Abstract

**Purpose:** Interleukin-10 (IL-10) determines virus persistent infection and promotes viral-associated tumor progression via tumor immune escape. However, the role of IL-10 in tumor progression and prognosis in lung adenocarcinoma remains controversial.

**Experimental Design:** To investigate how IL-10 is regulated by HPV E6, IL-10 promoter was constructed to understand which transcriptional factor could be responsible for its transcription. To verify which molecule could be responsible for IL-10-mediated soft agar growth and invasion capability, PCR array and mechanistic strategies were conducted. IL-10 and CIP2A mRNA levels in lung tumors from patients with lung cancer were determined by real-time reverse transcription PCR. The prognostic value of both molecules on survival was estimated by Cox regression model.

**Results:** Mechanistic studies showed that IL-10 protein and mRNA expression was decreased in E6 knockdown TL1 cells and increased in E6-overexpressing TL4 cells. In addition, IL-10 transcription was predominantly regulated by E6-mediated phosphorylation of cAMP response element-binding protein (CREB) and C/enhancer-binding protein β (C/EBPβ) via phosphoinositide 3-kinase (PI3K) signaling pathway. IL-10–mediated tumor aggressiveness in vitro and in vivo occurs through increased CIP2A expression via PI3K signaling pathway. Among patients, IL-10 mRNA expression in lung tumors was positively correlated with CIP2A mRNA expression. Cox-regression analysis showed that IL-10 and CIP2A mRNA levels may independently predict survival in patients with lung adenocarcinoma, especially in patients with E6-positive tumors.

**Conclusion:** IL-10 production from lung tumors and immune cells promotes lung adenocarcinoma aggressiveness and patients with poor survival. We thus suggest that PI3K inhibitor combined with chemotherapy may potentially enhance tumor regression and improve patients’ outcome and life quality.

**Introduction**

Interleukin-10 (IL-10) belongs to T helper 2 cytokine for anti-inflammation and it also inhibits T-cell immunity to block tumor immune surveillance (1–3). Most studies have indicated that IL-10 expression in immune cells, including macrophages, infiltrating T lymphocytes, and NK cells, promotes progression of tumors in kinds of cancer types including lung cancer (4, 5). In lung cancer cases, some reports have indicated that loss of IL-10 in lung tumors may promote tumor progression and result in poor clinical outcomes in patients; however, an opposite effect has been reported in other studies (6–8). Interestingly, the absence of IL-10 expression has been associated with poor outcome in stage I lung cancer, whereas in late-stage lung cancer, the presence of IL-10–positive macrophages at the tumor margins can be an indicator of poor prognosis (6–8). In addition, shorter survival times have been reported in patients with advanced lung cancer who had high serum IL-10 levels, when compared with similar patients who had low serum IL-10 levels (8). Therefore, the role of IL-10 in lung tumorigenesis remains elusive.

The infection of human papillomavirus (HPV) 16/18 has been documented to associate with cancers of squamous epithelia. However, in Taiwan, HPV16/18 infection rate was significantly higher in lung squamous cell carcinoma (9, 10). A high HPV infection rate in Taiwanese lung cancer reflects the possibility that imbalanced immune function might play an important role in

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The role of interleukin-10 (IL-10) in tumor progression and prognosis of lung adenocarcinoma remains controversial. In this study, we provided evidence to show that IL-10 production from E6-positive lung cancer cells via phosphoinositide 3-kinase (PI3K)/AKT signaling pathway directly promotes cell proliferation, soft agar growth, cell invasion, and xenograft tumor formation. In addition, CIP2A induced by IL-10 via PI3K/AKT pathway is responsible for IL-10-mediated cell invasion. Among patients with lung adenocarcinoma, those with high IL-10 and CIP2A mRNA expression detected in tumors had poorer survival and relapse than those with low IL-10 and CIP2A mRNA detected in tumors. Therefore, we suggest that PI3K/AKT inhibitor combined with chemotherapy may be potentially useful to reduce tumor progression and consequently to improve drug sensitivity and clinical outcome in patients with high IL-10 mRNA levels.

Materials and Methods

Study subjects

This study consisted of 98 patients with lung cancer. All patients were unrelated ethnic Chinese and residents of central Taiwan. The inclusion criteria for patients were: primary diagnosed with lung adenocarcinoma; no metastatic disease at diagnosis; no previous diagnosis of carcinoma; no neoadjuvant treatment before primary surgery; no evidence of disease within 1 month of primary surgery. Lung tumor specimens were collected by surgical resection, and surgically resected tissues were stored at -80°C at the Division of Thoracic Surgery, Taichung Veterans General Hospital. Patients were consecutively recruited between 1993 and 2004. This study was approved by the hospital's Institutional Review Board (Institutional Review Board, Chung Shan Medical University Hospital; CSMUH No: CS11177). The TNM stage, tumor type, and stage of each collected specimen were histologically determined according to the WHO classification system. The age of all patients was between 26 and 84 years (mean ± SD: 64.2 ± 11.2). Clinical parameters and overall survival data were collected from chart review and the Taiwan Cancer Registry, Department of Health, Executive Yuan, China. The survival time was defined to be the period of time from the date of primary surgery to the date of death. The median follow-up time after surgery was 21.5 months and the median overall survival of all patients was 21.9 months. During this survey, 63 patients died. On the basis of the follow-up data, 35 patients relapsed (15 had local recurrence, 35 had distant metastasis, and 11 had local and distant metastasis). Among these patients, tumors frequently relapsed in the lung (15 patients) and metastasized in the bone (13 patients), brain (10 patients), liver (5 patients), pleura (4 patients), chest wall (3 patients), and mediastinum (1 patient). In total, 11 patients had tumors that metastasized to more than one organ.

Cell culture

SiHa, HeLa, C33A, A549, and H1299 cancer cell lines were obtained from The American Type Culture Collection (ATCC; ref. 18). TL1, TL2, and TL4 cells were kindly provided by Dr. Cheng YW (10). All of these 3 cell lines are p53 wild type. TL1 and TL2 cell lines are HPV16 E6 positive and TL4 is HPV E6 negative. Cells were cultured and stored according to the suppliers’ instructions.

Genomic DNA extraction from tissues and cells

Genomic DNA was extracted from tissues and cell lines by conventional methods, as described previously (19).

RNA extraction and cDNA synthesis from tumor tissues and cells

RNA extraction and cDNA synthesis were conducted as described previously (19).

Real-time RT-PCR

The detail method was described previously (19). Real-time RT-PCR primers are listed in Supplementary Table S1.
There is no clinically defined cutoff point of IL-10 and CIP2A mRNA expression level, and the median value of both gene mRNA expression levels in lung tumors was used to categorize the study population into "low" and "high" expression groups.

**Immunohistochemical staining**

Immunohistochemical (IHC) staining to evaluate HPV16/18 E6 expression in tumor tissues was conducted as described previously (10). Briefly, formalin-fixed and paraffin-embedded specimens were sectioned at a thickness of 3 μm. Sections were deparaaffinized in xylene, rehydrated through serial dilutions of alcohol, and washed in PBS, the buffer which was used for all subsequent washes. Sections were heated in a microwave oven twice for 5 minutes in citrate buffer, and then incubated with polyclonal anti-HPV16 or HPV18 E6 antibody (Santa Cruz Biotechnology and Chemicon International, Inc.) for 90 minutes at 25°C. The conventional streptavidin peroxidase method (DAKO, LSAB Kit K675) was conducted to develop signals and the cells were counterstained with hematoxylin. Negative E6 immunostaining was defined to be with 0% to 10% positive nuclei, and cases with more than 10% positive nuclei were decided to be positive for E6 immunostaining. Three observers independently evaluated the intensities of the signals.

**Plasmid construction, transfection, and stable clone selection**

IL-10 shRNA was purchased from National RNAi Core Facility. The expression vector of HPV16 E6 and RNA interference target sequences for HPV16 E6 shRNA have been previously verified (18). Nonspecific shRNA control (NC) of scramble sequence was used as the control in the knockdown experiment and vector control (VC) was used as the control of HPV E6 overexpression. The procedures and methods were as described previously (19).

**CIP2A reporter plasmid**

The CIP2A-Luc plasmid was constructed by inserting a 972, 452, or 162 bps XhoI/KpnI fragment into an XhoI/KpnI-treated pGL3 vector (Promega). The primer sequences are listed in Supplementary Table S1.

**Cell doubling time, Migration, invasion assay, and anchorage-independent soft agar growth**

The procedures and methods were as described previously (18). In anchorage-independent soft agar growth assay, the colonies larger than 150 μm in diameter were counted.

**Chromatin immunoprecipitation assay**

Chromatin immunoprecipitation (ChIP) analysis was conducted as described in previous reports (18). The primers are listed in Supplementary Table S1.

**Animal model**

BALB/cAnN.Cg-Foxn1nu/CrlNarl mice were maintained in a standard mouse facility at Chung Shan Medical University (Taichung, Taiwan). When these nude mice were 7 weeks of age, nonspecific shRNA control and IL-10 knockdown TLL1 stable cells were injected via the tail vein (1 × 10⁶). The mice were then sacrificed after 4 months. The tumor nodules (diameter >1 mm) on the surface of lung were counted. Some tumor nodules were frozen at −80°C for the determination of IL-10 expression by real-time RT-PCR. The remaining lung specimens were stained with hematoxylin and eosin (H&E) and the pathology was confirmed by pathologists.

**Nested PCR**

Tumor genomic DNA was extracted from the tumor portion of whole-mount paraffin sections. SiHa and HeLa cervical cancer cells were used as positive controls for the detection of HPV16 and HPV18 DNA, and PBS was used as a negative control. HPV viral DNA was first amplified with type consensus primers MY09 and MY11 followed by a second round of amplification with type-specific primers flanking the L1 region to identify the subtype. The detailed procedures were described previously (9).

**Protein extraction from cells and Western blotting**

The procedures and methods were as described previously (18).

**Chemicals and antibodies**

PD153035 was purchased from Calbiochem. All other chemicals were acquired from Sigma Aldrich. Anti-IL-10Ra (C-20), anti-CIP2A (HL1916), anti-p-CREB (Ser133), anti-CREB (Thr217), and anti-c-Myc (9E10) antibodies were purchased from Santa Cruz Biotechnology, Inc. Anti-Akt and anti-p-Akt (Ser 473) antibodies were purchased from Cell Signaling Technology. Anti-human IL-10 antibody (MAB2171) was purchase from R & D Systems, Inc. The antibody for p53 (BP53-12), β-actin, and secondary antibodies were purchased from Sigma Aldrich.

**Statistical analysis**

All statistical analyses were conducted using the SPSS statistical software program as described previously (version 11.0; SPSS, Inc.; refs. 18, 19). Median survival time and 5-year survival rate for the whole-test set were estimated using the Kaplan–Meier product limit method. Multivariate and univariate Cox regression analysis were conducted to assess the prognostic value of IL-10 and CUP2 mRNA expression level with or without adjustment of the parameters including age, gender, smoking history, and tumor stage. All statistical tests were 2-sided and P values less than 0.050 were considered to be statistically significant.

**Results**

IL-10 expression was higher in E6-positive lung cancer cells than in E6-negative lung cancer cells

We explored whether IL-10 expressed from lung tumors could promote tumor progression by enrolling a panel of lung cancer cells to evaluate IL-10 protein and mRNA expression. IL-10 protein and mRNA expression was higher
IL-10 Promotes Tumor Aggressiveness via CIP2A

in HPV16 E6-positive TL1 and TL2 than in E6-negative lung cancer cells (Fig. 1A). Higher expression was also found in E6-positive SiHa and HeLa cervical cancer cells than in E6-negative C33A cervical cancer cells (Fig. 1A). Therefore, E6 seemed to promote IL-10 expression.

Knockdown and overexpression of E6, by shRNA and a cDNA plasmid, respectively, were then used to examine whether IL-10 expression could be modulated by E6 in TL1 and TL4 cells. E6 expression was decreased and p53 expression was increased by E6 knockdown in TL1 cells. Conversely, E6 expression was increased and p53 expression was decreased by E6 overexpression in TL4 cells (Fig. 1B). In addition, IL-10 protein expression was modulated by E6 knockdown or overexpression in a pattern consistent with the IL-10 mRNA levels found in TL1 or TL4 cells (Fig. 1B). Therefore, IL-10 induction due to E6 oncprotein expression in lung cancer cells might occur through transcriptional activation.

Upregulation of IL-10 by E6 is mediated through PI3K/AKT signaling pathway

We verified which signaling pathway might be linked with E6-induced IL-10 transcription by using different specific inhibitors. Western blotting data showed that IL-10 expression was significantly reduced in a dose-dependent manner in TL1 cells treated with wortmannin or LY294002 (PI3K inhibitors), and was slightly decreased by treatment with PD153035 (an EGFR inhibitor); however, IL-10 expression was not changed by treatment with PD98059 or U0126 (MEK inhibitors) or BAY11-7082 (a NF-κB inhibitor; Fig. 2A, upper panel). We further tested whether IL-10 production in E6-positive cells was mediated through PI3K/AKT pathway by treating TL1 and E6-overexpressing TL4 cells with LY294002 and wortmannin. IL-10 expression was reduced in a dose-dependent manner in both cell types by LY294002 and wortmannin (Fig. 2A, bottom).

We then explored which transcriptional factor(s) might be responsible for IL-10 transcription by using software analysis to predict the putative binding sites of transcription factors (http://www.genome.jp/tools/motif/). As shown in Fig. 2B, the IL-10 promoter (−858 to +1) had putative binding sites of C/enhancer-binding protein α (C/EBPα), C/EBPβ, C/EBPδ, C/EBPε, and MZF-1 (Fig. 2B, top). Three promoter regions for the IL-10 gene (−855 to +1, −458 to +1, and −349 to +1) were constructed for evaluation of luciferase reporter activity. Separately transfected each of these 3 promoters into TL1 cells resulted in activities of the −458 to +1 and −349 to +1 promoters that were 95% and 38%, respectively, of the reporter activity of −855 to +1 promoter. This finding suggests that C/EBPβ and CREB, located at −458 to −349 promoter region, might play an important role in IL-10 transcription. The luciferase reporter activity of the −458 to +1 promoter in TL1 cells was markedly reduced by E6 knockdown and by the inhibitors of PI3K, but to a lesser extent by inhibitors of the EGFR signaling pathway (Fig. 2B, bottom). This suggested a crucial role for phosphorylation of CREB and C/EBPβ, via the PI3K/AKT signaling pathway, in IL-10 transcription.
Figure 2. CREB and C/EBPβ may be responsible for IL-10 transcription via PI3K pathway in TL1 and TL4 cell lines. A, TL1 cells were treated with MEK (PD98059, 20 μmol/L and U0126, 10 μmol/L), EGFR (PD153035, 0.5 μmol/L), NF-κB (BAY11-7082, 20 μmol/L), and PI3K inhibitors (LY294002, 30 μmol/L and wortmannin, 10 μmol/L) and protein expression of IL-10, AKT, p-AKT, and β-actin was measured by Western blot. TL1 cells were treated with PI3K inhibitors at various concentrations as indicated. TL4 cells were transfected with 3 μg HPV16 E6 cDNA plasmid or vector control plasmid for 48 hours. The medium was renewed and then those cells were treated with PI3K inhibitors at various concentrations as indicated. Protein expression was measured by Western blot. B, diagram summarized the positions of the putative binding sites of transcriptional factors on IL-10 promoter constructs (−855 to +1) predicted by software analysis. Luciferase reporter assay was conducted to evaluate the promoter activity of these 3 constructs including −855 to +1, −458 to +1, and −349 to +1. TL1 cells were transfected with these 3 promoter constructs separately and β-gal was served as an internal control. The luciferase reporter activity of these 3 constructs was determined and the reporter activity of IL-10 (−349 to +1) construct was served as control (activity = 1) for presentation. Luciferase reporter assay was conducted to measure the promoter activity of IL-10 (−458 to +1) construct in TL1 cells, which were transfected with HPV E6 shRNA or treated with EGFR or PI3K inhibitors as indicated. TL1 cells transfected with IL-10 (−458 to +1) construct were treated with E6 shRNA, EGFR (PD153035, 0.5 μmol/L), and PI3K inhibitors (LY294002, 30 μmol/L and wortmannin, 10 μmol/L) for 48 hours, and then were determined to the
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reporter activity by luciferase reporter assay, 
β-gal was served as an internal control. C, TL1 cells were treated with EGFR (PD153035, 0.5 μmol/L) and PI3K inhibitors (LY294002, 30 μmol/L, and wortmannin, 10 μmol/L). Phosphorylated CREB (p-CREB), total CREB, p-C/EBP/β, and total C/EBP/β expression levels were evaluated by Western blot, and β-actin was used as a protein-loading control. ChIP assay was conducted to evaluate the DNA binding ability of p-CREB and p-C/EBP/β on the putative binding site of IL-10 promoter region. TL1 cells were treated with EGFR (PD153035, 0.5 μmol/L) and PI3K inhibitors (LY294002, 30 μmol/L, and wortmannin, 10 μmol/L) and fixed for ChIP assay. The products were amplified by PCR and the result was presented by gel-electrophoresis. Experiments in this figure were repeated at least 3 times and similar results were obtained.

Figure 3. IL-10 promotes the capability of soft-agar growth, invasiveness, and lung tumor nodule formation in nude mice in TL1 and TL4 cells. A, shRNA and cDNA plasmid of IL-10 were, respectively, transfected into TL1 and TL4 cells, and then IL-10 protein expression was determined by Western blot and β-actin was used as a protein loading control. B, Matrigel invasion and soft-agar colony formation assay were used to evaluate the invasiveness and soft-agar growth capability after TL1 cells transfected with IL-10 shRNA and TL4 cells transfected with IL-10 cDNA plasmid as compared with their control cells. The results were shown as representative pictures in the left and as the quantitative graph in the right. C, IL-10 and β-actin protein expression of stable clones was shown on the top. NC and IL-10 knockdown TL1 stable cells were injected into nude mice via tail vein (1 × 10⁶). The mice were sacrificed after 4 months (N = 5 for each group). Pictures of the tumor nodules formed in mice lung and quantitative graphs are shown (P = 0.0003). Experiments of Fig. 2A and B were repeated at least 3 times and similar results were obtained.

Phosphorylation of CREB and C/EBP/β by E6 via PI3K/AKT signaling pathway plays a crucial role in IL-10 transcription

We next questioned whether phosphorylation of CREB and C/EBP/β by E6, via the PI3K/AKT pathway, could play an important role in E6-mediated IL-10 transcription. Western blotting data showed that levels of phosphorylated CREB and C/EBP/β protein were markedly reduced by PI3K inhibitors (LY294002 and wortmannin), but the total protein levels of CREB and C/EBP/β were not changed by these inhibitors. As expected, the phosphorylation of both proteins was decreased by treatment with an EGFR inhibitor (PD98059; Fig. 2C, left). ChIP analysis further indicated that the DNA binding activities of CREB and C/EBP/β were diminished by PI3K inhibitors, but not by the EGFR inhibitor (Fig. 2C, right). Therefore, phosphorylation of CREB and C/EBP/β via PI3K/AKT signaling pathway seemed to play a crucial role in E6-mediated IL-10 transcription in lung cancer cells.

IL-10 induced by E6 is responsible for soft-agar growth, invasion, and xenograft tumor nodule formation

We used soft-agar colony formation and Boyden chamber assays to explore whether IL-10 induced by E6 could promote anchorage independent soft-agar growth and invasiveness, respectively. As expected, IL-10 expression was reduced in IL-10 knockdown TL1 cells and elevated in IL-10 overexpressing TL4 cells (Fig. 3A). The doubling time was significantly elevated in IL-10 knockdown TL1 cells and reduced in IL-10 overexpressing TL4 cells (23.4 ± 0.2, 26.1...
± 0.5, and 35.1 ± 1.0 for IL-10 knockdown TL1; 30.1 ± 0.3, 25.8 ± 0.3, and 20.6 ± 1.5 for IL-10–overexpressing TL4; Supplementary Fig. S1). The representative soft-agar growth colony sizes decreased markedly in IL-10 knockdown TL1 cells and increased in IL-10 overexpression TL4 cells when compared with nonspecific shRNA control and vector control cells (Fig. 3B). The capability for soft-agar growth and invasiveness was significantly reduced in IL-10 knockdown TL1 and elevated in IL-10 overexpressing TL4 cells in a dose-dependent manner when compared with nonspecific shRNA control and vector control cells (Fig. 3B). We further established a stable clone of IL-10 knockdown TL1 cells, in which IL-10 expression had almost disappeared (Fig. 3C). We then injected nude mice with these clonal cells via the tail vein to determine whether a lower number of lung tumor nodules would form after 4 months, compared with injection with nonspecific shRNA control cells. The number of tumor nodules was significantly lower in nude mice injected with the IL-10 knockdown stable clone than in nude mice injected with nonspecific shRNA control cells (10.5 ± 7.6 vs. 26.5 ± 6.7; \( P = 0.003 \); Fig. 3C). Therefore, IL-10 expression induced by E6 oncoprotein may be responsible for soft-agar growth, invasion, and xenograft tumor nodule formation.

**IL-10 promotes tumor aggressiveness via upregulation of CIP2A**

We explored the underlying mechanism of tumor aggressiveness induced by IL-10, using a PCR-array to examine which molecule might involve in IL-10-induced tumor progression. PCR-array analysis showed a marked decrease in c-Myc expression in IL-10 knockdown TL1 cells compared with expression in nonspecific shRNA control cells among the 94 gene examined. c-Myc expression has been shown to be regulated by a CIP2A-PP2A axis (20). Therefore, we expected that the IL-10 induced by E6 might upregulate CIP2A, thereby contributing to c-Myc expression and consequently promoting tumor aggressiveness. Western blot analysis showed that c-Myc and CIP2A expressions were concomitantly decreased in IL-10 knockdown TL1 cells and increased in IL-10 overexpressing TL4 cells (Fig. 4A). The elevated expression of c-Myc and CIP2A by E6 was restored by IL-10 knockdown in E6-transfected TL4 cells (Fig. 4A). Interestingly, CIP2A mRNA expression was consistent in its protein expression in IL-10 knockdown TL1, E6-transfected TL4, and IL-10-knockdown E6-transfected TL4 cells, suggesting that IL-10 could transactivate CIP2A transcription in E6-positive lung cancer cells (Fig. 4A).

**Phosphorylation of CREB via PI3K/AKT pathway is responsible for IL-10–mediated CIP2A transcription**

We next examined which signaling pathway might be linked with the upregulation of CIP2A transcription induced by IL-10. Three promoters of the CIP2A gene (−972 to +1, −452 to +1, and −162 to +1) were constructed: the putative transcriptional factors on these promoter regions are shown in Fig. 4B (top). These promoters were transfected into TL1 cells to verify which promoter region might be more important for CIP2A transcription. The luciferase reporter activity assays indicated that the −452 to +1 promoter had 71% of the reporter activity of the −972 to +1 promoter, whereas the −162 to +1 promoter had only 11% of the reporter activity of −972 to +1 promoter (Fig. 4B, middle). This finding suggests that CREB, NF-kB, and AP-1 might be involved in CIP2A transcription.

The reporter activity of the −452 to +1 promoter in TL1 cells was markedly suppressed by E6 knockdown, LY294002, and wortmannin, but not by PD153035. Therefore, we expected that the PI3K/AKT pathway might be involved in IL-10–mediated CIP2A transcription via phosphorylation of CREB. Western blot analysis indicated that the total CREB protein expression was not changed by E6 knockdown or by treatment of different inhibitors, but expression of phosphorylated CREB protein almost disappeared after treatment with LY294002 and wortmannin followed by E6 and IL-10 knockdown and PD98059. ChIP analysis further confirmed that phosphorylated CREB was bound to the CIP2A promoter (Fig. 4C). Phosphorylation of CREB therefore clearly played a crucial role in IL-10–mediated CIP2A transcription. We further verified whether IL-10–mediated CIP2A could be responsible for IL-10–induced cell invasion. TL4 cells were transfected with 2 doses of IL-10. Western blotting showed that CIP2A and c-Myc expression was concomitantly increased by IL-10 transfection in a dose-dependent manner (Fig. 4D top). The invasion capability of TL4 cells was significantly elevated by IL-10 transfection (Fig. 4D bottom). However, the invasion capability of IL-10–transfected TL4 cells was restored by CIP2A knockdown (Fig. 4D, bottom). This result clearly indicates that CIP2A is responsible for IL-10–mediated cell invasion.

**IL-10 mRNA expression levels are positively correlated with HPV16/18 E6 oncoprotein and CIP2A mRNA expression in tumors of patients with lung adenocarcinoma**

We verified whether IL-10 expression could be associated with HPV16/18 E6 oncoprotein expression by evaluating IL-10 mRNA expression levels and E6 oncoprotein levels in lung tumors from 98 patients with lung adenocarcinoma using real-time RT-PCR and immunohistochemistry. The distribution and prognostic value of parameters of patients were summarized in Supplementary Table S2. Univariate analysis showed that patients with advanced stage (II, III), higher T-value (T3, T4), and advanced nodal involvement (N1, N2) had shorter overall survival periods than with early stage (I), lower T-value (T1, T2), and nonnodal involvement (N0; \( P = 0.004 \) for stage, \( P = 0.001 \) for T, and \( P = 0.002 \) for N; Supplementary Table S2). As shown in Supplementary Table S3, IL-10 mRNA expression levels were higher in E6-positive tumors than in E6-negative tumors (168.1 ± 40.5 vs. 64.7 ± 24.5; \( P = 0.032 \); Supplementary Table S3). We next examined whether IL-10 expression could be related to CIP2A expression in lung tumors.
Figure 4. IL-10 upregulates CIP2A transcription by CREB phosphorylation via PI3K/AKT pathway in TL1-E6-positive and E6-negative TL4 cells. A, shRNA and cDNA plasmid of IL-10 were, respectively, transfected into TL1 and TL4 cells and various concentrations of IL-10 shRNA transfection in both cells were as indicated. Protein expression of HPV E6, IL-10, CIP2A, and c-Myc was determined by Western blot and β-actin was used as a protein loading control. The change of CIP2A mRNA expression levels was evaluated by real-time RT-PCR in IL-10 knockdown TL1 cells and E6-overexpressed TL4 cells and then transfected with IL-10 shRNA. B, diagram summarized the positions of the putative binding sites of transcriptional factors on CIP2A promoter constructs (-972 to +1) predicted by software analysis. Luciferase reporter assay was conducted to evaluate the promoter activity of these 3 constructs including -972 to +1, -452 to +1, and -162 to +1. TL1 cells were transfected with these 3 promoter constructs separately and β-gal was served as an internal control. C, TL1 cells were transfected with 5 μg HPV E6, IL-10, or NC shRNA; treated with EGFR (PD153035, 0.5 μmol/L) or PI3K inhibitors (LY294002, 30 μmol/L, and wortmannin, 10 μmol/L). Protein expression of p-CREB, total CREB, and β-actin was measured by Western blot. ChIP assay was conducted to evaluate the DNA binding ability of CREB on CIP2A promoter (-425 to -346). Transfected or inhibitor-treated TL1 cells were fixed for ChIP assay. The products were amplified by PCR and the result was presented by gel-electrophoresis. D, shRNA plasmid of CIP2A was, respectively, transfected into TL4 cells and various concentrations of IL-10 shRNA transfection in both cells were as indicated. Protein expression of IL-10, CIP2A, and c-Myc was determined by Western blot and β-actin was used as a protein loading control. Matrigel invasion assays were used to evaluate the invasiveness after TL4 cells were transfected with IL-10 cDNA and CIP2A shRNA plasmid as compared with their control cells. Experiments in this figure were repeated at least 3 times and similar results were obtained.
Real-time RT-PCR analysis showed that CIP2A mRNA expression was significantly higher in tumors expressing high levels of IL-10 mRNA than in tumors expressing low levels (424.4 ± 85.5 vs. 188.5 ± 50.9; \( P = 0.020 \)). These in vivo observations in lung tumors from patients with lung adenocarcinoma were consistent with the earlier in vitro findings in lung cancer cell cultures.

**IL-10 mRNA and CIP2A mRNA expression may independently predict survival in patients with lung adenocarcinoma**

Kaplan–Meier analysis showed that patients with high IL-10 mRNA and CIP2A mRNA tumors had shorter overall survival than those with low IL-10 mRNA and CIP2A mRNA tumors (Supplementary Fig. S2A). The prognostic significance of IL-10 and CIP2A mRNA levels was observed in patients with E6-positive tumors (Supplementary Fig. S2B), not in patients with E6-negative tumors (Supplementary Fig. S2C). Multivariate Cox regression analysis was used to estimate whether IL-10 and CIP2A mRNA expression level could independently predict survival in patients with lung adenocarcinoma. As expected, patients with stage II–III tumors had shorter median survival and lower 5-year survival percentage than did patients with stage I tumors (19.2 vs. 79.3 months and 18.3 vs. 57.4%; \( P = 0.003 \); Table 1). Patients with high IL-10 mRNA levels had poorer survival than those with low IL-10 mRNA levels (HR: 2.083, 95% CI: 1.241–3.495, \( P = 0.005 \); Table 1; Supplementary Fig. S2). In addition, poorer survival was found in patients with high CIP2A mRNA levels than in patients with low CIP2A mRNA levels (HR: 1.809, 95% CI: 1.063–3.079, \( P = 0.020 \); Table 1; Supplementary Fig. S2). Therefore, shorter median survival and lower 5-year survival rates were observed in patients with high IL-10 and CIP2A mRNA levels in tumor than in those with low IL-10 and CIP2A mRNA levels in tumor. Moreover, the prognostic significance of IL-10 mRNA and CIP2A mRNA expression levels was seen only in patients with E6-positive tumors and not in patients with E6-negative tumors (Table 2; Supplementary Fig. S1). We further confirm the finding by the presence or absence of HPV 16/18 DNA in this study population. The prognostic significance of IL-10 mRNA and CIP2A mRNA levels were also observed in patients with HPV 16/18 DNA-positive tumors and not in patients with HPV 16/18 DNA-negative tumors (Supplementary Table S4). These clinical observations for patients with lung adenocarcinoma were consistent with the findings from the mechanistic studies in cell models. Therefore, we suggest that IL-10 and CIP2A mRNA may independently predict survival in patients with lung adenocarcinoma.

**Discussion**

Early studies reported that IL-10 is commonly expressed in human lung tumors and suggest that it may play an active immunoregulatory role in the lung tumor microenvironment (2, 21–25). IL-10 is considered to be an autocrine growth factor of immune cells, and it participates notably in increases of tumor cell proliferation of melanoma, gastric, and thyroid cancers (26, 27). The majority of reports indicate that IL-10 produced from immune cells may promote lung cancer growth via suppressing immune surveillance (28, 29). This suppression is due to defected function of both \( T \) cells and antigen presenting cells (2). No evidence has yet shown that IL-10 expressed in tumor cells could promote tumor progression. Therefore, the nature of IL-10–promoted tumor malignancy of lung cancer cells, i.e., whether it occurs via an autocrine or paracrine pathway, is still unclear. In the present study, we provided the molecular evidence to show that IL-10 is induced by HPV E6 oncoprotein and acts as an autocrine growth factor that not only promotes lung cancer growth, but also promotes anchorage-independent soft-agar growth and invasiveness (Fig. 3). We also tested the effect of exogenous IL-10 on migration capability of lung cancer cells. As expected, the capability was decreased by IL-10 neutralized antibody in TL1 cells, but the capability was increased by IL-10 recombinant protein in TL4 cells (Supplementary Fig. S3). The autocrine regulation of cell growth by IL-10 is mediated through the IL-10 receptor (IL-10R). The results presented here for TL1 cells consistently showed that the capability for

**Table 1. Multivariate analysis of the influence of IL-10 and CIP2A on overall survival in patients with lung adenocarcinoma**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Case no.</th>
<th>Median survival, mo</th>
<th>5-year Survival, %</th>
<th>HR (95% CI)</th>
<th>( P )</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Stage</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>I</td>
<td>32</td>
<td>79.3</td>
<td>57.4</td>
<td>1.000 (Ref)</td>
<td>0.003</td>
</tr>
<tr>
<td>II and III</td>
<td>66</td>
<td>19.2</td>
<td>18.3</td>
<td>2.498 (1.373–4.546)</td>
<td></td>
</tr>
<tr>
<td><strong>IL-10</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Low</td>
<td>49</td>
<td>34.2</td>
<td>36.8</td>
<td>1.000 (Ref)</td>
<td>0.005</td>
</tr>
<tr>
<td>High</td>
<td>49</td>
<td>17.2</td>
<td>23.8</td>
<td>2.083 (1.241–3.495)</td>
<td></td>
</tr>
<tr>
<td><strong>CIP2A</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Low</td>
<td>49</td>
<td>42.2</td>
<td>40.2</td>
<td>1.000 (Ref)</td>
<td>0.029</td>
</tr>
<tr>
<td>High</td>
<td>49</td>
<td>19.2</td>
<td>19.8</td>
<td>1.809 (1.063–3.079)</td>
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migration and invasion promoted by IL-10 could be diminished by IL-10R knockdown (Supplementary Fig. S4). This strongly suggests that IL-10 induced by E6 can directly promote lung cancer cell invasiveness and soft-agar growth via the autocrine loop of IL-10/IL-10R.

IL-10 may play a dual role in the development and progression of human cancers (30). A recent report showed that IL-10 deficiency increases chemical-induced tumor incidence, growth, and foci formation in IL-10 knockout C57BL/6 mice compared with wild-type mice in a colitis-associated colon cancer model (31). The authors further indicated that IL-10 deficiency increases the numbers of myeloid-derived suppressor cells in which high levels of IL-1β was expressed to block tumor growth (31). In melanoma, IL-10 has been shown to suppress tumor growth and metastasis via inhibition of angiogenesis, indicating an antitumor action of IL-10 (32). However, in animal models and in human tumors, IL-10 was shown to promote metastatic potential in lung tumor cells in vivo by promoting angiogenesis and resistance to apoptosis (22, 33). IL-10 is not only expressed by tumor cells but also expressed by different types of immune cells (4, 5). The limitation of this study is to quantify the IL-10 expression from tumor cells, and to exclude IL-10 expression from the surrounding nontumor and immune cells. In the present study, tumor tissues from patients with lung cancer were obtained from the frozen section of surgically resected lung tumor parts according to the pathology examination. Therefore, we considered that IL-10 was largely expressed from tumor cells. Elevation of serum or tumor-expressed IL-10 may independently predict poor prognosis in patients with advanced lung cancer (8, 34). Moreover, after chemotherapy, patients whose serum IL-10 levels were stable or elevated showed a greater risk of tumor recurrence and distant metastasis, and of chemoresistance, when compared with patients with lower serum IL-10 expression (8). Our results seem to support this observation as we found that tumor-derived and exogenous IL-10 may promote tumor aggressiveness and poor outcome in patients with lung adenocarcinoma who had HPV 16/18 E6-positive tumors.

Upregulation of IL-10 production by phosphorylation of CREB via the PI3K/AKT pathway has been shown in immune cells such as monocytes and macrophages (35, 36). Notably, HPV E6 upregulates cIAP2 via the EGFR/PI3K/AKT cascades, and in turn contributes to cisplatin resistance in HPV-associated lung cancer. These results give the clue that HPV E6 might regulate IL-10 expression in lung cancer via the PI3K/AKT signaling pathway (37). In the present study, IL-10 production in E6-positive lung cancer cells was predominantly regulated by phosphorylation of CREB via the PI3K/AKT signaling pathway (Fig. 2). Unexpectedly, IL-10 was able to activate CIP2A transcription via the phosphorylation of CREB induced by the PI3K signaling pathway and also promoted tumor malignancy (Fig. 4). CIP2A has been shown to have an oncogenic role in human malignancies, operating via inactivation of PP2A and stabilization of c-Myc protein (20). CIP2A overexpression has been associated with poor prognosis in various human carcinomas,

### Table 2. Multivariate analysis of the influence of IL-10 and CIP2A mRNA on overall survival in patients with HPV E6-positive lung adenocarcinoma

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Case no.</th>
<th>Median survival, mo</th>
<th>5-year Survival, %</th>
<th>HR (95% CI)</th>
<th>P</th>
</tr>
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<tr>
<td>E6 Positive</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Stage</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>I</td>
<td>16</td>
<td>83.8</td>
<td>56.3</td>
<td>1.000 (Ref)</td>
<td>0.044</td>
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<tr>
<td>II and III</td>
<td>29</td>
<td>22.8</td>
<td>23.1</td>
<td>2.449 (1.026-5.850)</td>
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<td>IL-10</td>
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<td></td>
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</tr>
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<td>Low</td>
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<td>55.4</td>
<td>41.7</td>
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<td>0.009</td>
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<tr>
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<td>23</td>
<td>16.6</td>
<td>25.4</td>
<td>3.096 (1.333-7.193)</td>
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<td>CIP2A</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Low</td>
<td>20</td>
<td>55.4</td>
<td>48.1</td>
<td>1.000 (Ref)</td>
<td>0.016</td>
</tr>
<tr>
<td>High</td>
<td>25</td>
<td>26.1</td>
<td>21.7</td>
<td>3.152 (1.236-8.038)</td>
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<tr>
<td>E6 Negative</td>
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<td></td>
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</tr>
<tr>
<td>Stage</td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>I</td>
<td>16</td>
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<td>60.9</td>
<td>1.000 (Ref)</td>
<td>0.025</td>
</tr>
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<td>II and III</td>
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<td>2.762 (1.138-6.701)</td>
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<tr>
<td>IL-10</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Low</td>
<td>27</td>
<td>20.4</td>
<td>33.4</td>
<td>1.000 (Ref)</td>
<td>0.159</td>
</tr>
<tr>
<td>High</td>
<td>26</td>
<td>17.5</td>
<td>19.2</td>
<td>1.618 (0.829-3.158)</td>
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<tr>
<td>CIP2A</td>
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<td></td>
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<tr>
<td>Low</td>
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<td>31.2</td>
<td>33.6</td>
<td>1.000 (Ref)</td>
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<tr>
<td>High</td>
<td>24</td>
<td>17.5</td>
<td>20.4</td>
<td>1.545 (0.778-3.068)</td>
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</table>
including lung cancer (38–40). A prognostic value of CIP2A and IL-10 mRNA levels was also indicated in the present study population (Table 1). Moreover, the correlation of CIP2A with IL-10 expression in lung tumors was also supported by our mechanistic studies from lung cancer cell models (Fig. 4).

Recently, ectopic CIP2A expression in hepatocellular carcinoma and head and neck squamous cell carcinoma cells has been suggested to enhance PI3K/AKT activation (41, 42). Therefore, it is conceivable that a feedback loop of IL-10–CIP2A–phosphorylated–CREB may be involved in the progression of E6-mediated IL-10 lung adenocarcinoma. Previous studies indicated that a proteasome inhibitor, bortezomib, significantly reduced CIP2A expression and increased apoptosis in hepatocellular carcinoma and head and neck carcinoma cells (41–45). Therefore, we expected that bortezomib or a PI3K inhibitor could be used to suppress tumor invasiveness and to improve the outcome in patients with HPV-associated lung adenocarcinoma who had high IL-10 expression. In summary, we provide evidence that IL-10–mediated CIP2A may play a crucial role in the tumor aggressiveness of lung adenocarcinoma, particularly in patients with HPV 16/18 E6-positive tumors.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

Authors' Contributions
Conception and design: W.W. Sung, C.Y. Chen, H. Lee
Development of methodology: W.W. Sung
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): W.W. Sung, Y.C. Wang, P.L. Lin, T.C. Wu
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): W.W. Sung, Y.C. Wang, P.L. Lin, Y.W. Cheng
Writing, review, and/or revision of the manuscript: W.W. Sung, H. Lee
Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): W.W. Sung, Y.W. Cheng, C.Y. Chen, T.C. Wu
Study supervision: C.Y. Chen, H. Lee

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References
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