Hypoxia Inducible Factor 1α and Hypoxia Inducible Factor 2α Play Distinct and Functionally Overlapping Roles in Oral Squamous Cell Carcinoma

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Abstract

Purpose: This study aimed to investigate the functional difference between hypoxia inducible factor (HIF)-1α and HIF-2α in oral squamous cell carcinomas (OSCC).

Experimental Design: We evaluated the correlations between HIF-1α and HIF-2α expression and the clinical-pathologic characteristics of 97 patients with OSCC by immunohistochemical staining. OSCC cell lines transfected with lentivirus encoding short hairpin RNA against HIF-1α/2α were used to investigate the HIF-1α/2α–dependent target genes. Xenograft tumors in nude mice were established using cells affected by lentivirus, and tumor growth, angiogenesis, proliferation, and apoptosis were measured.

Results: HIF-1α expression was significantly associated with T stage (P = 0.004), lymph node involvement (P = 0.006), histologic differentiation (P = 0.013), and microvessel density (P = 0.014), whereas that of HIF-2α was associated with T stage (P = 0.011) and microvessel density (P = 0.005). Patients with positive HIF-1α nuclear staining had a significantly worse overall survival (P < 0.001) and disease-free survival (P < 0.001) than those with negative HIF-1α staining. When OSCC cells were cultured at 5% O₂, only HIF-2α contributed to the expression of vascular endothelial growth factor. At 1% O₂, vascular endothelial growth factor was regulated by both HIF-1α and HIF-2α, but glucose transporter 1, carbonic anhydrase 9, and urokinase-type plasminogen activator receptor were regulated by HIF-1α rather than by HIF-2α. Knocking down HIF-1α or HIF-2α individually inhibited the xenograft tumor angiogenesis and growth, and knocking them down simultaneously revealed a better inhibitory effect than knocking down either unit alone.

Conclusions: HIF-1α and HIF-2α correlated with different clinical-pathologic parameters, stabilized at different oxygen levels, and regulated different genes in OSCC. However, both HIF-1α and HIF-2α showed promoting roles in tumor angiogenesis and growth, and therapeutic outcome may benefit from combined targeting of HIF-1α and HIF-2α. Clin Cancer Res; 16(19); 4732–41. ©2010 AACR.
MDA 468 cells (breast cancer; ref. 10). HIF-2α, however, seems to regulate VEGF, GLUT-1, uPAR, and plasminogen activator inhibitor-1 (PAI-1) in RCC4 cells (renal carcinoma; ref. 9), erythropoietin in Hep3B cells (8), and PAI-1 in adenocarcinoma A549 cells (12). Despite these differences, both HIF-1α and HIF-2α showed promoting roles in tumor growth, and simultaneously knocking down HIF-1α and HIF-2α would produce a better inhibitory effect than knocking down HIF-1α or HIF-2α individually. As such, we suggest that therapeutic outcome in terms of inhibiting tumor growth and angiogenesis may benefit from nonselectively targeting HIF-1α and HIF-2α in OSCC. Fortunately, a small-molecule inhibitor, NSC-134754, has been tested to block both HIF-1α and HIF-2α in Von Hippel-Lindau–defective renal carcinoma cells. Whether NSC-134754 can be applied to oral squamous cell carcinomas therapy needs further exploration.

However, contradicting results related to the roles of HIF-1α in oral carcinomas have been reported as well, e.g., HIF-1α overexpression was found to indicate a favorable prognosis of patients with T1 and T2 OSCC (23). Moreover, no study, to the best of our knowledge, has investigated the functional role of HIF-2α in oral carcinomas. Therefore, to better understand the differences between these two HIF-α units, we investigated the correlation between HIF-1α/HIF-2α and clinical-pathologic characteristics in patients with OSCC respectively. We knocked down HIF-1α/HIF-2α by lentivirus encoding short hairpin RNA (shRNA, a sequence of RNA that makes a tight hairpin turn that can be used to silence gene expression via RNA interference) to further address the question as to whether certain genes are preferentially regulated by HIF-1α or by HIF-2α in human OSCC cell lines. Finally, we examined the contribution of HIF-1α/HIF-2α knockdown to the xenograft tumor growth as well as to angiogenesis, proliferation, and apoptosis.

Materials and Methods

Patients and specimens

The cohort was assembled from patients who were histologically diagnosed with OSCC and who underwent radical surgery at West China Hospital of Stomatology, Sichuan University, between 2003 and 2004. Exclusion criteria included recurrence at presentation, preoperative radiotherapy, chemotherapy, or hormone therapy, with residual tumor at surgical margin, and incomplete medical records. We retrospectively reviewed the medical records of patients with OSCC according to the inclusion and exclusion criteria. Finally, 97 patients (52 male and 45 female; median age, 58 years; range 40–79) were recruited in this study. The formalin-fixed, paraffin-embedded specimens from these patients were used for immunohistochemical analysis. Follow-up time was calculated from the date of surgery to the date of death, loss of follow-up, or the 60th month, whichever came first (median follow-up period of 47 months). A total of 36 tumors were early stage (T1/T2), and 61 were late stage (T3/T4). Among 97 cases, 18 with T1 stage received local resection only, 31 with clinically negative nodal involvement underwent radical resection plus selective neck dissection (level I-III), 48 with clinically positive nodal involvement underwent radical resection plus modified radical neck dissection (level I-V), 19 received postoperative radiotherapy, and 20 received postoperative chemotherapy because of their advanced stage. During the whole follow-up period, lymph node metastases were detected histologically in 64 patients. This study was approved by the Institutional Ethics Committee of Sichuan University. The principal clinical and pathologic characteristics of the patient cohort are summarized in Table 1.

Immunohistochemical staining

Sections (4 μm) were deparaffinized in xylene and rehydrated, and endogenous peroxidase was blocked with 3% H2O2. Antigen retrieval was accomplished by 0.01 mol/L
citrate buffer solution (pH 6.0) in a 700 W microwave oven for 15 minutes. After incubation with 5% normal goat serum for 20 minutes, the slides were exposed for 1 hour at 37°C and overnight at 4°C to the mouse anti-HIF-1α (1:200; NOVUS), rabbit anti-HIF-2α (1:100; Abcam), rabbit anti-VEGF (1:200; Santa Cruz), rabbit anti-CA-IX (1:100; Santa Cruz), rabbit anti-GLUT-1 (1:200; Santa Cruz), mouse anti-CD34 (1:100; Zymed), and mouse anti-uPAR (1:100; Santa Cruz). Sections were then incubated with biotinylated goat anti-rabbit IgG/goat anti-mouse IgG (Zhongshan Goldenbridge Biotechnology) for 1 hour, and streptavidin-peroxidase for 30 minutes. The 0.02% diaminobenzidine tetrahydrochloride was used as a chromogen, and the slides were counterstained with hematoxylin. The percentage of positive cells was estimated using an image analysis system (Leica). Microvessel density (MVD) was assessed by microscope as described previously (19). The median values for VEGF, CA-IX, GLUT-1, uPAR, and MDV were regarded as the cutoff values for low and high expression. Nuclear expressions of HIF-1α and HIF-2α were graded as negative and positive.

Cloning, lentivirus preparation, and titration

The Lenti-X shRNA expression system (Clontech) was used for the construction of the lentiviral expression construct according to the manufacturer’s instructions. Short pairs of sense and antisense DNA oligo encoding a sense-loop-antisense sequence to HIF-1α and HIF-2α genes were synthesized for the validated corresponding siRNAs (10), and sequences are listed in Supplementary Table S1. The cDNA oligos were annealed and cloned to the BamH I/EcoR I-digested pLVX-shRNA1 vectors (Clontech). The recombinant vectors were purified and cotransfected with Lenti-X HT packaging Mix (Clontech) into HEK 293T packaging cells using Lipofectamine 2000 (Invitrogen). The virus-containing cell culture supernatants were collected 48 hours after transfection, passed through a 0.45-μm filter, and stored at -80°C. The virus titration was determined using puromycin selection following the manufacturer’s protocol.

Cell culture and virus infection

Two malignant OSCC cells lines, Tca8113 (24) and BcaCD885 (25), were obtained from the State Key Laboratory of Oral Disease, Sichuan University. Cells were cultured in RPMI 1640 medium (Gibco) supplemented with 10% heat-inactivated FCS (Hyclone), 2 mmol/L L-glutamine, 25 mmol/L HEPES, and 100 units/mL penicillin and streptomycin in a humidified 5% CO2 atmosphere. The cells were cultured under 1% O2, 5% O2, and 20% O2 conditions respectively, balanced with N2 in a 3-gas incubator (Binder). After 24 hours, the cells were infected with recombinant lentivirus vectors at a multiplicity of infection of 5.

Immunofluorescence

OSCC cells were seeded onto coverslips at a density of 10^4/mL and cultured in a 6-well culture plate for 24 hours. Cells grown on coverslips were washed in cold PBS and fixed in 2% paraformaldehyde-PBS for 10 minutes, permeabilized in 0.5% Triton X-100 in PBS for 10 minutes at 4°C, and blocked in 1% bovine serum albumin for 30 minutes at room temperature. Cells were incubated overnight with 1:100 dilution of mouse anti-HIF-1α (NOVUS) or 1:100 dilution of rabbit anti-HIF-2α (Abcam), and then incubated with FITC-conjugated goat

Table 1. Clinical-pathologic characteristic of 97 patients with oral squamous cell carcinoma, and the association between HIF-1α/HIF-2α expression and these variables

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anti-mouse/rabbit IgG (1:500; Zhongshan Goldenbridge Biotechnology) at 37°C for 1 hour. Cells were counterstained with 4′, 6-diamidino-2-phenylindole (DAPI; 1 μg/μL), and examined using a fluorescence microscope (Olympus BX51).

Quantitative real-time reverse transcriptase-PCR

Total RNA was isolated with TRIzol reagent (Invitrogen) and treated with RNase-free DNase I (Takara) to avoid genomic DNA contamination. Samples with a 260:280 nm absorbance ratio of ≥1.9 were reverse-transcribed using a RevertAid First-Strand cDNA Synthesis Kit (Fermentas) with random hexamer primer. PCR amplification of the cDNA template was done using Thunderbird SYBR qPCR mix (TOYOBO) on ABI PRISM 7300 sequence detection system (Applied Biosystems). PCR conditions were 95°C for 1 minute followed by 40 cycles of amplification consisting of 95°C for 15 seconds, 55°C for 15 seconds, and 72°C for 1 minute. Reactions were run in triplicate, and results were averaged. Each value was normalized to GAPDH as the housekeeping gene to control for variations in the amount of input cDNA. Supplementary Table S1 shows the sequences of PCR primers used in this study. The relative expression level of the genes was calculated using the ΔΔCt method comparing with cells transfected with shRNA-neg.

Western blot

Total proteins were isolated from the cultured monolayer cells with a total protein extraction kit (Keygen), and protein concentrations were detected by a bicinchoninic acid protein assay kit (Pierce) as described previously (26). Thirty-microgram proteins from each sample were separated on 8% SDS-PAGE and transferred electrophoretically to polyvinylidene difluoride membranes (Millipore). Membranes were blocked with 2% bovine serum albumin in TBS containing 0.1% Tween20 (TBST) at 37°C for 2 hours and then incubated for 2 hours respectively with 1:500 dilution of mouse anti-HIF-1α, 1:200 dilution of rabbit anti-HIF-2α, 1:400 dilution of mouse anti-uPAR, 1:500 dilution of rabbit anti-GLUT1, and 1:1000 dilution of mouse anti-GAPDH. Horseradish peroxidase–conjugated antimouse or antirabbit IgG were used as secondary antibody (1:5,000 diluted in TBST with 2% bovine serum albumin, incubated for 1 hour). Bands were scanned using a densitometer (GS-700, Bio-Rad Laboratories), and quantification was done using Quantity One 4.4.0 software.

Enzyme-linked immunosorbent assay

VEGF protein contents in supernatant were measured by enzyme-linked immunosorbent assay (ELISA) using the Human VEGF Quantikine ELISA Kit (R&D systems) following the manufacturer's instructions. The intensity of color was measured at 540 nm in a microtest plate spectrophotometer. The concentration of protein in culture media was determined in triplicate wells and was normalized to standard curves generated for each set of samples assayed.

Cell proliferation

The cell proliferation was quantified by the colorimetric MTT assay. In brief, cells were incubated with 0.5 mg/mL MTT for 4 hours at 37°C. Then supernatant was removed and 150 mg DMSO were added. Optical densities at 490 nm were measured using culture medium as a blank.

Xenografts in nude mice

The nude mice (female, 6 weeks of age) were obtained from the Laboratory Animal Center of Sichuan University (Chengdu, Sichuan, China). Thirty-two mice were randomized and divided into four groups (shRNA-1, shRNA-2, shRNA-1+shRNA-2, and shRNA-neg), eight mice each. Lentivirus-transfected cells were then injected s.c. (5 × 10^6 cells/200 μL PBS/mouse) on the back of nude mice. Tumor size was monitored by measuring diameters using vernier caliper weekly, and was calculated as πl^2/6, where l = long side and s = short side as described previously (2). Tumors were harvested at the 7th week and fixed by 4% paraformaldehyde and then embedded by paraffin for immunohistochemistry analyses.

Proliferation and apoptosis in OSCC xenograft tumors

Proliferation was measured by immunohistochemical staining of the proliferation marker ki-67 (1:200; Santa Cruz). Cell apoptosis was detected by terminal deoxynucleotidyl transferase–mediated dUTP nick end labeling (TUNEL) method using In Situ Cell Death Detection Kit, POD (Roche Applied Science) according to the manufacturer's protocol. Cells were observed in a bright field microscope, and the number of apoptotic cells was counted in 10 different microscopic fields.

Statistics

The association between the levels of the HIF-1α/HIF-2α and the patients' sex, age, T stage, lymph node involvement, MVD, histologic differentiation, and recurrence was compared using Pearson's χ² test. Overall survival and disease-free survival curves were estimated using the Kaplan-Meier method, and differences between groups were compared using the log-rank test. A Cox proportional hazards model was applied to identify prognostic variables that predict overall survival and disease-free survival. The power calculation was done with PASS (V. 08.0.3, NCSS), assuming the 5-year survival rate to be 50% (27), hazard ratio to vary from 2.17 to 4.53 (21, 28), the proportion in control group 1 to be 47.5% (HIF-1α negative) or 39.2% (HIF-2α negative), and two-side α as 0.05. The log-rank test with an overall sample size of 97 subjects achieved 81.72% to 99.94% power for HIF-1α and 76.69% to 99.74% power for HIF-2α. The comparisons of means among groups were analyzed by one-way ANOVA, and the Dunn's Multiple Comparison Test was further used to determine the specific differences between groups. All statistical analyses were done using the SPSS package (version 13.0). A value of P < 0.05 was considered statistically significant.
Results

HIF-1α and HIF-2α expression and clinical outcomes

Representative immunohistochemical images are shown in Fig. 1. We found that the nuclear staining of HIF-1α was detected in 51 of 97 (52.5%) OSCC specimens, and that of HIF-2α was detected in 59 of 97 (60.8%). The nuclear staining of HIF-1α was significantly associated with T stage (P = 0.004), lymph node involvement (P = 0.006), histologic differentiation (P = 0.013), and MVD (P = 0.014), whereas that of HIF-2α was associated with T stage (P = 0.011) and MVD (P = 0.005; Table 1, Supplementary Fig. S1).

The Kaplan-Meier survival analysis revealed a significantly worse overall survival (P < 0.001) and disease-free survival (P < 0.001) for patients who had nuclear staining of HIF-1α compared with those who had negative HIF-1α staining (Fig. 1B and C). HIF-2α had no significant association with either overall survival (P = 0.396) or disease-free survival (P = 0.279; Fig. 1E and F). HIF-1α and HIF-2α expression levels as well as patients' gender, age, T stage, lymph node involvement, histologic differentiation, neck dissection, postoperative radiotherapy, and postoperative chemotherapy were included in the univariate and multivariate analysis done by Cox proportional hazard regression model. Multivariate analysis were carried out using a forward variable selection technique (entry P < 0.05, removal P > 0.1). In the univariate analysis, HIF-1α, T stage, lymph node involvement, histologic differentiation, and neck dissection were correlated with the overall survival, whereas HIF-1α, T stage, lymph node involvement, histologic differentiation, and postoperative radiotherapy were correlated with the disease-free survival (Supplementary Table S2). In the multivariate analysis, nuclear HIF-1α staining [P = 0.002; hazard ratio (HR), 2.641; 95% confidence interval (95% CI), 1.433-4.868] and neck dissection (P = 0.055; HR, 2.767; 95% CI, 0.98-7.81) remained in the final model for overall survival, and nuclear HIF-1α staining (P = 0.013; HR, 1.976; 95% CI, 1.154-3.385) and differentiation (P = 0.023; HR, 1.554; 95% CI, 1.064-2.27) were correlated with disease-free survival (Supplementary Table S2). These results suggest that HIF-1α but not HIF-2α expression may predict a worse survival of patients.

The OSCC specimens were simultaneously immunostained for several hypoxia-related proteins (VEGF, CA-IX, GLUT-1, and uPAR) that are potentially relevant to different aspects of tumor biology (Supplementary Fig. S1). HIF-2α protein was significantly associated with VEGF (P = 0.005), whereas HIF-1α was found to be significantly associated with VEGF (P = 0.012), GLUT-1 (P = 0.018), and CA-IX (P = 0.004; Supplementary Table S3).

HIF-1α and HIF-2α induction pattern in OSCC cells

We exposed OSCC cells to normoxic condition (20% O2), physiologically conditioned oxygen level (5% O2), and hypoxic condition (1% O2). After 24 hours of exposure,
HIF-α expression was detected by immunofluorescence. At 20% O₂, neither HIF-1α nor HIF-2α was detected in either cell line. Nuclear staining of HIF-1α, however, was detected in cells cultured at both 5% O₂ and 1% O₂ (Fig. 2A). The protein levels of HIF-α were further analyzed by Western blot. HIF-1α protein was hardly detectable under 20% O₂ and 5% O₂ conditions, and was remarkably increased at 1% O₂ in both cell lines. HIF-2α protein was undetectable at 20% O₂, and was remarkably increased at 5% O₂ and 1% O₂ in both cell lines (Fig. 2B). The mRNA levels of HIF-α were analyzed by quantitative real-time RT-PCR (RT-PCR) after 24-hour exposure. The HIF-1α mRNA levels were significantly increased at 1% O₂, but not at 5% O₂, whereas HIF-2α mRNA levels were significantly upregulated at 5% O₂ and 1% O₂ in both cell lines (Fig. 2C). These results suggest that HIF-2α protein expresses at a physiologic oxygen level, whereas HIF-1α protein should be stabilized at a much lower oxygen level (1% O₂).

**HIF-1α primarily contributes to cell proliferation under hypoxia**

We exposed cells to different oxygen levels, and infected them respectively with lentivirus encoding shRNA targeting HIF-1α (shRNA1), lentivirus encoding shRNA targeting HIF-2α (shRNA2), shRNA1 plus shRNA2 (shRNA1+shRNA2), and lentivirus encoding a negative control shRNA (shRNA-neg). Cell proliferation was measured by MTT assay. In both cell lines, no significant difference was observed among four groups at 20% O₂ or 5% O₂ (Supplementary Fig. S2A-D). At 1% O₂, however, the cells treated by shRNA1 and shRNA1+shRNA2 had a significantly lower proliferation rate than those treated with shRNA2 and shRNA-neg (Supplementary Fig. S2E and F). These results suggest that under hypoxic conditions (1% O₂), HIF-1α but not HIF-2α primarily contributes to the cell proliferation.

**Different genes regulated by HIF-1α and HIF-2α**

We analyzed the mRNA and protein expression of VEGF, GLUT-1, CA-IX, and uPAR in Tca8113 and BcaCD885 cells after being respectively treated with shRNA-neg, shRNA1, shRNA2, and shRNA1+shRNA2. The mRNA levels of genes were measured by quantitative RT-PCR, and the protein levels were measured by ELISA (VEGF) or Western-blot (GLUT-1, CA-IX, and uPAR). In both cell lines that cultured at 5% O₂, VEGF mRNA (Fig. 3A and C) and protein levels (Fig. 4A) were significantly decreased after shRNA2 and shRNA1+shRNA2 treatments, but were not significantly affected by shRNA1 in comparison with shRNA-neg. GLUT-1, CA-IX, and uPAR mRNA (Fig. 3B and D-H) and protein levels (Fig. 4B) were not significantly affected by either shRNA1 or shRNA2.

In both cell lines that cultured at 1% O₂, VEGF mRNA (Fig. 3A and C) and protein levels (Fig. 4A) were significantly decreased in the shRNA1 and shRNA2 groups, and were further decreased in the shRNA1+shRNA2 group compared with the shRNA-neg group. GLUT-1, CA IX, and uPAR mRNA (Fig. 3B and D-H) and protein levels (Fig. 4B) were significantly decreased in the shRNA1 and shRNA1+shRNA2 groups but were not decreased in shRNA2 group compared with the shRNA-neg group. These results indicate that at 1% O₂, VEGF was regulated by both HIF-1α and HIF-2α, whereas GLUT-1, CA IX, and uPAR were regulated by HIF-1α but not HIF-2α.
Different roles of HIF-1α and HIF-2α in the xenograft growth

We established xenograft using cells treated respectively with shRNA-neg, shRNA1, shRNA2, and shRNA1+shRNA2, and documented the tumor volume weekly.

As shown in Fig. 5, no difference of tumor volume was observed between the shRNA1 and the shRNA-neg groups in the first three weeks, but the growth of tumor significantly slowed down since the 4th week in the shRNA1 group compared with the shRNA-neg group. In contrast, the volume of the shRNA2-treated tumor was significantly smaller than that of the shRNA-neg-treated tumor since the 2nd week. Although it was still significantly slower than the shRNA-neg-treated tumor, there was a tendency to speed up after the 5th week. In addition, the shRNA1+shRNA2-treated tumor kept a much slower growth than other three groups during the whole period (Fig. 5A and B).

We harvested the tumors at the 7th week, and then evaluated the proliferation, apoptosis, and MVD of the tumors. The ki-67 immunohistochemical stainings in the shRNA1-, shRNA2-, and shRNA1+shRNA2-treated tumors were remarkably lower than that in shRNA-neg-treated tumors (Fig. 5C-E), indicating that interference for either or both HIF-α units may restrain the proliferation of tumor
The TUNEL assay showed stronger apoptosis in shRNA1-, shRNA2-, and shRNA1+shRNA2-treated tumors than in shRNA-neg-treated tumors (Fig. 5F-H). The MVD in shRNA1- and shRNA2-treated tumors was significantly lower than that in the shRNA-neg-treated tumor (Fig. 5I-K). Moreover, shRNA1+shRNA2-treated tumors had a much lower ki-67 staining, more apoptosis cells, and lower MVD than both shRNA1- and shRNA2-treated tumors alone (Fig. 5E, H, and K).

Discussion

A number of previous studies have provided evidence that HIF-1α and HIF-2α play different roles in different types of tumors (2, 9, 11, 16). Microarray analyses have identified a set of unique and common target genes regulated by HIF-1α and HIF-2α in a cell type--specific manner (2, 5–7). In the present study, we analyzed four approved HIF-α target genes (VEGF, GLUT-1, CA-IX, and uPAR) that are potentially correlated with different aspects of tumor biology. VEGF, a key angiogenic stimulator, is a well-known target gene of HIF-1α (31). Recently, regulatory roles of HIF-2α on VEGF have been reported in a few types of cells (2, 9, 16). Here, we show that both HIF-1α and HIF-2α regulated the expression of VEGF in OSCC cells, and that both HIF-1α and HIF-2α were correlated with VEGF and MVD in OSCC specimens. These results suggest essential roles of HIF-1α and HIF-2α in the angiogenesis of OSCC. GLUT-1 regulates the glucose uptake, and plays an important role in cell adaptation to hypoxic environment. CA-IX, an enzyme that catalyzes the reversible conversion of CO2 to carbonic acid, allows cancer cells to maintain an alkaline intracellular pH and an acidic extracellular pH, which are critical for cell proliferation and invasion, respectively (1, 32). We found that HIF-1α, but not HIF-2α, regulated the expression of GLUT-1 and CA-IX at 1% O2, indicating that HIF-1α rather than HIF-2α mediates the OSCC cellular adaptation to hypoxia. This may explain why knockdown of HIF-2α had no effect on cell proliferation at either 5% O2 or 1% O2, whereas knockdown of HIF-1α significantly inhibited the cell proliferation at 1% O2. uPAR, a serine proteinase receptor, activates plasminogen and matrix metalloproteinase, and finally facilitates matrix remodeling and cell migration (24). We observed that the hypoxic induction of uPAR was regulated by HIF-1α, but not HIF-2α, in OSCC cells, indicating a prometastatic role of HIF-1α in OSCC. We also observed a correlation between HIF-1α and lymph node involvement in patients with OSCC, which further supported the notion that HIF-1α may participate in the metastasis process of OSCC. Moreover, consistent with the results reported by Holmquist-Mengelbier et al. (2), we found that HIF-2α protein was stabilized at 5% O2 and 1% O2, whereas HIF-1α protein was stabilized at 1% O2. Because HIF-1α and HIF-2α stabilized at different oxygen levels and regulated different target genes, we
therefore argue that the specific roles of HIF-1α and HIF-2α in the tumor biology depend not only on which genes are transcribed by HIF-1α or HIF-2α, but also on the conditions under which HIF-1α and HIF-2α are stabilized.

In agreement with previous reports (21, 33, 34), we observed that HIF-1α expression was correlated with T stage, overall survival, and disease-free survival of patients with OSCC. It was suggested that rapid tumor growth results in large tumor size and hypoxic area, which thereby induces the stabilization of HIF-1α (21). Once stabilized, HIF-1α transactivates a set of genes that in turn facilitate tumor growth, angiogenesis, and metastasis. In this view, the correlation between HIF-1α and patients’ survival is intelligible. It has been reported that targeting the HIF-1α pathway in tumor cells inhibits tumor growth in mouse xenograft (9, 11, 35–37). Consistently, we observed that knockdown of HIF-1α reduced proliferation and MVD, and increased the apoptosis in OSCC xenograft tumors. These findings provide further evidence that HIF-1α participates in the progression of OSCC. However, Beasley et al. (4) found in surgically resected head and neck squamous cell carcinoma that HIF-1α was associated with improved disease-free survival. Recent studies have revealed a tumor suppressive role of HIF-1α as well, probably due to HIF-1α–induced apoptosis or transactivation of genes that are themselves targets for negative selection in human cancers (16, 38). In light of these discrepancies among different tumors, there may be tissue-specific differences in response to HIF-1α regulation.

Although HIF-2α has been claimed to have either a promoting (2, 16, 39) or a suppressing (11, 40) role in different types of tumors, the contribution of HIF-2α to tumor angiogenesis has been widely accepted (2, 11, 16, 39, 40). We observed that HIF-2α protein was significantly associated with MVD and VEGF in OSCC specimens, and that knockdown of HIF-2α inhibited the VEGF expression in vitro. In addition, knockdown of HIF-2α inhibited the xenograft tumor growth and reduced the MVD of xenograft tumor. These findings show an important role of HIF-2α in the angiogenesis and growth of OSCC.

Both HIF-1α and HIF-2α exhibited promoting roles in the xenograft tumor growth individually; however, their patterns were different. Knockdown of HIF-2α inhibited the tumor growth from the early days (2nd week) of xenograft growth, whereas the inhibitory effects of HIF-1α shRNA occurred during the latter period of time (4th week later). Holmquist-Mengelbier et al. (2) found that transient knockdown of HIF-1α did not affect neuroblastoma xenograft tumor growth within 15 days. In agreement with them, we found that knockdown of HIF-1α did not affect the OSCC xenograft tumor growth in the first three weeks. The reason for this may be that HIF-2α was stabilized at a wide range of oxygen levels (from physiologic oxygen level to hypoxia), but HIF-1α was stabilized at hypoxic condition which arises from a large tumor lacking oxygen delivery. More importantly, our results revealed that simultaneously knocking down HIF-1α and HIF-2α led to a better inhibitory effect on OSCC xenograft than knocking down HIF-1α or HIF-2α individually. Therefore, we suggest that therapeutic outcome in terms of inhibiting tumor growth may benefit from simultaneously targeting HIF-1α and HIF-2α in OSCC. Hitherto, targeting HIF-1α has become an attractive approach for anticancer agents, e.g., PX-478 (a HIF-1α inhibitor) is now undergoing phase I clinical trials. Although HIF-2α has been shown to exert the effects of an oncogene (2, 16, 39), drugs that specifically target HIF-2α have been poorly identified. Recently, a small-molecule inhibitor of HIF-1α, NSC-134754, has been tested to block HIF-2α as well in Von Hippel-Lindau–defective renal carcinoma cells. Whether NSC-134754 can inhibit both HIF-1α and HIF-2α in OSCC cells needs further exploration.

In conclusion, our results suggest that HIF-1α and HIF-2α may play distinct but functionally overlapping roles in OSCC, and that combined inhibition of HIF-1α and HIF-2α may be a suitable therapeutic strategy for OSCC.

Disclosure of Potential Conflicts of Interest

None declared.

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Play Distinct and Functionally Overlapping Roles in Oral
Squamous Cell Carcinoma

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