OncoTargets and Therapy

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ORIGINAL RESEARCH

RETRACTED ARTICLE: KIF4A Promotes Clear Cell Renal Cell Carcinoma (ccRCC) Proliferation in vitro and in vivo

This article was published in the following Dove Press journal:
OncoTargets and Therapy

Guang-Hua Yang[1,*]
Zhi-Xing Ren[2,*]
Xiong Yang[3]
Yan-Gang Zhang[1]

[1]Department of Urology, Shanxi Bethune Hospital, Shanxi Academy of Medical Sciences, Taiyuan City, Shanxi Province 030032, People's Republic of China; [2]Education and Research Center, Taiyuan Radio and Television University, Taiyuan City, Shanxi Province 030024, People's Republic of China; [3]Department of Urolith Center, Tianjin Institute of Urology, The Second Hospital of Tianjin Medical University, Tianjin 300211, People's Republic of China

*These authors contributed equally to this work

Purpose: To evaluate the expression in human clear cell renal cell carcinoma (ccRCC) tissues and explore the effects of kinesin family member 4A (KIF4A) on ccRCC progression.
Methods: GEPIA was used to evaluate the mRNA levels of KIF4A in human ccRCC tissues from TCGA database, and Immunohistochemistry (IHC) assays were performed to assess its expression in human ccRCC tissues collected in our hospital. The clinical-pathological analysis was performed to explore the correlation with KIF4A expression. The effects of KIF4A on ccRCC cell proliferation were detected through colony formation and MTT assays. Finally, the effects of KIF4A on tumor growth were measured using a mice model.
Results: Bioinformation results showed the expression of KIF4A mRNA was upregulated in ccRCC tissues and high expression of KIF4A was related with poor prognosis in ccRCC patients. We also found a high expression of KIF4A in human ccRCC tissues collected in our hospital. We also found its expression level was correlated with clinical characteristics, including T stage (P=0.035*) and lymphatic metastasis (P=0.028*). We further confirmed that knockdown of KIF4A suppressed cell proliferation in HTB-47 and CRL-1932 cells. Furthermore, KIF4A contributes to tumor growth of ccRCC cells in mice.
Conclusion: We found the abnormal high expression of KIF4A in human ccRCC tissues and demonstrated that KIF4A could serve as a tumor induction gene.
Keywords: clear cell renal cell carcinoma, ccRCC, KIF4A, proliferation, prognosis, clinicopathological characteristics

Introduction

Renal cell carcinoma is a common urinary disease with a high incidence.[1] In the United States, more than 65, 340 newly diagnosed RCC patients and approximately 14, 970 deaths in 2018.[2–4] While in 2019, there were 73, 820 new diagnosed RCC patients and approximately 14, 770 deaths.[2–4] Clear cell renal cell carcinoma (ccRCC) represents the highly aggressive renal malignant tumor which accounts for nearly 80% of renal cell carcinoma.[5] Existing traditional treatments, such as surgical resection, radiation and chemotherapy, seem to be ineffective against this highly aggressive tumor.[6] Recently targeted therapy for ccRCC is promising.[7] VHL was reportedly considered a potential molecular target for ccRCC, but more mutations were subsequently discovered, such as these mutations in ccRCC leading to further identification of their possible therapeutic role in this cancer.[8,9] In order to fight this disease in the future, the development of new molecular tars has potential clinical value.

The kinesin proteins (KIFs) that are mainly involved in cargo transportation belong to the microtubule-based kinesin family.[10] More than 45 kinesins have

Correspondence: Guang-Hua Yang; Yan-Gang Zhang
Department of Urology, Shanxi Bethune Hospital, Shanxi Academy of Medical Sciences, No. 99 Longcheng Street, Taiyuan City, Shanxi Province 030032, People's Republic of China
Tel +86 351-8368114
Email 836413443@qq.com; urozyg@163.com

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http://doi.org/10.2147/OTT.S240734

already been identified in human cells.[11] Kinesins carry out critical functions in the processes of mitosis and cytokinesis.[11] Additionally, previous studies demonstrated that kinesins could promote the separation of sister chromatin.[12] Kinesin family member 4A (KIF4A), a motor protein involved in multiple cellular processes such as spindle formation, chromosome segregation, and cytokinesis.[13] KIF4A also associates with the regulation of DSB repair-related proteins.[14] In recent years, the key role of KIF4A in cancer development has gradually been revealed.[15] KIF4A is widely expressed in a variety of human tissues.[15] Various studies have reported that KIF4A promoted the progression of several cancers, such as cervical cancer and oral cancer.[16] In addition, KIF4A promotes cell proliferation via cell cycle regulation and metastasis in colorectal cancer.[15] KIF4A ablation also leads to inhibition of lung cancer cell proliferation.[17] However, it is unclear whether KIF4A is involved in the occurrence and development of ccRCC in highly malignant tumors.

Here, we declared that KIF4A is involved in the development of ccRCC and found that KIF4A is highly expressed in ccRCC tissue samples. Our data further confirmed that KIF4A is correlated with the clinical pathology of ccRCC patients such as tumor stage and tumor size. Furthermore, our results indicated that KIF4A depletion dramatically inhibited ccRCC cell proliferation and exhibited tumor growth in mice. Therefore, KIF4A may become a promising therapy for ccRCC.

Materials and Methods

Bioinformatical Analyze

GEPIA (http://gepia.cancer-pku.cn/detail.php?gene=KIF4A) was used to analyze data from TCGA (The Cancer Genome Atlas) for differentially expressed genes, and the median was utilized as the threshold to separate the patients into two groups for Kaplan–Meier survival analysis.

Antibodies, Primers and shRNA Plasmids

Anti-KIF4A (for IHC assays, 1:400 dilution, for immunoblot assays, 1:1000 dilution, ab12227, Abcam, Cambridge, UK), Anti-β-actin (1:1000 dilution, ab8226, Abcam), Anti-Ki67 (1:1000 dilution, ab16667, Abcam), Anti-proliferating cell nuclear antigen (PCNA) (1:500 dilution, ab92552, Abcam).

The quantitative RT-PCR primer sequences of KIF4A were as follows: Forward, 5′ -TCTGTTTCAGGCTG CTTTCA-3′ and Reverse, 5′-GGATGACCTTGCCCACA GCCT-3′; The quantitative RT-PCR primer sequences of GAPDH were as follows: Forward, 5′-CATCTCTGCC CCCTCTGCTGA-3′ and Reverse, 5′-GGATGACCTTGCC CACAGCCT-3′.

KIF4A shRNA clone was conducted in our laboratory, and the targeted sequences were as follows: 5′-AACA GGAAGAAGTCTTCAATACA-3′.

Human Tissues Collection and Analysis

The ccRCC tissue samples and paired adjacent non-tumor tissues were obtained from 78 ccRCC patients at Shanxi Bethune hospital. The clinical-pathological characteristics, including ages, genders, tumor stage, tumor grades, and tumor size were collected and briefly listed in Table 1. The use of human samples in this study was approved by the Ethics Committee of Shanxi Bethune Hospital. The research involving human participants experiment had been approved by our hospital and our equivalent committee. The participants provided their written informed consents to participate in this study.

To investigate the possible relationship between KIF4A level and ccRCC, immunohistochemistry (IHC) assays were subsequently performed. Briefly, the samples were

Table 1 Relationships of KIF4A and Clinicopathological Characteristics in 78 Patients with Clear Cell Renal Cell Carcinoma

Feature	All n=78	KIF4A Expression		χ^2	P
		Low	High		
		n=40	n=38		
Age (year)				2.834	0.092
< 55	48	21	27		
≥ 55	30	19	11		
Gender				1.238	0.266
Male	44	25	19		
Female	34	15	19		
T stage				4.468	0.035*
T_{1-2}	32	21	11		
T_{3-4}	46	19	27		
Tumor grade				2.651	0.103
Low	34	21	13		
High	44	19	25		
Tumor size				4.803	0.028*
< 4 cm	28	19	9		
≥ 4 cm	50	21	29		

Note: *P < 0.05.

fixed with 4% PFA, then cut into 5-um slices and blocked with 2% BSA in PBS for 30 mins. The Slides were then incubated with an antibody targeting KIF4A at 4°C overnight. Subsequently, after rinsing in PBS several times, the slides were maintained in a biotinylated secondary antibody conjugated to horseradish peroxidase (HRP). Subsequently, a staining reaction was performed by using a DAB kit.

KIF4A is mainly located in the nucleus of ccRCC cells. The percentage of positively stained cells was scored as follows: 0, negative staining; 1, 10–50% positive tumor cells and 2, >50% positive-stained cells. The intensity of KIF4A staining was evaluated as 0 (no staining), 1 (moderate staining) and 2 (strong staining). The expression level of KIF4A was analysed based on the staining index: the staining intensity score was multiplied by the positive tumor cell staining score. KIF4A staining scored 0, 1 and 2 were considered low-expression, other scores of 3 and 4 were evaluated as high-expression.

Cell Culture and Transfection

Human ccRCC cell lines, HTB-47 and CRL-1932, were obtained from ATCC. Both HTB-47 and CRL-1932 cells were maintained in RPMI1640 medium with 10% fetal bovine serum addition (Gibico, CA, USA) in a 5% CO_2 incubator.

KIF4A shRNA plasmids were transfected into HTB-47 and CRL-1932 cells were conducted using lipofectamine 2000 (11668019, Invitrogen, Carlsbad, CA, USA). Stable knockdown of HTB-47 cells was obtained by its shRNA lentivirus infection and the selection was performed by puromycin supplementation and used in animal experiments.

Quantitative RT-PCR Assay

Total RNA from human ccRCC cells were extracted via Trizol reagent (15596026, Invitrogen, Carlsbad, CA, USA). Then, the RNA was reverse-transcribed into cDNA by M-MLV reverse transcriptase (M1701, Promega, Madison, Wisconsin, USA).

SYBR Ex Taq kit (638319, Takara, Japan) was utilized to conduct Quantitative RT-PCR and the relative KIF4A expression level was normalized to the level of GAPDH.

Immunoblot Assays

Extract ccRCC cells or tissue proteins with RIPA buffer (9800, Cell Signaling, Danvers, MA). Then, the protein was separated by SDS-PAGE, and subsequently transferred protein onto polyvinylidene fluoride (PVDF) membranes and blocked with 5% BSA. Membranes were incubated with primary antibodies targeting KIF4A, Ki67, PCNA, and β-actin, respectively, and then incubated with HRP-conjugated secondary antibodies for 1 hr. Visualize signals with ECL kit. To analyze the intensity of each band, ImageJ software was used.

Cell Proliferation Assays

For colony formation assay, about 500 ccRCC cells transfected with control or KIF4A shRNA plasmids were seeded into 6-well culture plates for culturing for 2 weeks, the cells were fixed with PFA and dyed with 0.2% crystal violet for 20 min at room temperature, and then manually counted the number of colonies.

For MTT assay, cells were seeded in 96-well culture dishes at a density of about 1000 cells. After adherence, incubated cells with MTT. After washing with PBS, dimethyl sulfoxide (DMSO) was added to each well, and the absorbance was measured at 570 nm using a microplate reader.

Tumor Growth Assays

Nude BalB/c mice (6–8 weeks, 18–22 g, female) were purchased from Beijing Vital River Laboratory Animal Technology Co., Ltd. (Beijing, China). For tumor growth assays, HTB-47 cells transfected with control or KIF4A shRNA lentivirus were injected subcutaneously into athymic Nude BalB/c mice. After 2 weeks, the tumor of each mouse was isolated and photographed. And the tumor volume was monitored every 3 days and marked the growth curve of tumor growth. All applicable international, national, and/or institutional guidelines for the care and use of animals were followed. The animal study was carried out in accordance with the guidelines approved by the Animal Experimentation Ethics Committee of Shanxi Bethune Hospital. The protocol was approved by the Committee, and all surgery and all efforts were made to minimize suffering.

Semi-Quantitative Analysis Assay for the Results of Immunohistochemistry in vivo

The expression of KIF4A or Ki67 was determined with anti-KIF4A or anti-Ki67 antibody in paraffin tumor using an immunohistochemistry kit (ZSGB-BIO, pv6000, Chian) according to the manufacture's protocols. Briefly, isolated tumor tissues were fixed into 10% neutral-buffered formalin and then embedded in paraffin blocks. Then, the embedded tissues were cut into 4 μm sections. After antigens retrieval in a microwave oven for 15 mins and endogenous

peroxidase blockage, sections were added with indicated antibodies overnight at 4°C. And then, goat anti-rabbit antibody was added at 37°C for 1 hr. Added DAB to visualize signals. Images were taken under a microscope (Olympus BX43).

Statistics

GraphPad 6 was used for data analysis in this study. All results were represented as mean ± SD. For statistical significance, Student's *t*-test was used. The Kaplan–Meier curve method was performed for survival analysis. Additionally, $P<0.05$ was considered significantly different.

Results

KIF4A Expression Correlates with ccRCC

KIF4A has been reported to be important in the promotion of cancer development. Bioinformatic analysis was conducted to analyze the expression level of KIF4A in ccRCC tissues and normal kidney tissues. As shown in Figure 1, KIF4A expression in ccRCC tissues (n = 523) was increased at mRNA levels compared to normal tissues (n = 100) (Figure 1A). According to the expression pattern KIF4A in patients, all ccRCC patients can be divided into high grou (n=254, from TCGA dataset) and low group (n=257, from TCGA data set), as shown in Figure 1B. We noti[illegible]ients with high KIF4A expression had poor overa[illegible] survival (OS) and disease-free survival (DFS). These da[illegible] sug[illegible]est th[illegible] KIF4A may be an adverse prognosis in ccRCC patients. To further verify the potential role of KIF4A in ccRCC, we detected its expression level in ccRCC tissue samples by IHC assays. We found KIF4A mainly located in the nucleus of ccRCC cells (Figure 2A). Consistently, adjacent tissues exhibited low or no KIF4A expression compared with ccRCC tissues (Figure 2A and B).

Then, 78 patient samples were divided into KIF4A low and high-expression groups based on the staining scored listed in Materials and methods (Figure 2A and Table 1). Forty patients were evaluated as low expressio[illegible] KIF4A, whereas 38 of them exhibited high-expressio[illegible]evels (Ta[illegible]e 1).

We then analysed the clinica[illegible]thological c[illegible]aracteristics, such as age, gender, tu[illegible]r stage, [illegible]umor gra[illegible]e and size in ccRCC patients. It is[illegible]worth noting [illegible]t [illegible]o significant correlations were fou[illegible] betwe[illegible]n patient age, gender and tumor grade bet[illegible]een KI[illegible]A low [illegible]nd high-expression groups (Table[illegible] Interestin[illegible]e expression level of KIF4A was correla[illegible]d with tumor stage (P=0.034) and tumor [illegible]P=0.028) i[illegible]cRCC patients (Table 1).

Taken together, our results demonstrated that KIF4A cor[illegible]lates with c[illegible]RCC.

Knockdown of KIF4A Weakened ccRCC Cell Proliferation in vitro

To explore the potential function of KIF4A in ccRCC, the KIF4A shRNA plasmids were transfected into t HTB-47 and CRL-1932 cells, to knockdown KIF4A expression.

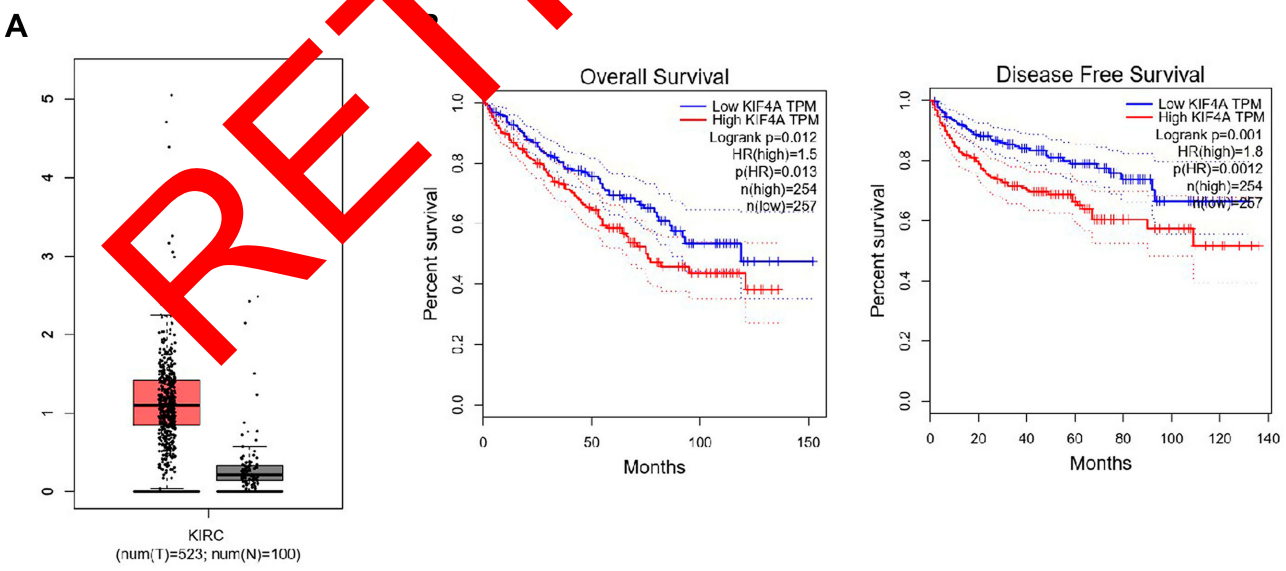

Figure 1 KIF23 expression at mRNA level on pancreatic tumor tissue and normal pancreatic tissues and is associated with poor prognosis. (**A**) KIF4A expression at mRNA level was high in 523 tumor tissues and low in 100 normal tissues. (**B**) Pancreatic cancer patients with high KIF4A expression had poor overall survival (OS) and poor disease-free survival (DFS).

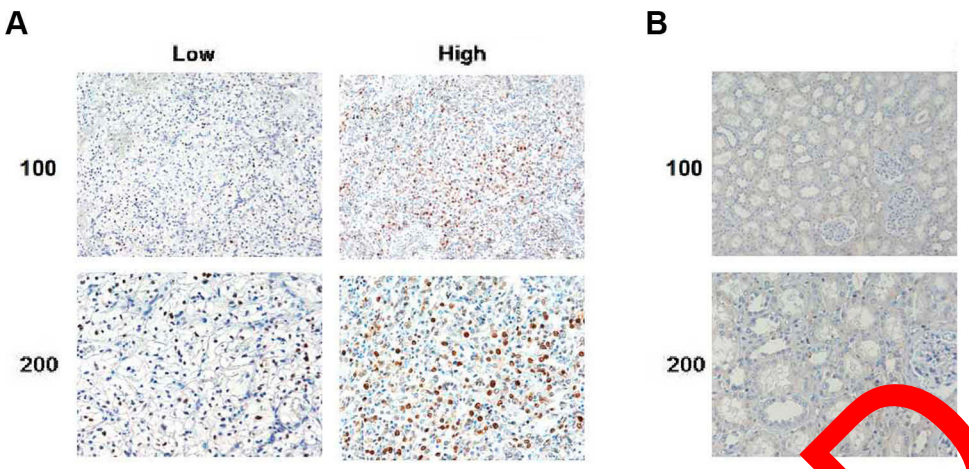

Figure 2 KIF4A was highly expressed in human ccRCC tissues. (**A**) Immunohistochemical assays were performed, and the representative photographs of KIF4A expression in ccRCC tissues were shown (×100 and ×200 magnification, respectively). (**B**) IHC staining revealed the expression level of KIF4A in the adjacent liver tissues (×100 and ×200 magnification, respectively).

The reduction of KIF4A in HTB-47 and CRL-1932 cells confirmed the knockdown efficiency by quantitative RT-PCR assays (Figure 3A). The reduction of KIF4A expression was further proved via Immunoblot assays in HTB-47 and CRL-1932 cells (Figure 3B).

To evaluate the role of KIF4A in cell proliferation, colony formation assays were performed. The knockdown of KIF4A dramatically inhibited the proliferation of ccRCC cells, assessed by the significant reduction in colony numbers (Figure 4A). Similarly, through MTT assays, we observed an obvious decreased absorbance value in both HTB-47 and CRL-1932 cells with KIF4A ablation (Figure 4B). We also assessed the expression levels of cell proliferation markers, Ki67 and PCNA. Consistently, KIF4A ablation resulted in an obvious reduction in Ki67 and PpCNA expression levels in HTB-47 and CRL-1932 cells (Figure 4C and D).

In conclusion, our data suggested that KIF4A promotes ccRCC cell proliferation in vitro.

KIF4A Promotes ccRCC Growth in Mice

Similar to our previous results, KIF4A ablation led to the inhibition of ccRCC cell proliferation in vitro, and then we speculated that KIF4A stimulated the development of ccRCC in mice.

To confirm our hypothesis, HTB-47 cells with control or KIF4A shRNA lentivirus infection were subcutaneously injected into nude mice. After 2 weeks, the tumor was isolated, photographed, and measured. According to the tumor volume measured every 3 days, we plotted the tumor growth curve in each group. Representative photographs of tumors are displayed in Figure 5A. Interestingly, the volume of tumors in KIF4A depleted groups was significantly smaller than control groups (Figure 5A).

Additionally, silencing of KIF4A was confirmed by IHC assays (Figure 5B). We also examined the expression level of Ki67 in control and KIF4A knockdown groups by IHC assays. As expected, Ki67 reduction was observed in tumors in the KIF4A knockdown groups, which indicates that KIF4A knockdown impaired proliferation capacity (Figure 5C). Therefore, we showed that the involvement of KIF4A in the regulation of ccRCC development in mice.

Discussion

There are four types of renal carcinoma: clear cell renal carcinoma, granulosa cell renal carcinoma, mixed cell renal carcinoma, and undifferentiated cell renal carcinoma.[18] Among them, the vast majority are renal clear cell carcinoma, accounting for 70%~80% of renal carcinoma.[19,20] Renal clear cell carcinoma is often asymptomatic in the early stage, or only fever, fatigue and other systemic symptoms; tumor volume was found to increase. However, in the advanced stage, existing treatments have little effect on ccRCC.[21,22] New treatments are urgently needed to combat this disease. Through the bioinformation analysis, we noticed the high mRNA levels of KIF4A in human ccRCC tissues, and KIF4A expression was correlated with the prognosis of ccRCC patients, indicating that KIF4A can be used as a prognostic indicator of ccRCC.

Performing IHC assays, we noticed 78 human ccRCC tissue samples and their corresponding non-tumor adjacent tissue samples, we found a relatively high-expression level

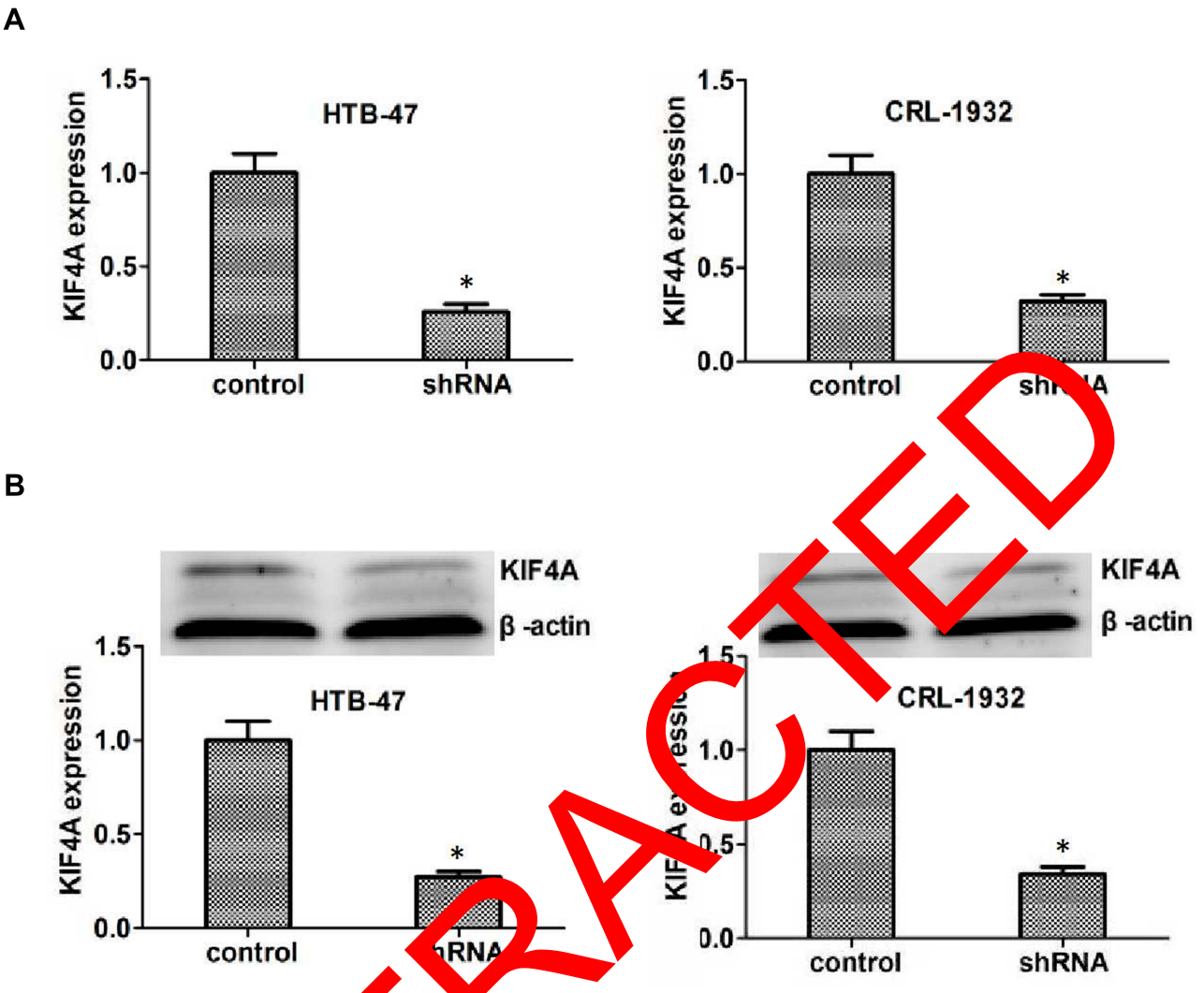

Figure 3 KIF4A expression was effectively inhibited in both HTB-47 and CRL-1932 human ccRCC cells caused by its shRNA plasmids. (**A**) Quantitative RT-PCR assays revealed the dramatically reduced expression level of KIF4A caused by its shRNA in HTB-47 and CRL-1932 cells, respectively. (**B**) Immunoblot assays confirmed the efficiently silencing of KIF4A caused by its shRNA in HTB-47 and CRL-1932 cells. Results are presented as mean ± SD, *P < 0.05.

of KIF4A in tumor tissues, and the expression level of KIF4A was remarkably associated with clinical features including tumor size and the number of tumor nodes. Similarly, another study indicated that high expression of KIF4A is correlated with lymph node metastasis in patients with colorectal cancer.[16] These clinical data testified the possible role of KIF4A in the histopathology and progression of tumorigenesis. Further investigations are consistent with the hypothesis that KIF4A serves as a trigger of ccRCC progression. Performing IHC assays, we also found the decrease expression of Ki67 in tumor tissues isolated from mice of KIF4A depletion groups, which further confirmed the critical role of KIF4A on the regulation of ccRCC cell proliferation.

KIF4A is a member of KIF4 subfamily, which consists of KIF4A, KIF4B, KIF21A and KIF21B.[23,24] Various studies have reported that the KIF4 subfamily is critical in tumorigenesis and progression.[25,26] It is reported that KIF4A was a new component of the chromosome segregation machinery and acted critical roles in mediating spindle organization and cytokinesis.[23] All these functions suggest that KIF4A may have an impact on tumorigenesis and development. In fact, KIF4A plays as an oncogene and participates in the progression of several malignancies, including breast cancer, oral cancer, and cervical cancer.[16,27] KIF4A stimulates cell migration and invasion in lung cancer,[17] and it was found to regulate cell proliferation by the activation of spindle assembly checkpoint

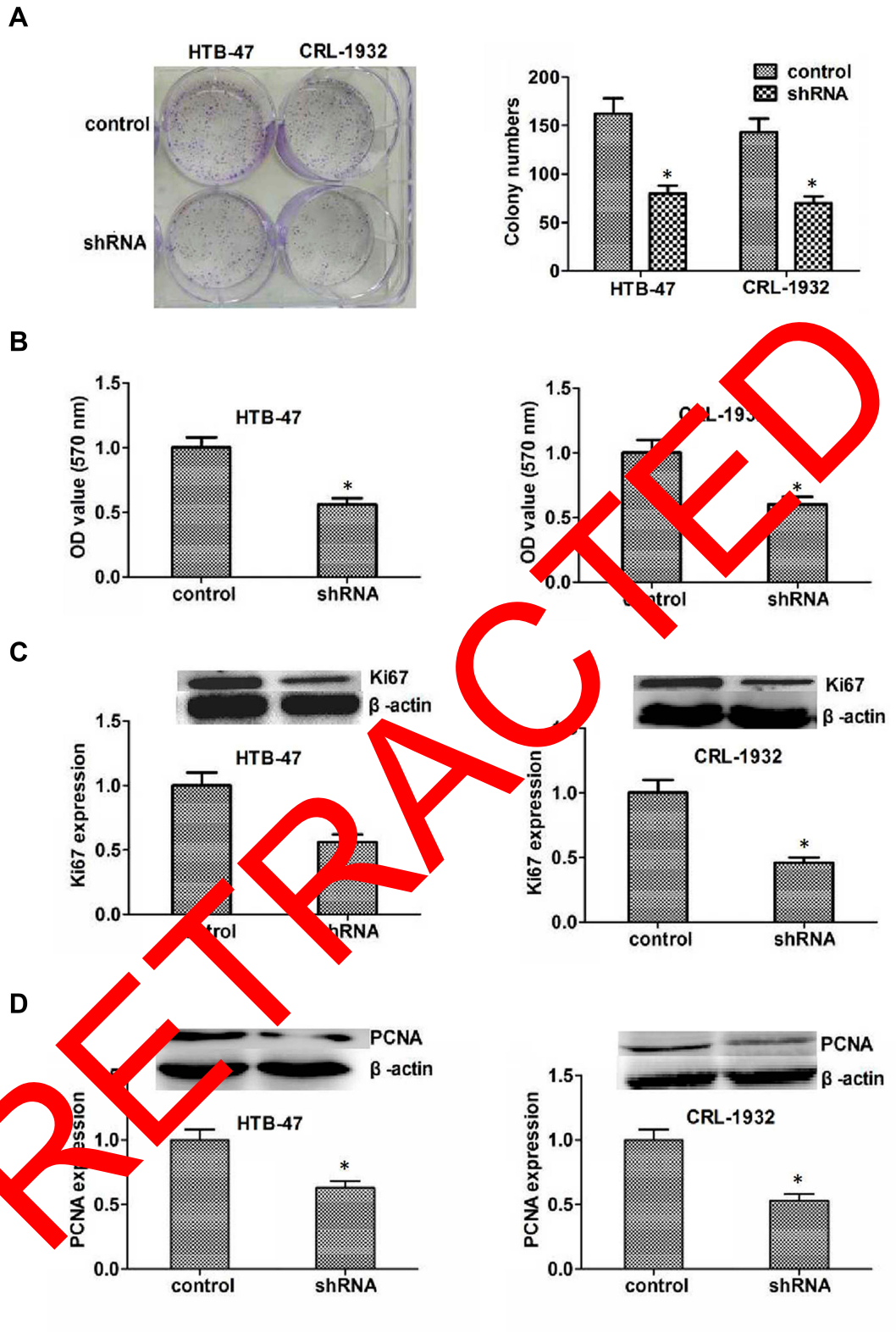

Figure 4 KIF4A promotes ccRCC cell proliferation in vitro. (**A**) HTB-47 and CRL-1932 cells transfected with control or KIF4A shRNA, and the proliferation capacity was quantified by colony formation assays. (**B**) The results of MTT assays showed the inhibition of cell proliferation caused by KIF4A depletion. (**C**) Immunoblot assays showed Ki67 expression level in control or KIF4A knockdown HTB-47 and CRL-1932 cells. (**D**) Immunoblot assays revealed the expression level of PCNA in control or KIF4A ablation ccRCC cells. Results are presented as mean ± SD, *P < 0.05.

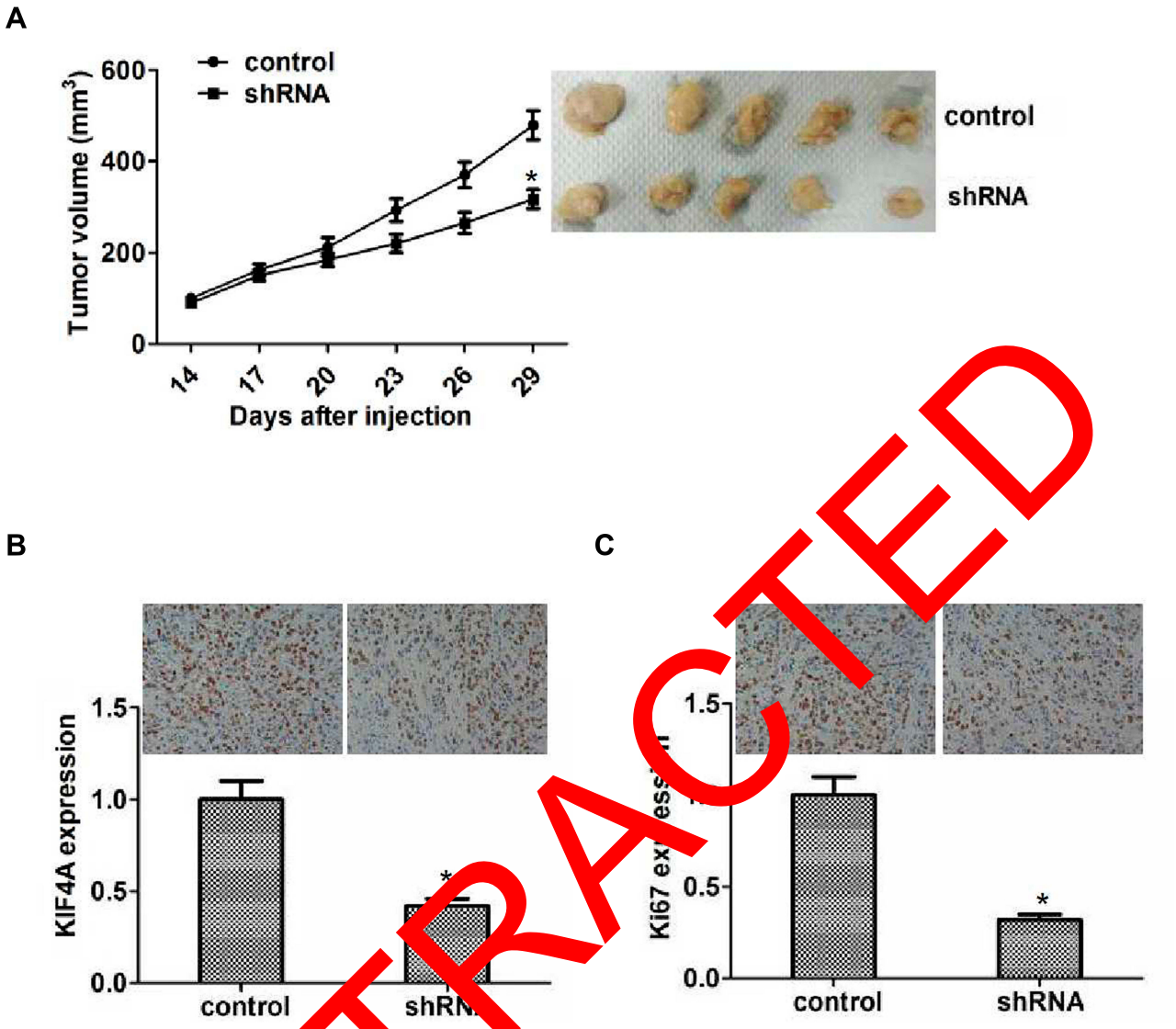

Figure 5 KIF4A facilitated ccRCC growth in mice. (**A**) Hep cells infected with control or KIF4A shRNA lentivirus were subcutaneously implanted into nude mice. After 2 weeks, tumors were isolated, and vol e was examined every days (n=5 in each group). Tumor growth curve was calculated and analyzed according to the average volume of six tumors in each group. (**B**) IH assays indicated the expression level of KIF4A in control or KIF4A depletion tumor tissues isolated from mice. (**C**) IHC assays revealed the expression level of Ki67 in trol or K A depletion tumor tissues taken from mice. Results are presented as mean ± SD, *P < 0.05.

(SAC).[28] Additionally, KIF4A promotes the proliferation of colorectal cancer by the regulation of p21-mediated cell cycle progression and they found KIF4A knockdown obviously decreased the expression level of pAKT, and the expression level of MEK and ERK was comparable, suggesting that KIF4A promotes CRC proliferation through PI3K/AKT signaling pathway.[15] Interestingly, we found that KIF4A contributed to cell proliferation of ccRCC in vitro and in mice. Whether KIF4A promotes ccRCC through this signaling pathway also requires further study.

KIF4A was known to be involved in the regulation of mitosis.[29] Previous studies have indicated KIF4A could be phosphorylated by CDK1 at S1186, triggered chromosome compaction.[23,30] Meanwhile, KIF4A affected the spindle formation and chromosome segregation in oocytes.[31,32] These studies suggest KIF4A has the potential to affect the cell cycle and proliferation of cancer cells. Interestingly, here we noticed that KIF4A promoted cell proliferation in ccRCC, and therefore thought KIF4A affected the proliferation via mediating mitosis.

In addition to KIF4A, other members of KIF family also play various roles in the tumor development and metastasis.[33] KIF7 could promote the growth of prostate tumor through LKB1-mediated AKT inhibition.[34] KIFC1 was associated with the progression of HCC.[35] Additionally, KIF3A

participated in the development of breast cancer.[36] These studies, together with our results, indicate the possible roles of KIFs as potential therapeutic targets.

Collectively, our results demonstrated that KIF4A was highly expressed in human HCC tissues. We also found a correlation between KIF4A expression level and clinical characteristics in ccRCC patients. Furthermore, KIF4A promoted the proliferation of ccRCC cells in vitro and in mice. Therefore, we have a preliminary mechanism study of KIF4A in ccRCC development and provide a novel therapeutic target for the treatment of ccRCC.

Data Sharing Statement

The dataset supporting the conclusions of this article is included in the article.

Disclosure

The authors declare that they have no competing interests in this work.

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