

# The Role of Estrogen Receptors in Proliferation of Non-Small Cell Lung Cancer

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## Abstract

To explore the expression pattern of ERs in NSCLC tissues and assess their relationship with tumor histopathological variable. In our study, Ers expression was examined using Real-time PCR with specimens of 28 NSCLC patients. It was shown that both ERα and ERβ were over expression in NSCLC tissues, and also the Mrna concentration of both ERα and ERβ were significantly higher in primary tumor T2 stage than in T1 stage and higher in squamous carcinoma than in adenocarcinoma. However, the activation of ERα and ERβ were completely different. To further explore the role of Ers in development and progression of NSCLC, we used Ers selective siRNA or antagonist *in vitro* experiments. The results showed that ERβ but not ERα can mediate E2 induced cell growth, since siRNA targeting ERβ but not ERα gene can induce cell cycle arrest at G1 phase by down regulation of cyclinD1 expression, and also cell cycle regulators p21<sup>Waf1/Cip1</sup> and p53 were involved in this signaling pathway.

**Keywords:** Estrogen receptors; Non-small cell lung cancer; siRNA; P53; Proliferation

## Introduction

Estrogens and its receptors are key signaling molecules that regulate various physiological processes, such as cell growth, development, and differentiation [1,2]. Ers are also involved in the development of many types of malignant tumors, including breast and gynecologic cancers [3-6], endocrine gland cancers [7-15], digestive cancers [16-18] and lung cancer [19-22]. Estrogens exert their biological effect through two classical estrogen receptors(Ers) subtypes, ERα and ERβ, and novel estrogen receptor G protein coupled receptor 30 (GPR30) [23].

Lung cancer, especially Non-small cell lung cancer (NSCLC) is the leading cause of cancer-related mortality for both men and women worldwide. Estrogen signaling pathways may play an important role in development of lung cancer. The cellular response to estrogen is mainly mediated by ERα and ERβ. There was increasing evidence to show that NSCLC express both ERα and ERβ in nucleus as well as extra-nuclear sites [19]. It was observed that ERβ but not ERα is the dominant form in normal lung cancer cell line and tissues, and loss of ERβ leading to abnormal lung structure and systemic hypoxia [24,25]. Moreover, when expression of either ERα or ERβ was suppressed by small interfering RNA (siRNA), the proliferation of NSCLC cells were significantly reduced [20], and also, blockage of Ers by Ers antagonist ICI 182780 lead to the inhibition of NSCLC cell line growth [26]. Therefore, the function of ERα and ERβ seems to prompt the cell proliferation since block of both of them lead to arrest of tumor growth. However, the role of ERα and ERβ are complicated by found that Era positive and ERβ negative lung cancer patients are associated with poor prognosis [21], and absence of ERβ expression is a marker showing high risk of lung cancer patients even an early clinical stage [21]. While some study found that Era was elevated in tumor but was not predictive of survival [27]. Although these studies reveal the importance of estrogen receptors in promoting the growth of lung cancers, but it is not clear which ER subtype is involved.

In our study, we explored the expression pattern of Ers in NSCLC tissues, and also the relationship between Ers expression with the

tumor histological subtype, pathological stage and histological stage of NSCLC. To elucidate the role of ERα and ERβ in NSCLC cell lines were chosen.

## Materials and Methods

### Patients

Lung cancer tissues and normal tissues from 28 patients with NSCLC were collected during primary debulking surgery from January 2009 to January 2011. The patients were selected according to the following criteria: (a) primary none small cell lung cancer; (b) previously untreated; (c) complete patient characteristics information; and (d) surgery as the first treatment.

The patient information was recorded as follows: clinical diagnosis, pathological stage, histologic subtype and histologic grade. The tissues were classified into two groups; one is lung tumor tissues group; and the other is corresponding tumor-free lung tissues from the same patient. All the tissues were obtained according to protocol of lung cancer patients during surgery to remove the tumors. Tissues were frozen immediately in liquid nitrogen and kept at -80°C. Patient characteristics are summarized in Table 1.

### Cell culture and transfection

NSCLC cell line, H1650 and A549 (ATCC, USA), were cultured in

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RPMI medium 1640 (ATCC, USA) supplemented with 10% fetal calf serum (ATCC, USA) at 37°C under 5% humidified CO<sub>2</sub> and 100 µg/ml each of streptomycin and penicillin G (GIBCO, USA). The anti-ERα, anti-ERβ and anti-GPR30 siRNA (Santa cruz, USA) were transfected by Lipofectamine™ RNAiMAX (Invitrogen, USA) according to the manufacturer's instructions. Briefly, approximately 2 × 10<sup>4</sup> cells/well were grown overnight in 24-wells plate. When the cells reached 80% confluence, they were transfected with anti-ERα siRNA (30 nM), anti-ERβ siRNA (30 nM) or anti-GPR30 siRNA (30 nM) and negative control siRNA (30 nM) separately in anti-body free medium using lipofectamine™ RNAiMAX. After incubation for 48 h at 37°C 200 µl RPMI 1640 with 10% FBS was added and then subjected to real-time RT-PCR and western blot analysis.

### RNA extraction and reverse transcription

Lung tumor tissue (N=28) and the corresponding tumor-free tissue (N=28) were homogenized and total RNA extraction from tissues was performed using RNeasy Mini Kit (Qiagen, Valencia, CA). RNA quality was checked with Spectrophotometer (NanoDrop 1000). Almost all samples had high-quality RNA. 1 µg RNA was reverse transcribed into cDNA with Omniscript RT kit (QIAGEN, Germany) according to the manufacturer's protocol.

### Quantitative real-time PCR

Primers (IDT, USA) for estrogen receptors and other genes were designed to locate into two exons, Sequences of the primers used in the Real-Time PCR analysis were shown in Table 2. The 18s gene was chosen as an endogenous house-keeping control gene. Quantitative real-time PCR was performed using Cyler iQ Real-time PCR Detection System (BIO RAD iQ5 Optical Module. Reaction mixtures contained 1 × SYBR Green PCR supermix (Bio-rad, USA), 0.1 µl Primer, 1 µl cDNA template in total volume of 25 µl. Thermal cycling conditions included activation at 95°C (10 min) followed by 40 cycles each of denaturation at 95°C (15 sec) and annealing at 60°C (1 min).

Each reaction was performed in triplicate and negative controls were included in each experiment. To compare the expression levels among different samples, the relative mRNA levels were calculated using the comparative delta CT (ΔCt) method.

### Western blot analysis

After transfection, cells were lysed in lysis buffer. Equivalent amounts of protein lysates from each sample were separated by

Patient characteristics	N=28
<b>Age</b>	
Mean	63
Range	43-71
<b>Pathological stage</b>	
T1, N0, M0	N=11
T2, N0, M0	N=17
<b>Histologic grade</b>	
G1 Well differentiated (Low grade)	N=2
G2 Moderately differentiated (intermediated grade)	N=14
G3 Poorly differentiated (High grade)	N=12
<b>Histologic subtype</b>	
Adenocarcinoma	N=16
Squamous cell lung carcinoma	N=10
Large Cell Carcinoma	N=1
Adeno-squamous cell carcinoma	N=1

**Table 1:** Patient characteristics.

**Table 2:** Sequences of the primers used in the real-Time PCR analysis.

RNAs	Primer sequences
Human estrogen receptor α mRNA	5'-GGAGACGGACCAAGCCACT-3'
	5'-TTCCCAACAGAAGACAGAAGATG-3'
Human estrogen receptor β mRNA	5'-CACGTCAGGCATGCGAGTAAC-3'
	5'-ACCCCGTGATGGAGGACTTG-3'
Human GPR30 mRNA	5'-ACGAGACTGTGAAATCCGCAACCA-3'
	5'-ATCAGGCTGGAGGTGCACCTTGGAA-3'
Human cyclin A2 mRNA	5'-CCTGCA AACTGCAAAGTTGA-3'
	5'-AAAGGCAGCTCCAGCAATAA-3'
Human cyclin D1 mRNA	5'-CAGGCGGCTCTTTTTCAC-3'
	5'-CCCTCGGTGTCCTACTTCAA-3'
Human P53 mRNA	5'-TGACTGTACCACCATCCACTA-3'
	5'-AAACACGCACCTCAAAGC-3'
Human P21 mRNA	5'-TGGACCTGTCACTGTCTTGT-3'
	5'-TCCTGTGGGCGGATTAG-3'
18s rRNA	5'-GGGAGGTAGTGACGAAAATAACAAT-3'
	5'-CCCTCCAATGGATCCTCGTTAAAGGA-3'

electrophoresis through pre-cast 10% Tris-HCL polyacrylamide gel and transferred to PVDF membranes. Nonspecific binding site were block by incubation in 1X PBS. Primary antibodies (Santa cruz, USA) were incubated with the membranes and recognized with secondary antibodies (Santa cruz, USA). ECL-Plus Western Blotting Detection Reagents (Amersham Biosciences, Piscataway, NJ, USA) were used to visualize the complexes.

### Cell viability analysis

Cells were seeded in phenol red-free RPMI 1640 medium supplemented with 10% 4X dextran-coated, charcoal-treated FBS (SFS) in 24-well plates or 96-well plates. After overnight attachment, the cell culture medium was removed. The adherent cell was washed twice with sterile PBS, and the cells were then treated with the indicated ligands for a total of 48 h. Selective siRNA or antagonist treatment were 1 h before E2. The effect of treatment on cell growth was determined by MTT assay. The MTT assay kits were purchased from ATCC, and assays were according to the manufacturer's protocol. The percentage of cell viability was calculated using a standard curve and normalized to non-treated control.

### Flow cytometric analysis

Cells were cultured overnight in RPMI-1640 medium and then treated with siRNA of ERα and ERβ for 48 h. The treated cells were fixed and stained with propidium iodide (Sigma USA). At least 1 × 10<sup>6</sup> stained cells were analyzed using FACSAria (BD Biosciences USA).

### Statistical analysis

All data shown as bar graphs are expressed as the mean ± SE. The statistical significance of differences was calculated by one-way ANOVA and two-tailed t test analysis. The correlation between gene expressions was evaluated by chi-square test. Two-tailed P<0.05 was considered to be statistically significant.

## Results

### Both ERα and ERβ mRNA were over-expression in NSCLC tissues

We examined the expression of ERs in all lung tumor tissues and the corresponding tumor-free lung tissues from same patient. Both the ERα and ERβ mRNA transcript expression levels were over-expression in NSCLC tissues Table 3. However, GPR30 mRNA transcript showed

Variables	ER $\alpha$ mRNA	ER $\beta$ mRNA
Normal(n=28)	1.01 $\pm$ 0.03	1.02 $\pm$ 0.03
Cancer(n=28)	5.17 $\pm$ 0.07	4.08 $\pm$ 0.05
P value	0.004*	0.002*
<b>Pathological stage</b>		
T1, N0, M0 (n=11)	1.93 $\pm$ 0.23	1.62 $\pm$ 0.12
T2, N0, M0 (n=17)	6.02 $\pm$ 0.50	5.07 $\pm$ 0.52
P value	0.009*	0.019*
<b>Histologic subtype</b>		
Adenocarcinoma(n=16)	4.09 $\pm$ 0.52	2.62 $\pm$ 0.62
Squamous(n=10)	7.64 $\pm$ 0.97	5.82 $\pm$ 0.26
P value	0.03*	0.05*

\* Difference is significantly at 0.05 level

**Table 3:** ER $\alpha$  and ER $\beta$  mRNA concentration in patients with NSCLC.

a lower-expression in NSCLC tissues. It was also shown the ER $\alpha$  and ER $\beta$  mRNA concentrations according to pathological stage. Significant increasing of ER $\alpha$  and ER $\beta$  mRNA concentration in T2 stage compared with T1 stage in NSCLC patients were found. Additionally, as shown in Table 3. ER $\alpha$  and ER $\beta$  mRNA concentrations were different according to the tumor histologic subtype by finding that squamous carcinoma has higher mRNA concentration than adenocarcinoma in both ER $\alpha$  and ER $\beta$  expression. However, there is no correlation between ERs mRNA concentration and histologic tumor grade.

### ER $\beta$ but not ER $\alpha$ mediates estrogen-dependent growth of NSCLC

To evaluate the role of ER $\alpha$  and ER $\beta$  in non-small cell lung cancer, we used receptor selective siRNA to down regulate the ER $\alpha$ , ER $\beta$  and GPR30 expression separately in H1650 cell lines, as well as A549 cell lines. and then Real-time RT-PCR and western blotting were performed to determine ER $\alpha$ , ER $\beta$  and GPR30 expression levels in transfected NSCLC cell lines (Figure 1). When H1650 cell line were transfected with anti-ER $\alpha$  siRNA, anti-ER $\beta$  siRNA or anti-GPR30 siRNA, the mRNA concentration (Figure 1) and proteins level (Figure 2) were down-regulated. The results obtained from A549 cells were same.

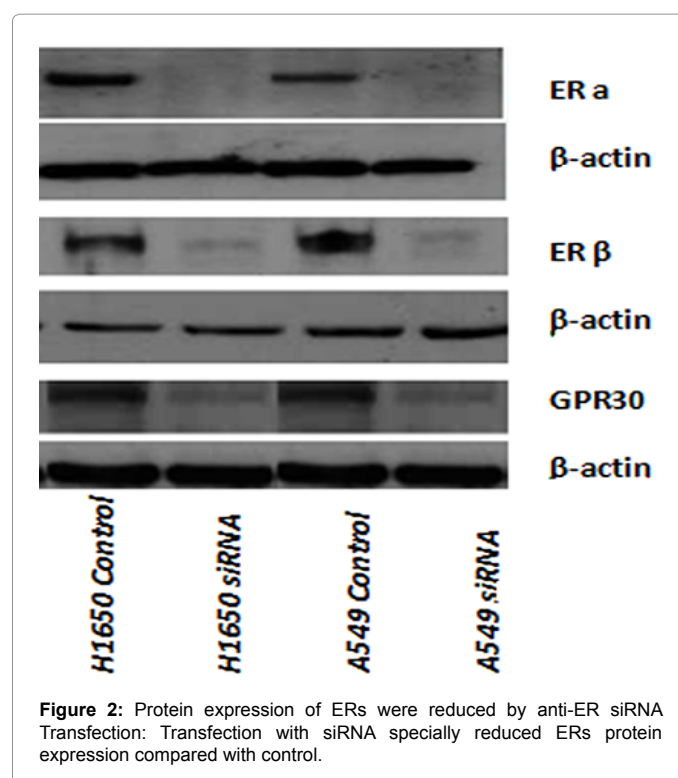
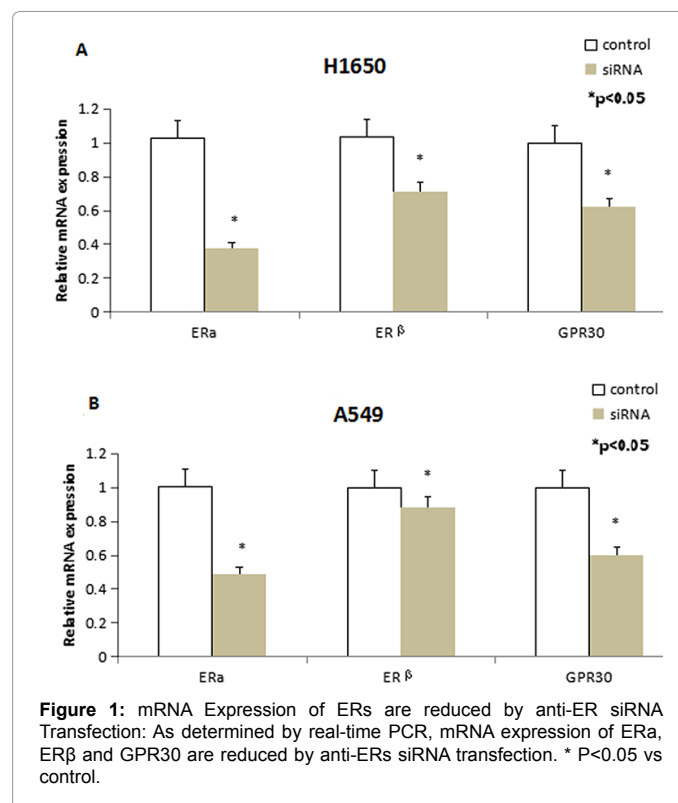
To determine whether the expression of ER $\alpha$  or ER $\beta$  affect the NSCLC cells proliferation, Cell viability was detected using MTT method. The cell growth in 10 nM E2 treatment group had no significant difference from that in control group. However, blocking of estrogen receptors before E2 treatment significantly decreased the proliferation of cells compared with that in E2-treatment group. Furthermore, the role of ER $\beta$  was detected by blocking both ER $\alpha$  and GPR30 expression by selective siRNA but left ER $\beta$  expression, and the result shown that the cell growth was increased compared with all ERs blockage group. However, no difference was found in ER $\beta$  and GPR30 blockage but ER $\alpha$  expression group compared with all ERs blockage group (Figure 3A). It indicated that up-expression and down-expression of ER $\beta$  but not ER $\alpha$  can accelerate and inhibit the cellular proliferation.

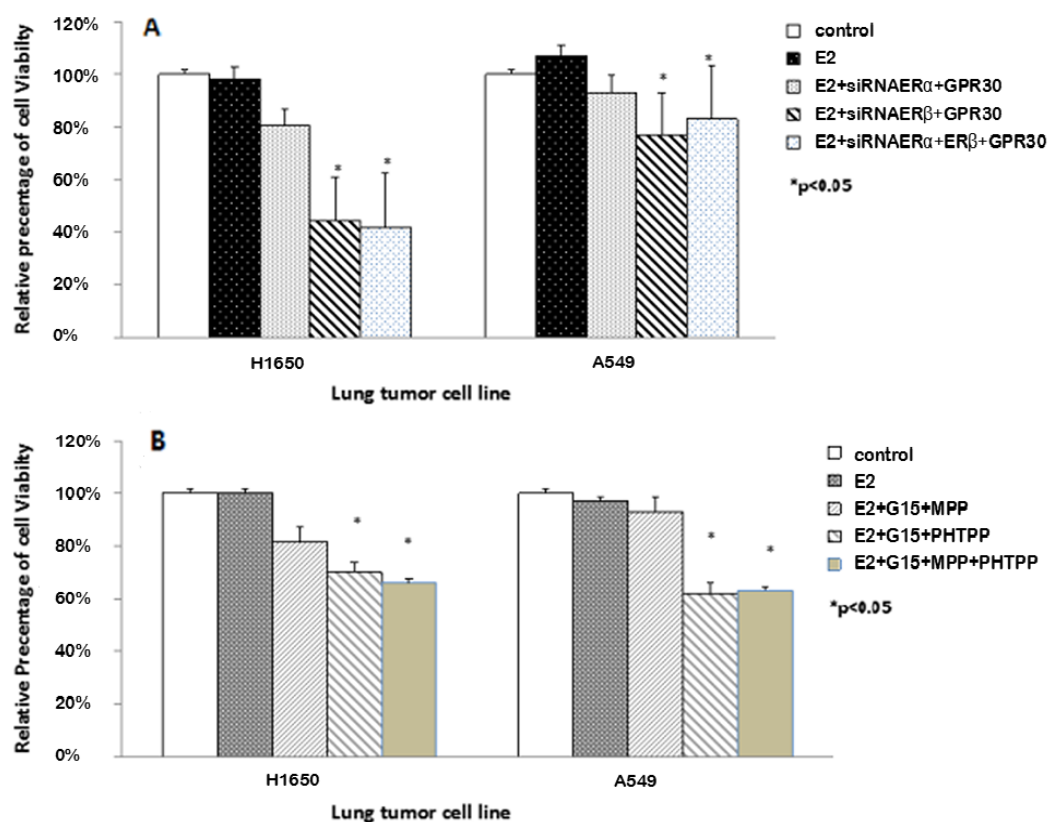
To further confirm that ER $\beta$  but not ER $\alpha$  is involved in NSCLC cells proliferation, we performed cell proliferation assays with ER $\alpha$ -, ER $\beta$ - and GPR30 selective antagonist. Combined with G15 and MPP, but not PHTPP can stimulate the growth of H1650 cells, while combined with PHTPP and G15 shows no difference (Figure 3B)

### Inhibition of ER $\beta$ induced a G1-phase cell-cycle arrest

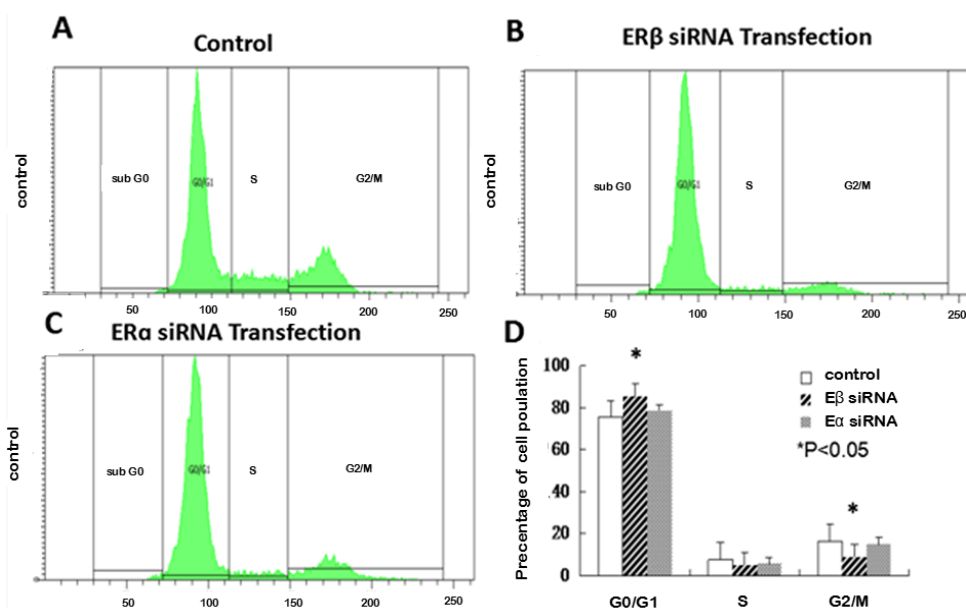
Flow cytometric analysis (Figures 4A-4D) showed a significant increase in the number of cells in G0/G1 phase after treatment of H1650 with anti-ER $\beta$  siRNA for 48 hr, as compared with that in control

cells. It indicated that the induction of a cell cycle arrest at G1 phase was induced by ER $\beta$  siRNA in H1650 cells. Further, the role of ER $\alpha$  was further determined by transfection with ER $\alpha$  siRNA, and the result showed no significantly difference in G0/G1 cell population compared with control group.





**Figure 3:** ER $\beta$  is Associated with Cell Growth induced by Estrogen: A: The inhibitory of ERs by siRNA before E2 treatment decrease the cell growth significantly (\*p<0.05 vs control). Pre-treatment with ER $\alpha$  siRNA and GPR30 siRNA transfection followed by 10 nM E2 increase the growth of cells significantly compared with E2+ GPR30 siRNA+ER $\alpha$  siRNA+ER $\beta$  siRNA (\*\*P<0.05 vs E2+GPR30 siRNA+ER $\alpha$  siRNA+ER $\beta$  siRNA). B: Also, treatment cells with ERs selective antagonist (1  $\mu$ M MPP, PHTPP and G15) can significantly reduce cell growth (\*p<0.05 vs control), and inhibitory of ER $\alpha$  and GPR30 by MPP and G15 can increase the cell relative viability (\*\*p<0.05 vs E2 +G15+MPP+PHTPP). So it shows that E2 induced H1650 cell proliferation through ER $\beta$ -mediated signaling.



**Figure 4:** Cell cycle distribution of H1650 Transfected with ER $\alpha$  or ER $\beta$  for 48 h: inhibitory of ER $\beta$  expression by siRNA induced cell cycle arrest at G1 phase, while the cell cycle distribution of cells transfected with ER $\alpha$  siRNA showed no difference compared with control, \* p<0.05 VS control.



To determine whether the anti-ER $\beta$  siRNA treated H1650 were arrested at the G0/G1 phase; we examined changes in the expression of panel cell-cycle-specific markers after 48 h. The mRNA concentration as well as the protein level of cyclin-D1 which functions in the transition from G1 to S phase of the cell cycle decreased (Figures 5A and 5B). The mRNA concentration and the protein level of cyclin-A2, which is involved in transition from S to G2, did not change significantly (Figure 5C and 5D). Collectively, these data support the notion that inhibition of ER $\beta$  induces cell-cycle arrest at the G0/G1 phase in H1650 cells, which is consistent with flow cytometric analysis. The results obtained from A549 also shown the changes of cyclinD1 and cyclinA2 when the expression of ER $\beta$  was blocked (Figure 5B).

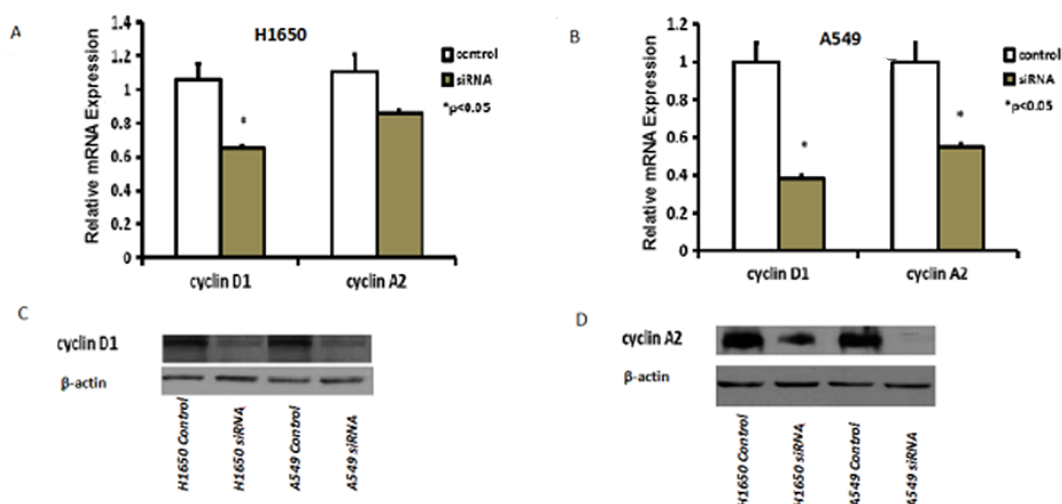
### P53 and P21 expression was involved in cell growth inhibition through ER $\beta$ -mediated signaling

Inhibition of ER $\beta$  expression by anti-ER $\beta$  siRNA markedly

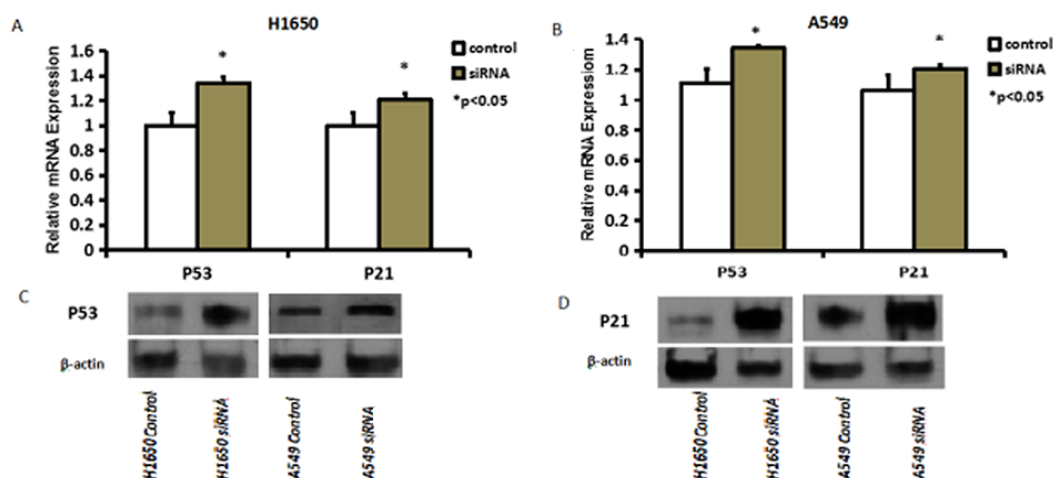
increased P53 expression at both mRNA level and protein level in H1650 cells as well as A549 cells. The overexpression was completely induced by anti-ER $\beta$  siRNA but not by a scramble siRNA control (Figures 6A-6D). Furthermore, the cyclin-dependent kinase cyclin inhibitors gene, P21 mRNA concentration were also upregulated by inhibition of ER $\beta$  siRNA. These finding establish that inhibition of ER $\beta$  induced upregulation of P53 and P21 as a direct mediator of the growth-inhibitory response.

### Discussion

It is well established that ERs play a major role in pathological processes of lung cancer, while the results remain inconsistent. Early studies detected for the presence of the classical ER $\alpha$  only, and then with the development of ER $\beta$  antibody, the expression of ER $\beta$  was also found in lung cancer [28-30]. Many studied have shown the expression of ER $\beta$  in majority of human NSCLC cell lines as well as primary



**Figure 5:** H1650 cells were subjected to real-time RT-PCR analysis to determine cyclinD1 and cyclinA2 mRNA levels after ER $\beta$  transfection for 48 h. The mRNA expression of cyclinD1 was decreased significantly, while the mRNA expression of cyclinA2 had no difference, \* $p < 0.05$ .



**Figure 6:** H1650 cells were subjected to real-time RT-PCR analysis to determine P53 and P21 mRNA levels after ER $\beta$  transfection for 48h. The mRNA expression of both P53 and P21 were increased significantly after ER $\beta$  transfection. \* $p < 0.05$ , \*\*  $p < 0.001$

tissues, however, the role of ER $\alpha$  in lung cancer is less clear, and also the relationship between ERs expression and tumor pathological stage, histology subtype and histologic grade are not clear. Our findings used NSCLC tissues and its corresponding tumor-free lung tissues to explore ERs expression in NSCLC, and the result is consistent with those in cell findings, which shown that both ER $\alpha$  and ER $\beta$  mRNA concentration of NSCLC tissues are higher than the corresponding normal lung tissues.

The other main question addressed in this study was whether expression of ER $\alpha$  or ER $\beta$  have relationships with tumor pathological stage, histology subtype or histologic grade. There is evidence suggests that in breast cancer, ERs is an important prognostic factor, which is the same case in lung cancer [31,32]. Our results showed that both ER $\alpha$  and ER $\beta$  were overexpressed in NSCLC tissues, and their mRNA concentration was related to the tumor pathological stage and histology subtype. Higher concentration of ERs mRNA has been found in T2 stage, and also that ER $\alpha$  and ER $\beta$  mRNA expression were higher in squamous carcinoma than in adenocarcinoma. In addition, evidence suggests that mRNA concentration of ER $\alpha$  was correlate with ER $\beta$ , since we found that the number of patients who have either low level of ER $\alpha$  but high level of ER $\beta$  or high level of ER $\alpha$  but low level of ER $\beta$  were relatively small in present study.

In order to explain the activation of ER $\alpha$  and ER $\beta$  in the development of NSCLC separately, we selected a NSCLC cell line] which deprived from lung adenocarcinoma patients. Selected ERs specific siRNAs were successfully transfected into H1650 cell lines separately. ER $\beta$  but not ER $\alpha$  affects NSCLC cells proliferation. MTT method was used in this study for cell viability. The results showed that inhibitory ERs by selective siRNA or antagonist can block the cell proliferation induced by 10 nM E2, however only the presence of ER $\beta$  but not ER $\alpha$  can accelerate cell growth. This is indicated that ER $\beta$  but not ER $\alpha$  was involved in cell proliferation. These results were consistent with other reports. A549 cells transfected with ER $\beta$  have increased proliferation in response to estrogen [33].

The progression of cells proliferation is associated with cell cycle, which is known to be positively regulated by a series of cyclin-dependent kinases (CDKs), as well as cyclins, and is negatively controlled by specific CDK inhibitors (CDKIs) [34-36]. CDKIs are separate into two classes, including this, the CIP/KIP family ((p21Waf1/Cip1, p27Kip1, and p57Kip2) which inhibits all CDKs by directly binding CDK complexes [37]. Wild-type P53 regulates cell transition from G1 to S phase in cell cycle and induce G1 arrest in response to DNA damage [38]. The *p21Waf1/Cip1* gene, which is transcriptional target of wild-type P53 [39,40], is activated by wild-type P53 and is downstream effectors for P53 function by inducing G1 arrest if cells are exposed to DNA damaging agents [41]. We found that inhibitory of ER $\beta$  but not ER $\alpha$  by selective siRNA can leading to upregulation of P53 and P21, which in turn downregulated cyclinD1, which is G1-checkpoint regulator [42], and led to cell-cycle arrest at the G1 phase in H1650 cells. These findings provide credence for P21-mediation of ER $\beta$ -induced-cell cycle arrest at the G1 phase in H1650 cells.

One major limitation of the present study was small tissue samples. Therefore, it cannot be test the level of ERs protein in both lung cancer tissues as well as tumor free tissues. A further limitation was that a more detailed demonstration of the relationship between the level of GPR30 and lung cancer proliferation was not carried out. This was not completed because of the relatively low expression of GPR30 in lung cancer tissue. A further study with more detail on the correlation between GPR30 and lung cancer should be performed.

## Conclusion

In conclusion, we showed that both ER $\alpha$  and ER $\beta$  play important role in development of NSCLC. ER $\beta$  were involved in proliferation of NSCLC induced by estrogen separately. The discovery of the expression pattern of ERs may open up an opportunity for development of estrogen-based therapy.

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