer’s instructions. Percent growth was determined relative to DMSO-treated controls.

Statistical Analysis

Statistical analysis was performed using JMP statistical software version 9.0.2 (SAS Institute Inc., Cary, NC). All variables are expressed as the mean ± standard deviation (SD). Qualitative variables were compared using χ^2 tests, and quantitative variables were compared using Wilcoxon tests. Multivariate models were constructed using logistic regression, including sex, smoking history and EGFR mutation status, with aromatase expression (high/low) as the outcome of research.
interest. Survival curves were drawn using the Kaplan–Meier method. Significant differences among subgroups were compared using the log-rank test. The Cox proportional hazard regression model was used to explore the effects of the clinicopathologic variables and aromatase expression on survival. Factors showing prognostic significance in the univariate analyses were adopted as variables in multivariate analysis. \( P < 0.05 \) was considered statistically significant.

**Results**

*Expression of aromatase mRNA in lung adenocarcinoma tissues and corresponding non-neoplastic lung tissues*

We first examined the mRNA expression level of aromatase in lung adenocarcinoma and corresponding non-neoplastic lung tissues, using quantitative RT-PCR. Relative aromatase mRNA expression in carcinoma tissues (0.83 ± 1.06) was significantly higher than in corresponding non-neoplastic lung tissues (0.55 ± 0.46; \( P = 0.025 \)) (Fig. 1). Aromatase mRNA expression in non-neoplastic lung tissues did not significantly differ among subgroups divided by age (<70 vs. ≥70), sex, smoking history or *EGFR* mutation status (\( P = 0.07, 0.58, 0.46 \) and 0.61, respectively).
Relationship between aromatase expression and clinicopathologic factors

In univariate analysis, no significant correlation was identified between tumor aromatase expression level and clinicopathologic factors that are associated with smoking-unrelated lung cancer, such as sex, smoking history and EGFR mutation status (Table 1). The same results were observed for other clinicopathologic characteristics; age, maximum standardized uptake value (SUV$_{\text{max}}$), tumor size, histological grade, pleural invasion, lymphatic invasion, vascular invasion and pathological stage. In addition, in multivariate analysis, no significant association between high aromatase expression and sex, smoking history or EGFR mutation status was identified (Supplementary Table 1). We also examined tumor aromatase expression as a continuous variable. However, any statistically significant correlation was still not found between aromatase expression level and clinicopathological factors, although tendencies were seen in vascular invasion ($P = 0.06$) and pathologic stage (I vs. ≥II, $P = 0.051$).

Influence of aromatase gene expression level on survival

A survival analysis was performed in 110 patients who underwent curative resections. Median follow-up time was 35 months (range: 9–66 months). High expression of aromatase was
associated with poor prognosis in terms of both recurrence-free survival (RFS) \((P = 0.004;\) Fig. 2A) and overall survival (OS) \((P = 0.003;\) Fig. 2B).

Cox regression analyses of clinical variables for RFS and OS are shown in Table 2. Among the variables, sex, aromatase expression and pathologic stage were identified as potential predictors of RFS. A multivariate analysis that included the above variables also showed aromatase expression to be a significant prognostic factor, with a relative risk of 2.37 (95% confidence interval [CI], 1.05–5.31; \(P = 0.039\)) for RFS. Multivariate analysis for OS was not performed because of the small number of events (deaths).

**Prognostic significance of aromatase expression in lung adenocarcinomas with EGFR mutations**

Next, we compared survival between subgroups divided by clinicopathologic factors that are related to smoking-unrelated lung cancer such as sex, smoking history and EGFR mutation status.

High aromatase expression was associated with a poor prognosis in females \((P = 0.008\) for RFS and \(P < 0.001\) for OS; Fig. 2C and D), in never-smokers \((P = 0.009\) for RFS and \(P < 0.001\) for OS; Fig. 2E and F), and in patients with EGFR mutations \((P = 0.005\) for RFS and \(P = 0.003\) for OS; Fig. 2G and H), but not in males \((P = 0.14\) for RFS and \(P = 0.65\) for OS; Supplementary
Fig. S1A and B), not in current or former smokers ($P = 0.16$ for RFS and $P = 0.58$ for OS;
Supplementary Fig. S1C and D) and not in patients without $EGFR$ mutations ($P = 0.19$ for RFS
and $P = 0.07$ for OS; Supplementary Fig. S1E and F). Eleven patients with $EGFR$ mutations had
recurrent disease, and among them 8 patients received EGFR-TKI gefitinib after recurrence.
There was no patient who received EGFR-TKI before recurrence.

Cox regression analyses for potential predictors of survival in patients with $EGFR$ mutations are
shown in Table 3. Among the parameters, aromatase expression and pathologic stage were
identified as potential predictors of RFS. Multivariate analysis was not performed because of the
small number of recurrences.

**Growth inhibition of lung adenocarcinoma cell line by aromatase inhibitor**

We examined aromatase mRNA expression in 21 human lung adenocarcinoma cell lines
(Fig. 3A). No correlation was demonstrated between aromatase expression level and driver
mutation type. Because patients with high aromatase expression had worse prognoses than those
with low aromatase expression among those with $EGFR$ mutations (Fig. 2G and H), we next
investigated whether aromatase had therapeutic potential in lung adenocarcinomas with $EGFR$
mutations. We chose 11-18 as high-aromatase mRNA-expressing cell line and HCC4006 as
low-aromatase mRNA-expressing cell line, both of which have \textit{EGFR} mutations. To test the
growth inhibitory effects of the aromatase inhibitor exemestane, we conducted an MTT assay.

HCC4006 was not sensitive to exemestane, either alone or combined with erlotinib (Fig. 3B). By
contrast, 11-18 was sensitive to exemestane alone (Fig. 3C), and its cell growth was significantly
inhibited by the combination of exemestane with erlotinib. We further tested the growth
inhibitory effects of exemestane in high-aromatase mRNA-expressing cell lines without \textit{EGFR}
mutations: H358 (Supplementary Fig. S2A), H2228 (Supplementary Fig. S2B) and ACC-LC-319
(Supplementary Fig. S2C). The antitumor effect of exemestane in H358, H2228 and
ACC-LC-319 was much weaker than in 11-18.

\textbf{Discussion}

Although increasing evidence indicates that female hormones affect development of lung cancer
(34–36), to our knowledge, the present study is the first report to elucidate the prognostic
significance of aromatase expression in patients with lung adenocarcinomas with \textit{EGFR}
mutations. We found that aromatase mRNA expression level was not correlated with
clinicopathologic factors, including \textit{EGFR} mutation status. However, high aromatase expression
was associated with poor prognosis in terms of both RFS and OS. Moreover, the prognostic
significance of aromatase expression was limited to females, never-smokers, and patients with

*EGFR* mutations, whereas such significance was not observed in their counterparts.

Aromatase is an enzyme that catalyzes the conversion from androgens to estrogens. In NSCLC
cells, estrogen is reported to be mainly produced by intrinsic aromatase (23), and stimulates the
ER signaling pathway, resulting in tumor development and progression (9–11, 13, 24). Here, we
found that aromatase mRNA expression levels in carcinoma tissues were significantly higher than
in corresponding non-neoplastic lung tissues. Niikawa et al. reported that the estradiol
concentration in NSCLC was significantly higher than that in the non-neoplastic lung tissues, and
intratumoral estradiol concentration in NSCLC was positively associated with aromatase mRNA
expression (23). In another study, levels of aromatase activity tested by radioassay were
significantly greater in tumors compared with those in nearby normal tissue (12). These studies
indicate that intrinsic aromatase expression levels are closely associated with the estrogen levels
in the lung cancer cells. Thus, increased aromatase level may have profound influence in
carcinoma tissues through estrogen function.

Most estrogenic actions are mediated by ER which exists in two forms, ERα and ERβ (37).

Although immunohistochemical expressions of ERα and/or ERβ has been associated with clinical
outcome in some studies (14–16, 26, 38), the findings for expression frequency and subcellular localization (nuclear or cytoplasm) of ERs are inconsistent (14–16, 27, 36, 38, 39). These differences could be due to variation in such factors as (a) antibodies and dilutions, (b) scoring systems for staining, and (c) patient cohort characteristics (16). This discrepancy may obscure the significance of hormone receptor expression in patients’ clinicopathologic characteristics or prognoses. For this reason, we found it difficult to clarify the effect of estrogen on the development of lung cancer using immunohistochemical analysis.

In the present study, no significant correlation was identified between tumor aromatase expression and clinicopathological factors, including EGFR mutations, when analyzed as either dichotomized or continuous variables. These results are consistent with previously reports (27, 39, 40). On the other hand, a correlation between EGFR mutation and ER expression, both ERα (14) and nuclear ERβ (15), in lung adenocarcinoma, was reported in previous studies, suggesting that some interaction between ER and the EGFR signaling pathway may exist.

High aromatase expression was associated with a poor prognosis in patients who underwent curative resections for lung adenocarcinoma. We also demonstrated that the prognostic significance of aromatase expression was limited to females, never-smokers, and patients with
EGFR mutations, whereas such significance was not observed in their counterparts. We conducted Cox proportional hazards analysis in patients with EGFR mutations by RFS, not by OS, because 8 of 11 patients (73%) with EGFR mutations had received EGFR-TKI treatment for recurrence. EGFR-TKI prolonged the survival of such patients; therefore, the follow-up period may not have been enough to evaluate OS in this study. Aromatase expression level and EGFR mutation status did not directly correlate, but aromatase expression only held prognostic significance for lung adenocarcinomas with EGFR mutations, which suggests that estrogenic signaling augments growth that depends on the EGFR pathway. Mah et al. reported that lower aromatase levels predicted greater chances of survival in women 65 years and older with NSCLC, particularly among women who had no smoking history (13). Although they did not investigate EGFR mutation status, their results are consistent with ours. Nose et al. reported that strong nuclear expression of ERβ correlated with better disease-free survival in patients with EGFR mutations, but found no such prognostic significance in patients without EGFR mutations (15). They also suggested that strong ERβ expression was a surrogate marker for good response to EGFR-TKI (26). These results, along with our own, indicate that female hormone-related factors, such as aromatase and ERβ, affect outcomes only in lung adenocarcinomas with EGFR mutation,
which suggests that hormonal and EGFR pathways may contribute in concert to progression of lung adenocarcinoma.

To investigate the influence of differences in aromatase expression between the tumor and normal tissues on patient survival, we classified patients into the following two groups: T>N, in whom aromatase expression in adenocarcinoma tissue was higher than in non-neoplastic lung tissue (n = 51); and T<N, in whom it was lower (n = 43). We performed survival analyses between the two groups, but saw no significant survival difference in RFS ($P = 0.22$) or OS ($P = 0.27$). We further compared RFS and OS between the two groups in subsets divided by sex, smoking history and $EGFR$ mutation status, but saw no significant difference in these analyses (data not shown).

Recently, interactions between the ER and EGFR pathways have been investigated in vitro. A nonnuclear ER pool has been proposed that works via rapid signaling through various kinase cascades, including EGFR pathway and its downstream effectors in the lungs, such as MAPK (10, 11). On the other hand, the ER and EGFR pathways appear to act as alternate signaling pathways, with one up-regulating when the other is inactivated (10, 41). This bi-directional crosstalk between ER and EGFR signaling suggests that simultaneous or combined therapy that targets both pathways could exert higher antitumor effect in patients with NSCLC.
Both *in vitro* and *in vivo* reports have demonstrated that estrogen down-modulator, alone or combined with EGFR-TKI, resulted in enhanced anti-tumor activity in NSCLCs (9–12, 23, 25, 41–44). Exemestane, an irreversible steroidal inactivator, either alone (41) or in combination with cisplatin (43) showed significant anti-tumor effects in two separate studies. Both letrozole and anastrozole, reversible steroidal inactivators, demonstrated similar anti-tumor activity in NSCLCs (12, 23, 44). However, lung cancer cell lines used in almost all of these studies were without *EGFR* mutations. We showed that the 11-18 cell line, which has an *EGFR* mutation accompanied with a high aromatase mRNA expression, was sensitive to exemestane alone and cell growth was significantly inhibited by the combination of exemestane and erlotinib. We also demonstrated that exemestane’s antitumor effects in H358, H2228 and ACC-LC-319, which have high aromatase expressions without *EGFR* mutations, were much weaker than in 11-18. These results suggest that sensitivity to the aromatase inhibitor may depend on crosstalk between ER and the EGFR pathway; reducing estrogenic signaling by inhibiting aromatase might inhibit cell growth that depends on the EGFR pathway. Therefore, our result suggests that selecting patients with high aromatase expression accompanied by *EGFR* mutation might improve clinical responses to the combination of EGFR-TKI and aromatase inhibitor. However, we tested the growth inhibitory
effects of only one cell line with high aromatase expression and *EGFR* mutation, thus this study remains limited. Further studies using *in vivo* and clinical models are needed to elucidate the therapeutic potential of aromatase inhibitor in lung adenocarcinomas with *EGFR* mutations.

Traynor et al. reported a pilot study of gefitinib and fulvestrant in the treatment of 22 postmenopausal women diagnosed as NSCLC (45). No significant results were obtained in this small study, but combination therapy was well tolerated. Three out of 12 patients tested for *EGFR* mutation status detected *EGFR* mutation. A trial of EGFR-TKI and estrogen down-modulator in NSCLC patients with *EGFR* mutations may be therefore needed in the future.

In conclusion, high aromatase expression is correlated with poor outcome in patients with lung adenocarcinoma, including those with *EGFR* mutations. Aromatase may be a useful therapeutic target in lung adenocarcinomas with high aromatase expression and *EGFR* mutations. Although our results provide potential insights into the influence of aromatase expression in lung cancer, further studies are required to better understand the mechanisms of aromatase expression and interaction with EGFR signaling, and to determine the clinical applicability of aromatase inhibitors.
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a rapid and sensitive detection system, the peptide nucleic acid-locked nucleic acid PCR

mesenchymal transition in an epidermal growth factor receptor-mutant lung cancer cell line

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Table 1. Clinicopathologic characteristics by aromatase expression (n = 110)

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<th>Aromatase expression</th>
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<td></td>
<td></td>
<td>Low (n = 83)</td>
<td>High (n = 27)</td>
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<td>Age (years)</td>
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<tr>
<td>&lt; 70</td>
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<td>SUV&lt;sub&gt;max&lt;/sub&gt;&lt;sup&gt;a&lt;/sup&gt;</td>
<td>6.1 ± 4.7</td>
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<td>Pathological stage</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>I</td>
<td>81</td>
<td>64</td>
<td>17</td>
</tr>
<tr>
<td>II, IIIA</td>
<td>29</td>
<td>19</td>
<td>10</td>
</tr>
</tbody>
</table>

<sup>a</sup>Data not available for 19 of the aromatase-low patients and 5 of the aromatase-high patients.
<sup>b</sup>Data not available for one of the aromatase-low patients.

SUV<sub>max</sub>: maximum standardized uptake value.
Table 2. Cox proportion hazards model for recurrence-free survival and overall survival (n = 110)

<table>
<thead>
<tr>
<th>Variable</th>
<th>Univariate</th>
<th>Multivariate</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Hazard ratio</td>
<td>95% CI</td>
<td>P</td>
</tr>
<tr>
<td><strong>Recurrence-free survival</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age (≥70 vs. &lt;70)</td>
<td>1.49</td>
<td>0.71–3.17</td>
<td>0.296</td>
</tr>
<tr>
<td>Sex (male vs. female)</td>
<td>2.30</td>
<td>1.09–5.06</td>
<td><strong>0.029</strong></td>
</tr>
<tr>
<td>Smoking (current or former vs. never)</td>
<td>1.05</td>
<td>0.49–2.21</td>
<td>0.907</td>
</tr>
<tr>
<td>EGFR mutation (positive vs. negative)</td>
<td>0.72</td>
<td>0.32–1.51</td>
<td>0.382</td>
</tr>
<tr>
<td>Aromatase (high vs. low)</td>
<td>3.01</td>
<td>1.35–6.64</td>
<td><strong>0.008</strong></td>
</tr>
<tr>
<td>Pathological stage (≥II vs. I)</td>
<td>5.33</td>
<td>2.53–11.5</td>
<td><strong>&lt;0.001</strong></td>
</tr>
<tr>
<td><strong>Overall survival</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age (≥70 vs. &lt;70)</td>
<td>2.85</td>
<td>1.06–8.97</td>
<td><strong>0.041</strong></td>
</tr>
<tr>
<td>Sex (male vs. female)</td>
<td>2.74</td>
<td>1.04–7.97</td>
<td><strong>0.038</strong></td>
</tr>
<tr>
<td>Smoking (current or former vs. never)</td>
<td>0.76</td>
<td>0.28–1.98</td>
<td>0.573</td>
</tr>
<tr>
<td>EGFR mutation (positive vs. negative)</td>
<td>0.25</td>
<td>0.06–0.78</td>
<td><strong>0.015</strong></td>
</tr>
<tr>
<td>Aromatase (high vs. low)</td>
<td>4.20</td>
<td>1.49–12.1</td>
<td><strong>0.007</strong></td>
</tr>
<tr>
<td>Pathological stage (≥II vs. I)</td>
<td>3.54</td>
<td>1.35–9.46</td>
<td><strong>0.011</strong></td>
</tr>
</tbody>
</table>

CI: confidence interval. Multivariate analysis for OS was not performed because of the small number of events (deaths).
Table 3. Cox proportion hazards model for recurrence-free survival in patients with *EGFR* mutations (n = 54)

<table>
<thead>
<tr>
<th>Variable</th>
<th>Hazard ratio</th>
<th>95% CI</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age: ≥70 (n = 21) vs. &lt;70 (n = 33)</td>
<td>0.85</td>
<td>0.22–2.82</td>
<td>0.795</td>
</tr>
<tr>
<td>Sex: male (n = 12) vs. female (n = 42)</td>
<td>3.48</td>
<td>0.99–11.6</td>
<td>0.050</td>
</tr>
<tr>
<td>Smoking: current/former (n = 15) vs.</td>
<td>1.60</td>
<td>0.42–5.30</td>
<td>0.466</td>
</tr>
<tr>
<td>never (n = 39)</td>
<td>4.97</td>
<td>1.50–19.0</td>
<td>0.009</td>
</tr>
<tr>
<td>Pathological stage: ≥II (n = 13) vs.</td>
<td>6.55</td>
<td>1.98–25.0</td>
<td>0.002</td>
</tr>
<tr>
<td>I (n = 41)</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

CI: confidence interval. Multivariate analysis was not performed because of the small number of recurrences.
Figure legends

Figure 1. Differences in aromatase mRNA expression levels between carcinoma tissues and corresponding non-neoplastic lung tissues (n = 94). Each value is shown in an open circle; paired values of the same patient are connected by a line. Two data groups are shown as box-and-whisker plots, with the bottom and top of the box at the first and third quartiles, and the band inside the box at the median. Upper and lower whiskers indicate 90th and 10th percentiles, respectively. Aromatase mRNA level for the human reference RNA is set as 1. Statistical difference was determined by a Wilcoxon matched-pair signed-rank test.

Figure 2. Kaplan–Meier postoperative RFS and OS curves according to aromatase expression level. N: number of patients in each category. (A) RFS and (B) OS curves for all cohort patients. (C) RFS and (D) OS curves for females. (E) RFS and (F) OS curves for never-smokers. (G) RFS and (H) OS curves for patients with EGFR mutations.

Figure 3. Effect of exemestane alone and in combination with erlotinib on EGFR mutant lung adenocarcinoma cell line proliferation. (A) mRNA expression levels of aromatase in 21 human lung adenocarcinoma cell lines. Quantitative real-time RT-PCR was performed with validated TaqMan probes; assays were done in triplicate. The expression value for each cell line was
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calculated relative to that of human reference. MCF-7: breast carcinoma cell line. (B) HCC4006 cells were not sensitive to exemestane alone or in combination with erlotinib. (C) 11-18 cells were sensitive to exemestane alone and in combination with erlotinib. HCC4006 and 11-18 cells were incubated for 24 hours and for an additional 72 hours with the indicated concentrations of exemestane or erlotinib; cell growth was then measured. Independent experiments were repeated three times. *$P < 0.05$ vs. erlotinib alone; †$P < 0.05$ vs. control (both erlotinib and exemestane were free) by Dunnett’s test. All data represent the mean ± SD from three independent experiments.
Figure 1

Box plots showing mRNA relative expression (relative to human reference) in non-neoplastic lung tissues compared to carcinoma tissues. The figure indicates a statistically significant difference with a p-value of 0.025.
Figure 2

A. All patients
Recurrence-free survival (%)

B. All patients
Overall survival (%)

C. Females
Recurrence-free survival (%)

D. Females
Overall survival (%)

E. Never smokers
Recurrence-free survival (%)

F. Never smokers
Overall survival (%)

G. Patients with EGFR mutation
Recurrence-free survival (%)

H. Patients with EGFR mutation
Overall survival (%)
Figure 3

A

Aromatase mRNA levels (relative to human reference)

KRAS mut.  EGFR mut.

H23  ACC-LC-94  AS809  H2009  LKCI  SK-LU1  H56  HCC827  HCC4006  H2225  PC-9  11-18  H56  H1993  ACC-LC-319  Ros fusion  HCC78  HER2 mut.  EML4/ALK  VMRC-LCS  SK-LC-3  MOF-7

B (%)

HCC4006

% growth

Erlotinib alone
Erlotinib + Exemestane 37.5 μM
Erlotinib + Exemestane 75 μM
Erlotinib + Exemestane 150 μM

Erlotinib concentration (nM)

0  31.25  62.5  125  250  500

C (%)

11-18

% growth

Erlotinib alone
Erlotinib + Exemestane 37.5 μM
Erlotinib + Exemestane 75 μM
Erlotinib + Exemestane 150 μM

Erlotinib concentration (nM)

0  125  250  500  1000  2000

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Mikihiro Kohno, Tatsuro Okamoto, Kenichi Suda, et al.

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