ORIGINAL ARTICLE

Clinicopathological significance of hypoxia-inducible factor-1 alpha (HIF-1 α) expression in gastric cancer

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Abstract

Background Hypoxia is a common feature of rapidly growing solid tumors. Therefore, cellular adaptation to hypoxia and altered glucose metabolism are fundamental to the biology of cancer cells. Hypoxia-inducible factor- 1α (HIF- 1α) is a transcription factor for more than 60 genes recognized to control the delivery of oxygen and nutrients through the induction of angiogenesis and glycolysis under hypoxic conditions. Therefore, inhibition of the expression of HIF-1 α can be expected to be potentially tumor-specific molecular targetbased therapy. In this study, we evaluated the significance of $HIF-1\alpha$ expression in relationship to clinicopathological factors, prognosis, vascular endothelial growth factor (VEGF) expression, and microvessel density (MVD).

Methods Paraffin-embedded tumor specimens from 128 patients who underwent gastrectomy at Kurume University from 2004 to 2005 were used to assess the clinical significance of HIF-1 α expression. We used the ABC method to perform an immunohistochemical analysis of the HIF-1 α and VEGF expression.

Results Eighty-four (65.6%) of gastric cancer specimens were positive for HIF-1 α expression. Multivariate analysis showed that histology, depth of invasion, VEGF expression, and MVD were significantly associated with HIF-1 α expression. On relapse-free and overall survival curves, the $HIF-1\alpha$ -negative group was significantly higher than the HIF-1 α -positive group. Moreover, HIF-1 α (+)/VEGF(+)

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A. Kawahara · T. Taira · M. Kage Department of Diagnostic Pathology, Kurume University Hospital, 67 Asahi-machi, Kurume, Fukuoka 830-0011, Japan patients had the worst prognosis. HIF-1 α expression was identified as a significant predictor of relapse-free survival and overall survival by multivariate Cox's proportional hazard analyses.

Conclusion Overexpression of HIF-1 α was found to be an indicator of poor prognosis for patients with gastric cancer and was significantly correlated with histology, depth of invasion, VEGF, and MVD.

Keywords $HIF-1\alpha \cdot VEGF \cdot Gastric \text{ cancer} \cdot$ Clinicopathological factors

Introduction

Gastric cancer is the second leading cause of cancer-related death in Japan [\[1](#page-9-0)]. Curative resection remains the only treatment associated with improvement in 5-year survival rates, but prognosis depends on the extent of lymph node (LN) metastasis and dissemination [\[2](#page-9-0)]. Therefore, a better understanding of the molecular mechanisms governing local invasion and systemic spread of gastric cancer is needed to design and evaluate new therapeutic strategies for this fatal disease [[3\]](#page-9-0).

Hypoxia is a common feature of rapidly growing solid tumors, because oxygen is only able to diffuse 100–180 μ m from the blood capillaries to cells [\[4–10](#page-9-0)]. When tumors grow larger, oxygen and nutrition must be delivered by newly generated vessels. Therefore, cellular adaptation to hypoxia and altered glucose metabolism are fundamental to the biology of cancer cells. Angiogenesis is essential for tumor growth and metastasis. Tumor neovascularization depends on the production of specific angiogenic factors. Vascular endothelial growth factor (VEGF) is one of the major factors that contribute to angiogenesis and metastasis in numerous tumor types, and VEGF overexpression has been associated with tumor progression and poor prognosis $[7, 8, 11-13]$ $[7, 8, 11-13]$ $[7, 8, 11-13]$ $[7, 8, 11-13]$ $[7, 8, 11-13]$.

Hypoxia-inducible factor-1 α (HIF-1 α) is a transcription factor for more than 60 genes recognized to control the delivery of oxygen and nutrients through the induction of angiogenesis and glycolysis under hypoxic conditions [\[2](#page-9-0), [14–17](#page-10-0)]. HIF-1 α activates the transcription of VEGF, and the expression of glucose transporters (GLUT-1), glycolytic enzymes, and growth factors, which may promote tumor cell survival under hypoxic conditions [\[17–19](#page-10-0)].

 $HIF-1\alpha$ plays a critical role in angiogenesis during vascular development. HIF-1 is a heterodimer composed of HIF-1 α and HIF-1 β subunits; HIF-1 α is the oxygen-regulated subunit that determines HIF-1 activity [\[7\]](#page-9-0). Under normoxic conditions, HIF-1 α is unstable. The instability is regulated, in part, by binding to the von Hippel–Lindau tumor suppressor protein. This binding occurs after hydroxylation of the two $HIF-1\alpha$ proline residues by $HIF-{\text{proj}}$ hydroxylases. The von Hippel–Lindau protein is one of the components of the multiprotein ubiquitin-E3-ligase complex. HIF-1 α is degraded by the ubiquitin-dependent proteasome pathway [[20](#page-10-0)]. However, under hypoxic conditions, proline hydroxylation is inhibited, allowing HIF-1 α to become stable. The stabilized HIF-1 α dimerizes with HIF-1 β , translocates from the cytoplasm into the nucleus, and binds to hypoxia-responsive elements (HRE) within the nucleus. Its target genes then promote cell proliferation and viability, angiogenesis, and also metabolic adaptations to hypoxia $[6, 21-24]$ $[6, 21-24]$ $[6, 21-24]$.

HIF-1 α is a primary determinant of HIF activity. HIF-1 α overexpression has been studied in several cancers, such as brain, bladder, breast, lung, esophagus, colon, ovary, pancreas, kidney, and prostate cancer [[15,](#page-10-0) [25–31](#page-10-0)]. These results revealed that HIF-1 α is related to the prognosis in these cancers. Therefore, inhibition in the expression of $HIF-1\alpha$ will be expected to be a tumor-specific molecular target-based therapy. So far, few studies have investigated the correlation between HIF-1 α and gastric cancer. In this study, immunohistochemical analysis was used to investigate HIF-1a protein and VEGF protein expression. We hypothesized that HIF-1 α expression would be correlated with clinicopathological factors, VEGF expression, and microvessel density (MVD) expressed as the mean count of CD34-immunostained vessels, and that this correlation would predict recurrence and overall survival.

Samples of gastric cancer were taken from the resected

Materials and methods

Patients

stomach of 128 patients who underwent gastrectomy for

gastric carcinoma at the Kurume University Hospital between 2004 and 2005, excluding mucosal cancer, multiple primary cancer, multiple gastric cancer, remnant cancer, and remnant cancer after endoscopic submucosal dissection (ESD). All patients were diagnosed histologically according to the General Rules for Japanese Classification of Gastric Carcinoma of the Japanese Gastric Cancer Association (14th edition) [\[32](#page-10-0)]. None of the patients had received any preoperative treatment. Samples were obtained from the central zone of the cancer lesion and preserved by formalin fixation, embedded in paraffin, and stained with hematoxylin and eosin for histological examination. The paraffin blocks were stored until required for immunohistochemistry of HIF-1 α and VEGF.

Immunohistochemistry

Paraffin-embedded tissues were subjected to immunohistochemical analysis performed by the avidin–biotin–peroxidase complex method (Vectastain ABC Kit; Vector, Burlingame, CA, USA). For immunohistochemistry of HIF- 1α and VEGF, paraffin sections were deparaffinized in xylene and rehydrated through graded ethanol solutions. For HIF-1 α antigen retrieval, sections were then irradiated by a domestic microwave oven at 99° C in 10 mM citrate buffer (pH 9.0) for 30 min, and cooled to room temperature. After microwave irradiation, the slides were washed with phosphate-buffered saline (PBS), treated with 0.3% hydrogen peroxide in methanol for 30 min to block endogenous peroxidase, and then incubated with the primary antibody in a humidified chamber at 4° C overnight. As the primary antibody, the rabbit polyclonal antibody H206 (Santa Cruz Biotechnology, Santa Cruz, CA, USA) for HIF-1 α , diluted at 1:200, and the rabbit polyclonal antibody A-20 (Santa Cruz Biotechnology) for VEGF, diluted at 1:200, were used. Sections were washed three times with PBS, then incubated with biotinylated horse anti-mouse/anti-rabbit immunoglobulin G antibody for 30 min, washed again three times with PBS, and then incubated with avidin-biotinylated peroxidase complex for 30 min. After three additional washings with PBS, staining was developed by incubating the sections in 3-amino-9-ethylcarbazole (Vector) for 10 min. The sections were then counterstained with hematoxylin and mounted. For evaluation of HIF-1 α expression, five fields were selected randomly and a total of more than 1,000 tumor cells were counted microscopically under high magnification (400 \times). The HIF-1 α expression through nuclear staining of positive cells was predominant at the invading edge of the tumor margin and at the periphery of necrotic regions within tumors. The HIF-1 α expression was defined as positive if nuclear staining was observed in $\geq 5\%$ of the tumor cells. Concomitant cytoplasmic staining was not counted because HIF-1 α in the nucleus determines the

Fig. 1 Immunoreactivity for hypoxia-inducible factor-1 alpha (HIF- 1α) is mainly identified as positive staining in the nucleus of cancer cells (a, b); for vascular endothelial growth factor (VEGF), immunoreactivity is mainly identified as supranuclear staining or diffuse

staining in the cytoplasm of cancer cells (c, d); and for CD34, immunoreactivity is recognized in the endothelium of microvessels (e). a, c, e $\times 100$; b, d $\times 200$

functional activity of the HIF-1 α complex (Fig. 1a, b) [\[3](#page-9-0)]. In regard to overall survival curve, the HIF-1 α expression was classified as one of four categories, depending on the percentage of tumor cells stained: $- (0-5\%)$, $1+ (5-10\%)$, $2+$ $(10-15\%)$, $3+ (215\%)$. The VEGF expression was defined as positive if cytoplasmic staining was observed in \geq 10% of the tumor cells (Fig. 1c, d). The ChemMate Envision method was used for CD34. Endogenous peroxidase activity was inhibited by incubating slides in 3% H₂O₂ for 5 min. CD34 antigen retrieval was performed by treating with proteinase K for 5 min. Each slide was incubated for 30 min with the antibody at room temperature (Novocastra, Newcastle, UK for CD34, diluted at 1:200). For staining detection, the ChemMate Envision method was used with DAB as chromogen (Fig. 1e). We extracted the digital data of expression using the following image analysis system. CD34-stained specimens were examined to identify the areas with high density. Expression analysis was performed

to measure the five expression areas of MVD in all cases, using 'Win ROOF' (version 5.7; Mitani, Osaka, Japan) computer software. The digitized data of the expression area were measured and averaged. MVD was classified as either $1,200$ or $\geq 1,200/\mu m^2$.

Statistical analysis

Differences in expression rate and association with clinical characteristics were compared by Fisher's exact test or the chi-square test. Significant factors were extracted for further analysis, carried out using multivariate analysis with a logistic regression method. Moreover, Pearson's correlation coefficient was used to examine the correlation of positive rate between $HIF-1\alpha$ expression and VEGF expression. The relapse free-survival (the time of surgical resection to the time of recurrence) and the overall survival (the time of surgical resection to patient death) rates were calculated using the Kaplan–Meier method. Univariate analysis of factors thought to influence the relapse-free survival and overall survival was carried out using the logrank test. The Cox proportional hazards model was used in the multivariate analysis of the factors that were determined to be significant for relapse-free survival and overall survival by univariate analysis. The statistical analyses were performed using a statistical analysis computer program (JUMP 8; SAS Institute, Cary, NC, USA). For all analyses, statistical significance was defined as $P < 0.05$.

Results

Patients

A total of 128 patients were included in this study; 91 patients were men, and 37 were women. Mean age was 67.3 years, with age ranging from 39 to 85 years. Curative resections were performed in 100 patients (78.1%), and noncurative resection was performed in the other 28 (21.9%). On histological differentiation, 53 cases were differentiated type (41.4%) and 76 cases were undifferentiated type (58.6%). Concerning tumor size, 68 (53.1%) were 6 cm or larger; 62 patients (48.4%) had LN metastasis, and 15 patients (11.7%) had peritoneal metastasis. The postoperative stages of patients were I, II, III, and IV in 48, 24, 34, and 22 patients, respectively.

Clinicopathological significance of HIF-1 α protein expression

Eighty-four (65.6%) of gastric cancer specimens were positive for HIF-1 α expression; 68 (53.1%) specimens were positive for VEGF expression. Univariate analysis showed

that tumor size, macroscopic type, histological type, depth of invasion, LN metastasis, distant metastasis, venous invasion, lymphatic invasion, infiltration (INF), VEGF expression, and MVD were significantly correlated with HIF-1 α expression ($P = 0.017$, $P = 0.021$, $P \lt 0.0016$, $P = 0.043$, $P = 0.006, P = 0.006, P = 0.015, P = 0.022, P = 0.0004,$ $P = 0.0001$, and $P = 0.0001$, respectively). However, there was no significant correlation between the expression of HIF-1a, age, sex, H, P factor, and cancer stroma. As for histological types, $HIF-1\alpha$ expression in signet-ring cell carcinoma or in mucinous adenocarcinoma was significantly higher than that in the other histological types (Table [1](#page-4-0)). Multivariate analysis was performed for 11 parameters [tumor size, macroscopic type, histological type, depth of invasion, LN metastasis, venous invasion, lymphatic invasion, distant metastasis, infiltration (INF), VEGF expression, and MVD] that had been found to be significant by univariate analysis, using the logistic regression method (Table [2](#page-5-0)). Multivariate analysis showed that histology, depth of invasion, VEGF expression, and MVD were significantly associated with HIF-1 α expression ($P = 0.006$, $P = 0.020$, $P = 0.0004$, and $P = 0.014$, respectively). However, the correlation of positive rate between $HIF-1\alpha$ expression and VEGF expression was not so strong by Pearson's correlation coefficient ($r = 0.507$, $P < 0.0001$) (Fig. [2\)](#page-5-0).

Relapse-free survival and overall survival curves

The median follow-up duration was 44.9 months (range, 0–60 months) after surgery. The relapse-free survival curve in the HIF-1 α -negative group was significantly higher than that in the HIF-1 α -positive group in 100 patients who underwent a curative resection (R0) $[P = 0.021;$ hazard ratio (HR), 7.685 (95% confidence interval (CI), 1.471–140.980)] (Fig. [3a](#page-6-0)). There was no significant correlation between VEGF expression and relapse-free survival $(P = 0.381)$ (Fig. [3b](#page-6-0)). During the follow-up period, 32 patients died of gastric cancer; the 5-year-overall survival rate was 97.7% in the HIF-1 α -negative group and 62.7% in the HIF-1 α -positive group. On the overall survival curve, the HIF-1 α -negative group was significantly higher than the HIF-1 α -positive group [$P < 0.0001$; HR, 19.480 (95% CI, 4.184–346.672)] (Fig. [3c](#page-6-0)), and the VEGF negative group was significantly higher than the VEGF positive group $[P = 0.034, HR \ 2.194 \ (95\% \ CI$ 1.066–4.846)] (Fig. [3](#page-6-0)d). In patients with stage III, The survival curve in the HIF-1 α -negative group was significantly higher than that in the $HIF-1\alpha$ -positive group $(P = 0.0319)$, but there were no significant difference in the other stages (Fig. [4\)](#page-7-0). The 5-year-overall survival rate according to the percentage of positive tumor staining was 55.6% in (3+), 59.5% in (2+), 69.1% in (1+), and (-) in 97.7%. The prognosis became worse according to the rate

Table 1 Correlation between expression of hypoxia-inducible factor-1 alpha (HIF-1 α) and clinicopathological features

Factor	No.	$(-)$	$(+)$	P value
Age (years)				
< 65	50	14	36	0.224
≥ 65	78	30	48	
Sex				
Male	91	35	56	0.127
Female	37	9	28	
Tumor size (mm)				
< 60	60	27	33	$0.017*$
≥ 60	68	17	51	
Macroscopic type				
Type 0	42	19	23	$0.021*$
1	5	2	3	
\overline{c}	20	11	9	
3	35	9	26	
$\overline{4}$	12	1	11	
5	14	\overline{c}	12	
Histological type				
pap.	3	2	1	$< 0.0016*$
tub1	28	19	9	
tub2	22	7	15	
por1	16	4	12	
por ₂	38	8	30	
sig.	14	3	11	
muc.	7	$\mathbf{1}$	6	
Differentiated	53	28	25	$0.0002*$
Undifferentiated	76	16	59	
Depth of invasion				
T ₁ b	42	20	22	0.131
\overline{c}	15	5	10	
3	11	4	7	
$\overline{4}$	60	15	45	
\leq T2	57	25	32	$0.043*$
\geq T3	72	19	52	
Lymph node metastasis				
N ₀	66	32	34	$0.006*$
1	10	3	7	
\overline{c}	12	2	10	
3	40	7	33	
Liver metastasis				
H ₀	124	44	80	0.141
H1	$\overline{4}$	0	$\overline{4}$	
Peritoneal metastasis				
P ₀	113	42	71	0.068
P ₁	15	2	13	
Distant metastasis				
M ₀	106	42	64	$0.006*$
M1	22	2	20	

 $* P < 0.05$ indicates statistical significance

of HIF-1 α expression ($P = 0.0004$) (Fig. [5\)](#page-7-0). When stratified for HIF-1 α -negative and HIF-1 α -positive patients in the VEGF-negative and VEGF-positive subgroups, a statistical difference was observed among the groups. The $HIF-1\alpha$ -negative and VEGF-negative patients had the most favorable prognosis, whereas the HIF-1 α -positive and VEGF-positive patients had the worst prognosis $(P = 0.0002)$ (Fig. [6\)](#page-7-0). On overall survival, HIF-1 α , VEGF, MVD, tumor size, macroscopic type, histological type, depth of invasion, LN metastasis, venous invasion, lymphatic invasion, liver metastasis, peritoneal metastasis, distant metastasis, cancer stroma, and INF ($P < 0.0001$, $P = 0.034, P = 0.004, P < 0.0001, P < 0.0001, P =$ 0.025, $P \lt 0.0001$, $P \lt 0.0001$, $P \lt 0.0001$, $P \lt 0.0001$, $P = 0.033$, $P < 0.0001$, $P < 0.0001$, $P = 0.026$, and $P = 0.0005$, respectively), and on relapse-free survival, HIF-1 α , macroscopic type, depth of invasion, LN metastasis, venous invasion, lymphatic invasion, and cancer stroma ($P = 0.021$, $P = 0.009$, $P = 0.001$, $P = 0.006$, $P = 0.002$, $P = 0.001$, and $P = 0.030$, respectively) were indicators for poor prognosis according to the log-rank test. Multivariate Cox's proportional hazard analyses of clinicopathological factors that appeared significant in the univariate analyses revealed that HIF-1 α was an independent prognostic factor on overall survival and relapse-free survival (Tables [3,](#page-8-0) [4](#page-9-0)). HIF-1 α expression was identified as a significant predictor of relapse-free survival $[P = 0.011;$

Factors	Characteristics		Hazard ratio	95% CI	P value*
	Unfavorable	Favorable			
Tumor size (mm)	>60	< 60	1.475	$0.462 - 4.764$	0.509
Macroscopic type	Type 3, 4, 5	0, 1, 2	2.348	$0.606 - 9.982$	0.218
Histological type	Undifferentiated	Differentiated	4.321	1.560-12.900	$0.006*$
Depth of invasion	T ₃ , T ₄	T ₁ b, T ₂	0.165	$0.033 - 0.711$	$0.020*$
LN metastasis	$(+)$	$(-)$	3.304	$0.765 - 15.152$	0.112
Venous invasion	$(+)$	$(-)$	4.244	0.877-22.091	0.075
Lymphatic invasion	1y0, 1	1y2, 3	0.205	$0.033 - 1.056$	0.069
Distant metastasis	M1	M ₀	2.265	$0.466 - 13.812$	0.334
Infiltration (INF)	$\mathbf c$	a, b	1.287	0.337-4.981	0.711
VEGF	$(+)$	$(-)$	4.215	1.634-11.624	$0.004*$
MVD (/ μ m ²)	>1,200	< 1,200	3.589	1.327-10.349	$0.014*$

Table 2 Multivariate logistic regression analysis of HIF-1 α expression

CI confidence interval

 $* P < 0.05$ indicates statistical significance

Fig. 2 Coefficients of correlation between $HIF-I\alpha$ and VEGF expression. Correlation of positive rate between $HIF-1\alpha$ expression and VEGF expression was not so strong by Pearson's correlation coefficient ($r = 0.507$, $P < 0.0001$)

HR, 9.723 (95% CI, 1.568–197.633)] and overall survival $[P = 0.016; HR, 7.366 (95\% CI, 1.368-137.169)].$

Discussion

Under hypoxic condition, angiogenesis is essential for growth and metastasis of solid tumors, because oxygen is only able to diffuse $100-180 \mu m$ from the blood capillaries to cells. When tumors grow larger, oxygen and nutrition should be delivered by newly generated vessels. Therefore, cellular adaptation to hypoxia and altered glucose metabolism are fundamental to the biology of cancer cells [[5–9,](#page-9-0) [11](#page-10-0)–[13,](#page-10-0) [21–24,](#page-10-0) [28,](#page-10-0) [33\]](#page-10-0). For this reason, inhibition in angiogenesis is emerging as a promising strategy for cancer treatment [[3\]](#page-9-0). Tumor angiogenesis and neovascularization require VEGF expression. Binding of HIF-1 α to the VEGF promoter is a major pathway resulting in the induction of VEGF expression under hypoxic conditions [[34\]](#page-10-0). VEGF, as well as functioning as a growth factor, is able to function as a vascular permeability factor. Increased permeability of blood vessels facilitates the extravasation of proteins and formation of ascites [[35–37\]](#page-10-0). In previous reports, the expression level of VEGF has been found to be directly associated with the production of ascites and carcinomatosis [\[37](#page-10-0), [38](#page-10-0)]. Aoyagi et al. [[39\]](#page-10-0) reported that VEGF was correlated with peritoneal metastasis from gastric cancer, and that VEGF was a useful indicator of peritoneal recurrence. Moreover, Imaizumi et al. [\[40](#page-10-0)] reported that bevacizumab, which is a humanized monoclonal antibody against VEGF, suppressed peritoneal dissemination from gastric cancer using peritoneal metastasis model. These studies provide clear evidence that VEGF is an essential element in the development of peritoneal metastasis from gastric cancer. Some hypoxia-independent mechanisms of HIF-1 activation in tumor cells have also been reported, such as genetic alterations in tumor suppressor genes (p53, VHL, and PTEN) and oncogenes (SRC, HER2, and H-RAS) [[41–44](#page-10-0)]. Activation of certain growth factor receptors (insulin-like growth factor I receptor) has also been shown to increase expression of HIF-1 α . Results from recent studies demonstrated that HIF-1 α may also regulate the invasiveness of colon cancer cells by altering the expression of genes encoding intermediate filaments (vimentin, keratins), extracellular matrix components (fibronectin), and proteases (matrix metalloproteinase 2 and the urokinase plasminogen activator receptor) [\[11](#page-10-0)]. Most studies have shown that HIF-1 α overexpression has

Fig. 3 Relapse-free survival and overall survival curves in HIF-1 α and VEGF. a Relapse-free survival curve in the HIF-1 α -negative group was significantly higher than that in the $HIF-1\alpha$ -positive group $[P = 0.021$; hazard ratio (HR), 7.685 (95% confidence interval (CI), 1.471–140.980)]. b There was no significant correlation between VEGF expression and relapse-free survival ($P = 0.381$). c On the

been detected in several human cancers, such as brain, bladder, breast, lung, esophagus, colon, ovary, pancreas, kidney, and prostate cancer [[15](#page-10-0), [25–31](#page-10-0)]. Furthermore, HIF- 1α overexpression has been reported to be significantly correlated with highly aggressive disease, resistance to radiation therapy and chemotherapy, and poor prognosis in some cancer types such as oligodendroglioma, breast, ovarian, and oropharyngeal cancer [[27,](#page-10-0) [28](#page-10-0), [30,](#page-10-0) [45](#page-10-0)[–50](#page-11-0)]. However, few studies have investigated the correlation between HIF-1 α and gastric cancer.

In this study, we have investigated the relationship between HIF-1a, VEGF, clinicopathological significance, and patient prognosis in gastric cancer. Our results showed that HIF-1 α expression significantly correlated with a malignant behavior category, including increased expression of tumor size, macroscopic type, histological type, depth of invasion, LN metastasis, distant metastasis, venous invasion, INF, VEGF expression, and MVD. However, there were no significant correlations between the HIF-1 α expression, H, P, factor, lymphatic invasion and cancer stroma. The multivariate analysis showed that the

overall survival curve, the HIF-1 α -negative group was significantly higher than the HIF-1 α -positive group [$P < 0.0001$; HR, 19.480 (95%) CI, 4.184–346.672)]. d VEGF-negative group was significantly higher than VEGF-positive group $[P = 0.034; HR, 2.194 (95\% CI,$ 1.066–4.846)]

histology, depth of invasion, VEGF expression, and MVD were significantly associated with the HIF-1 α expression. However, the correlation of the positive rate between HIF- 1α expression and VEGF expression was not so strong by Pearson's correlation coefficient, because $HIF-1\alpha$ is a transcription factor of more than 60 genes and HIF-1 α induces not only VEGF but also other many factors that affect tumor progression and prognosis. As for histological types, $HIF-1\alpha$ expression in the undifferentiated types was significantly higher than that in the differentiated types. Hypoxic tumors are aggressive and exhibit stem cell-like characteristics. Recent genomics studies have further revealed that poorly differentiated human tumors display a gene expression signature similar to that found in normal embryonic stem cells or lineage-committed progenitor cells [\[51](#page-11-0)]. Some clinical studies have shown significant associations between HIF-1 α expression and patient outcome in human solid tumors [\[28](#page-10-0), [49](#page-11-0), [50](#page-11-0)]. Our data also demonstrated that relapse-free survival and overall survival curves in the HIF-1 α -negative group were significantly higher than those in the HIF-1 α -positive group. Moreover,

Fig. 4 In patients at stage III, the survival curve in the HIF-1 α -negative group was significantly higher than that in the HIF-1 α -positive group $(P = 0.0319)$, but there were no significant differences at the other stages

Fig. 5 In regard to overall survival curve, HIF-1 α expression was classified as one of four categories, depending on the percentage of tumor cells stained: $-$ (0–5%), 1+ (5–10%), 2+ (10–15%), or 3+ $(\geq 15\%)$. The prognosis became worse according to the rate of HIF-1 α expression ($P = 0.0004$)

we classified HIF-1 α expression as four groups, and a statistical difference was observed among the groups. The prognosis was worse according to the rate of HIF-1 α expression. We also found that there was a significant difference among groups stratified to HIF-1a/VEGF expression ($P = 0.0002$). The patients with HIF-1 α (+)/

Fig. 6 There was a significant difference among groups stratified according to HIF-1 α /VEGF expression ($P = 0.0002$). Patients with $HIF-1\alpha(+) / VEGF(+)$ tumors had the worst prognosis

 $VEGF(+)$ tumors had the worst prognosis. Concerning the heterogeneity of the expression of the HIF-1 α and VEGF within each tissue, other pathways upstream can induce VEGF expression independent of HIF-1 α signaling. For example, the oncogene ras upregulates VEGF expression and downregulates endogenous angiogenic inhibitors such

Determined by the Cox proportional hazard model

CI confidence interval

 $* P < 0.05$ indicates statistical significance

as thrombospondin-1 (Tsp-1). Conversely, activation of the tumor suppressor genes p53, PTEN, and Smad4 increases Tsp-1 expression and inhibits the angiogenesis. p53 has been reported to inhibit angiogenesis through the regulation of other unidentified inhibitors [\[52](#page-11-0)]. In multivariate analysis, HIF-1 α was an independent prognostic factor for relapse-free survival and overall survival. These findings suggested that HIF-1 α plays an important role in tumor growth and progression of gastric cancer.

In conclusion, we have demonstrated in this study that $HIF-1\alpha$ expression was correlated with clinicopathological findings. HIF-1 α expression was found to be an indicator of poor prognosis for disease recurrence or progression in patients with gastric cancer. In addition, immunoreactivity

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	Table 4 Univariate and multivariate analysis of relapse-free survival		

Determined by the Cox proportional hazard model

CI confidence interval

 $* P < 0.05$ indicates statistical significance

of combination of HIF-1 α and VEGF was a useful marker of the prognosis of gastric cancer.

Conflict of interest No author has any conflict of interest.

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