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ORIGINAL RESEARCH

RETRACTED ARTICLE: Targeting of KDM5A by miR-421 in Human Ovarian Cancer Suppresses the Progression of Ovarian Cancer Cells

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Purpose: The retinoblastoma binding protein RBP2 (KDM5A) is a histone demethylase that promotes cell growth in many human cancers. A series of functional experiments were conducted to explore the role of miR-421/KDM5A in ovarian cancer cells and their underlying molecular mechanisms.

Materials and Methods: Public microarray databases were analyzed to assess KDM5A and miR-421 expression in ovarian cancer. KDM5A was predicted to be a target of miR-421 using software analysis. The expression of the miR-421/KDM5A regulatory axis in ovarian cancer and the mechanisms of its effects on proliferation, migration, and invasion of ovarian cancer cell lines were investigated.

Results: Compared with normal ovarian tissues, the expression of KDM5A mRNA and protein was elevated ($P<0.05$), and miR-421 expression was reduced in ovarian cancer tissue ($P<0.05$). miR-421 was found to bind specifically to the KDM5A gene. Silencing KDM5A or overexpressing miR-421 significantly inhibited proliferation, migration, and invasion of OVCAR-8 and SKOV-3 cells. Similarly, compared with nude mice injected with cells transfected with empty capsids, the in vivo proliferation rate of OVCAR-8 cells after miR-421 overexpression was reduced significantly.

Conclusion: The miR-421/KDM5A regulatory axis plays an important role in the development and progression of ovarian cancer cells.

Keywords: ovarian cancer, KDM5A/RBP2, miR-421, progression

Introduction

Ovarian cancer has the highest mortality rate in the reproductive system.[1] It is the fifth most frequent female cancer type in the western world and although the surgical techniques have been improving with more treatment options, the 5-year survival rate of ovarian cancer is still at 47.4% among American women based on 2008–2014 cases. The high mortality is due to the diagnosis at the late stages (stage III or IV) for most cases[2,3] and chemotherapy resistance. Thus, investigating novel targets of ovarian cancer treatment is urgently important.[4]

Histone methylation epigenetically controls gene expression[5] via histone-modifying enzymes, including methyltransferases and demethylases. KDM5A (Lysine specific demethylase 5A), also known as RBP2 (Retinol-binding protein) or JARID1A (jumonji, AT rich interactive domain 1A), is originally identified as a retinoblastoma protein (Rb)-binding partner.[6] Depending on its JmjC domain, KDM5A regulates gene expression by removing di- and trimethyl groups from

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H3K4 (lysine 4 of histone 3).[7–9] In recent years, accumulating shreds of evidence has shown that KDM5A is found to be dysregulated in some diseases including tumors, and has previously been convincingly revealed that KDM5A is overexpressed in gastric cancer. The inhibition of KDM5A triggers senescence of gastric cancer cells.[10] In human lung cancer tissues and cell lines, KDM5A was also overexpressed. Inhibition of KMD5A expression by shRNA (short hairpin RNA) impaired the proliferation, motility, migration, invasion, and metastasis of lung cancer cells. KDM5A enhances cell proliferation and metastasis potentially through upregulation cyclins D1 and E1 expression while downregulation the cyclin-dependent kinase inhibitor p27 (CDKN1B) expression.[11]

MicroRNAs (miRNAs) are around 21 nucleotides endogenous non-coding RNAs.[12,13] It can result in the cleavage or translation repression of target mRNAs by binding to the 3′-untranslated region (UTR) of target genes.[14–17] Numbers of miRNA that have been found promoted or suppressed the progression of ovarian cancer include Let-7, miR-200 family, miR-21, miR-145, and miR-23b.[18–20] However, there are still numerous miRNAs whose biological functions and molecular mechanisms remain unknown.[21] It was found that miR-421 is down-regulated in breast cancer tissues and metastatic cell lines. Moreover, miR-421 suppressed the metastasis of breast cancer by inhibiting the expression of MTA1 directly.[22] However, little is known about the physiologic targets of miR-421 in ovarian cancer.

In our study, we demonstrated that KDM5A up-regulation was a characteristic molecular change in ovarian cancer and it promoted the proliferation and metastasis of ovarian cancer in vitro and in vivo. Moreover, the mechanistic analysis revealed that KDM5A was a direct target of miR-421. Down-regulated miR-421 was positively correlated with the survival rate in ovarian cancer patients. Together, our present work provided the first evidence for an oncogenic role for KDM5A/miR-421 in ovarian cancer progression.

Materials and Methods

Expression Data Sets

We downloaded the set of microarray data (GSE66957) from the Gene Expression Omnibus (GEO) (http://www.ncbi.nlm.nih.gov/geo) to analyze the expression of KDM5A in ovarian tissues. The expression and clinical data of KDM5A and miR-421 were downloaded from The Cancer Genome Atlas Project (TCGA; http://tcga-data.nci.nih.gov/). It included a total of 304/438 samples for ovarian cancer patients. The correlation between the expression levels of KDM5A/miR-421 and the clinical characteristics were analyzed by BRB-array tools (v4.5.0Beta2).

miRNAs Target Prediction Algorithms

Online tools, including miRanda, miRWalk, and Targetscan were used to screen our candidate miRNAs that could regulate KDM5A. Several miRNAs were proposed and after integrating the results, downloading and analyzing the expression datasets and clinical data of miRNAs from TCGA, we selected miR-421 for further research because of its tumor suppressor properties in ovarian cancer.

Patient Samples

This research was approved by the ethics committee of the First Affiliated Hospital of Zhengzhou University. Tissue specimens of 51 ovarian cancer tissues, and 51 normal ovary subjects who had hysterectomy and salpingo-oophorectomy due to uterine myoma and confirmed as normal controls, were obtained from 2010 to 2014 from the Department of Gynecology in the First Affiliated Hospital of Zhengzhou University. The signed informed consent was obtained from the patients. The tissue samples were stored at −80°C for subsequent quantification of mRNA/miRNA expression and Paraffin-embedded specimens were used for immunohistochemical analysis. To further confirm the expression of KDM5A, we collected another 17 ovarian cancer tissues which were already embedded by paraffin in the pathology department. All of the 68 Paraffin-Embedded ovarian cancer tissues were made to a tissue microarray (TMA) to determine the protein expression level of KDM5A in ovarian cancer tissues. Those patients who have not received previous chemotherapy or radiation were included in the study and the patients with the severe concomitant diseases were excluded. Every archived frozen tissue was confirmed by two pathologists independently to be similar to those in the paraffin-embedded tissues.

Cell Culture

Human ovarian cancer cell lines (OVCAR-8 and SKOV-3) were purchased from the American Type Culture Collection (ATCC, Manassas, VA). Cell lines were incubated at 37°C in 5% CO_2 atmosphere in DMEM medium (Gibco, USA) containing 10% FBS (CLARK Bioscience, USA).

Polymerase Chain Reaction (PCR) Assays

Total RNA from cells and tissue samples were isolated using Trizol reagent (Invitrogen, US) following the manufacturer's protocols. Similarly, the reaction cDNA was synthesized using the Reverse Transcription System (TAKARA, Japan). After all the mRNA and miRNA were reverse transcribed, qRT-PCR was performed with the Applied Biosystems 7500 system (Life Technologies, US). The relative expression levels of KDM5A and miR-421 were calculated based on the $2^{-\Delta\Delta CT}$ method. The primers used in this study are listed in Table S1.

Western Blotting Analysis

Total proteins were extracted using a RIPA protein extraction reagent (Beyotime, People's Republic of China). Western blot analysis was performed as described.[23] The Odyssey infrared imaging system was used to scan membrane signals and the results were analyzed using Odyssey 3.0 software (LI-COR Biosciences).

Immunohistochemistry (IHC)

IHC was executed as previously described.[23] The antibodies used in the IHC were anti-KDM5A and anti-Ki-67 (Abcam, USA). The KDM5A protein would be quantified with the proportion and intensity of positively stained cells across three randomized images. We used the NanoZoomer 2.0-RS system (Hamamatsu Photonics, Inc., Germany) to obtain the images and the software NDP.view 2.5.14 version to analyze the digital slides.

Transfection of Cell Lines

Ovarian cancer cell lines (OVCAR-8 and SKOV-3) were transfected with miR-421 mimics or KDM5A siRNA using Lipofectamine3000 transfection reagent (Invitrogen, USA). miR-421 mimics were synthesized by GenePharma (Shanghai, China). The sequences of the miR-421 mimics are listed in Table S2.

Luciferase Activity Assay

The full-length KDM5A 3′UTR (KDM5A-wt) and the KDM5A mutant 3′UTR (KDM5A-mut) were amplified using the PCR system. Then the target sequence was subcloned into psiCHECK-2 vector (Promega, USA). Cells were transfected with the reporter constructs and then transfected with miR-421 mimics or control miRNAs. After 48 hours, reporter assays were determined with the Dual-Luciferase Reporter Assay System (Promega, USA).

MTT Assay

Ovarian cancer cells transfected with miR-421 mimics or KDM5A si-RNA (small interfering RNA) were seeded in 96-well plates and incubated overnight. Cell proliferation was assessed using the MTT solution (Beyotime, China) every 24 hours. MTT (0.5mg/mL) was added into each well for an additional incubation for 1 hour. To dissolve the formazan crystals and terminated the MTT reaction, 100μL DMSO was added. The results were determined by measuring the absorbance at 490 nm with a spectrophotometer (Molecular Devices, USA).

Wound-Healing Assay

Ovarian cancer cells were cultured in a six-well plate. When cells reached 80% confluence, the medium was replaced with serum-free medium and a gap was created by a 200μL pipette tip. The distances between two wounds were observed at 0, 24, and 36 hours.

Cell Invasion Assay

The invasion activity was assayed using Matrigel Invasion Chambers (BD Biosciences). The upper chamber was coated with Matrigel and dried at room temperature. 1×10^4 transfected cells or control cells were seeded on the upper surfaces of the filter in a serum-free medium. 24 hours later, the cells migrated to the lower chamber were stained with 0.5% crystal violet and counted under a microscope.

In vivo Tumor Growth Experiments

The institutional animal care and use committee of the First Affiliated Hospital of Zhengzhou University approved all the in vivo experiments performed in this study. This study was carried out in strict accordance with the Guide for the Care and Use of Laboratory Animals: Eighth Edition (2011).[24] miR-421-overexpressing OVCAR-8 cells and the control cells were implanted subcutaneously into the 4 or 6 week-old nude mice. Tumor volume was photographed once a week by the IVIS@ Lumina II system (Caliper Life Sciences, Hopkinton, MA). The mice were sacrificed 4 weeks after injection, and the tumor specimens were fixed in 10% formalin for histopathological analysis and IHC.

Statistical Analysis

The data were presented as mean ± SEM. The difference between the experimental and the control groups

was analyzed by Student's *t*-test with the SPSS 21.0 statistical software. The correlation between the expression of miR-421 and KDM5A was analyzed by Spearman rank analysis with GraphPad Prism 7.0. $P < 0.05$ was considered statistically significant.

Results

Association of High KDM5A Expression in Ovarian Cancer with Poor Clinical Prognosis

KDM5A mRNA (messenger RNA) was significantly elevated in ovarian cancer compared to normal ovarian tissues (Figure 1A). The overall survival (OS) of patients with high KDM5A mRNA expression was notably shorter than that of patients with low KDM5A expression (Figure 1B).

Tissue microarrays were used to compare KDM5A protein expression in normal ovarian and ovarian cancer tissues (Figure 2A–D). Besides, the relationship between KDM5A protein expression and the clinicopathological prognosis was evaluated. KDM5A expression was significantly elevated in ovarian cancer compared with normal ovarian tissue (Figure 2E and F). High KDM5A expression was associated with the FIGO stage (p=0.012) and lymph node metastasis (p=0.005), but there were no significant associations with age, histological type, and pathological grade (Table 1). Furthermore, overall survival was also significant in association with the FIGO stage (p=0.003), lymph node metastasis (p=0.000), and KDM5A expression (p=0.000) (Table 1). Multivariate analyses were utilized to evaluate whether the KDM5A expression level and various clinicopathological features were independent prognostic parameters of patient outcomes. KDM5A expression (RR =1.849, 95% CI: 1.616–2.20714; P = 0.041), lymph metastasis (RR =1.573, 95% CI: 1.309–2.014; P = 0.043), and the FIGO stage (RR =2.915, 95% CI: 2.561–3.452; P = 0.032) were independently associated with the overall survival (Table 2).

The Kaplan-Meier method was used to analyze the relationship between KDM5A expression and patient survival. OS of patients in the KDM5A-high group (median survival, 54.5 months) was significantly shorter than that of patients in the KDM5A-low group (median survival, 68.4 months) (Figure 2F).

Suppression of the Ovarian Cancer Cells Proliferation and Invasion Due to KDM5 Knockdown

To study the function of KDM5A in ovarian cancer, KDM5A siRNA was used to knock down its expression in OVCAR-8 and SKOV-3 ovarian cancer cells, and the proliferation and invasion of these cells were studied. After transfection, the efficiency of KDM5A siRNA was evaluated by RT-PCR (Reverse Transcription Polymerase Chain Reaction) and Western blotting. The results showed that KDM5A mRNA and protein expression was significantly reduced in transfected OVCAR-8 and SKOV-3 ovarian cancer cells. Optimal knockdown efficiency was reached when the siRNA concentration was 45 nmol/L (Figure 3A and B).

We examined the effects of KDM5A knockdown on the proliferation and migration of ovarian cancer cells using EdU assay (Figure 3C), MTT (Figure 3D), scratch, and

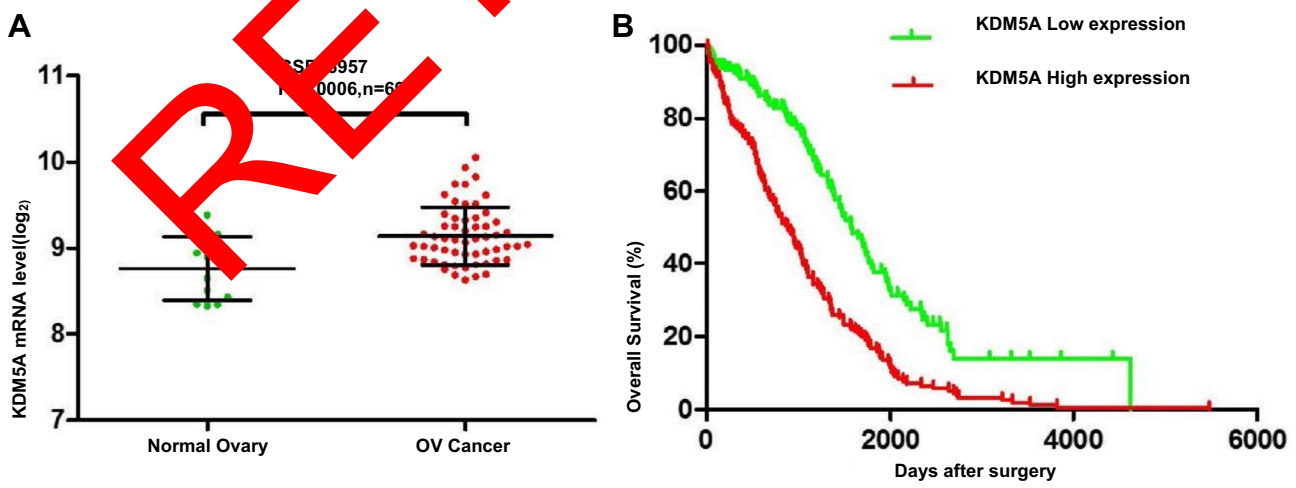

Figure 1 KDM5A is over-expressed in ovarian cancer tissues and was correlated with prognosis of ovarian cancer patients in public databases. (**A**) KDM5A expression levels in GEO ovarian cancer cohort. (**B**) Kaplan-Meier relapse-free survival analysis between expression of KDM5A (red, high KDM5A expression; green, low KDM5A expression).

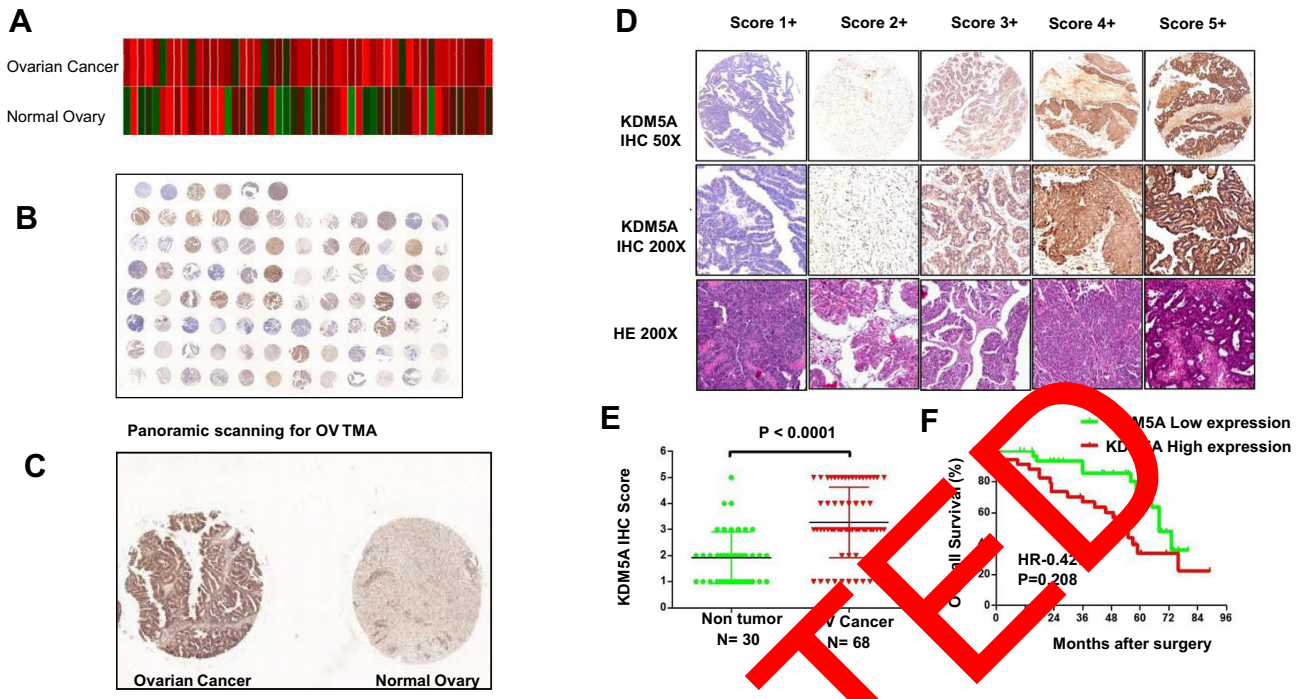

Figure 2 KDM5A is over-expressed in ovarian cancer tissues and was correlated with prognosis of ovarian cancer patients. (**A**) The mRNA expression level of KDM5A in ovarian cancer and normal ovary tissues. (**B**–**D**) Representative KDM5A and immunohistochemical staining patterns with different staining scores in ovarian cancer tissues. (**E**) Distribution of KDM5A immunohistochemical staining scores in normal ovary and ovarian cancer tissues. (**F**) Kaplan-Meier overall survival analysis between expression of KDM5A (red, high KDM5A expression; green, low KDM5A expression).

colony formation assays. The results showed that the proliferation capacity of OVCAR-8 and SKOV-3 cells transfected with KDM5A siRNA was profoundly reduced compared with untreated control cells and cells transfected with control siRNA (Figure 3C and D). The scratch assay showed that KDM5A silencing significantly suppressed the migration capacity of OVCAR-8 and SKOV-3 cells (Figure 3E) and the results of the cell invasion assay showed a notable

Table 1 The Relationship Between KDM5A Expression and Clinicopathological Features of Ovarian Cancer

Clinicopathological Feature		KDM5A Expression		χ^2	*P*	Survival		χ^2	*P*
		Low (n=21)	High (n=47)			Live (n=33)	Dead (n=35)		
Age (years)	>median ≤median	9 12	19 28	0.006	0.937	10 23	18 17	2.32	0.128
FIGO stage	Stage I and II III and IV	17 4	21 26	6.344	**0.012**	25 8	13 22	8.77	**0.003**
Histological type	Serous Mucinous and others	10 11	22 25	0.04	0.841	19 14	13 22	2.09	0.149
Grade	G1 G2/G3	8 13	22 25	0.163	0.686	17 16	13 22	0.89	0.343
Lymph node metastasis	Absent Present	16 5	17 30	7.773	**0.005**	25 8	8 27	16.97	**0.000**
KDM5A expression	Low High	– –	– –		–	17 16	4 31	10.978	**0.0009**

Notes: p<0.05 is considered statistically significant. Significant p-values are in bold.
Abbreviation: FIGO, International Federation of Gynecology and Obstetrics.

Table 2 Multivariate Survival Analyses of Independent Prognostic Factors in Patients with Ovarian Cancer

Multivariate Analysis	Relative Risk	(95% CI)	*P*-value
FIGO stage (III and IV vs I and II)	2.915	2.561–3.452	**0.032**
Lymph node metastasis (Present vs Absent)	1.573	1.309–2.014	**0.043**
KDM5A expression (High vs Low)	1.849	1.616–2.20714	**0.041**

Notes: p<0.05 is considered statistically significant. Significant p-values are in bold.
Abbreviations: FIGO, International Federation of Gynecology and Obstetrics; CI, confidence interval.

reduction of the invasive capacity of ovarian cancer cells transfected with KDM5A siRNA compared with that of cells transfected with control siRNA (Figure 3F).

KDM5A as a Direct Target of miR-421 in Ovarian Cancer

Bioinformatics analysis was utilized to screen and predict miRNAs with binding potential to the 3′UTR of KDM5A mRNA. Based on this analysis, miR-421 was predicted to target KDM5A mRNA and was selected for further study. RT-PCR was used to compare miR-421 expression in ovarian cancer and normal ovarian tissues. Also, the relationship between the miR-421 expression level in ovarian cancer specimens and patient prognosis in the TCGA database was analyzed. The results showed that miR-421 expression was reduced in ovarian cancer tissues, and this reduced expression correlated with the patient prognosis. After overexpression of miR-421, KDM5A mRNA and protein level[illegible] considerably reduced.

Next, we confirmed that the KDM5A 3′-UTR region was a direct target of miR-421 using a dual-luciferase gene reporter assay in which miR-421 and wild-type or mutated KDM5A reporter vectors were cotransfected. Cells transfected with the reporter plasmid pMIR-KDM5A-3′-UTR exhibited stable miR-421 expression and luciferase activity was significantly weaker than that in ovarian cancer cells transfected with control miRNA. These results suggested that miR-421 can bind directly to KDM5A mRNA. Further experiments confirmed that the proliferation and

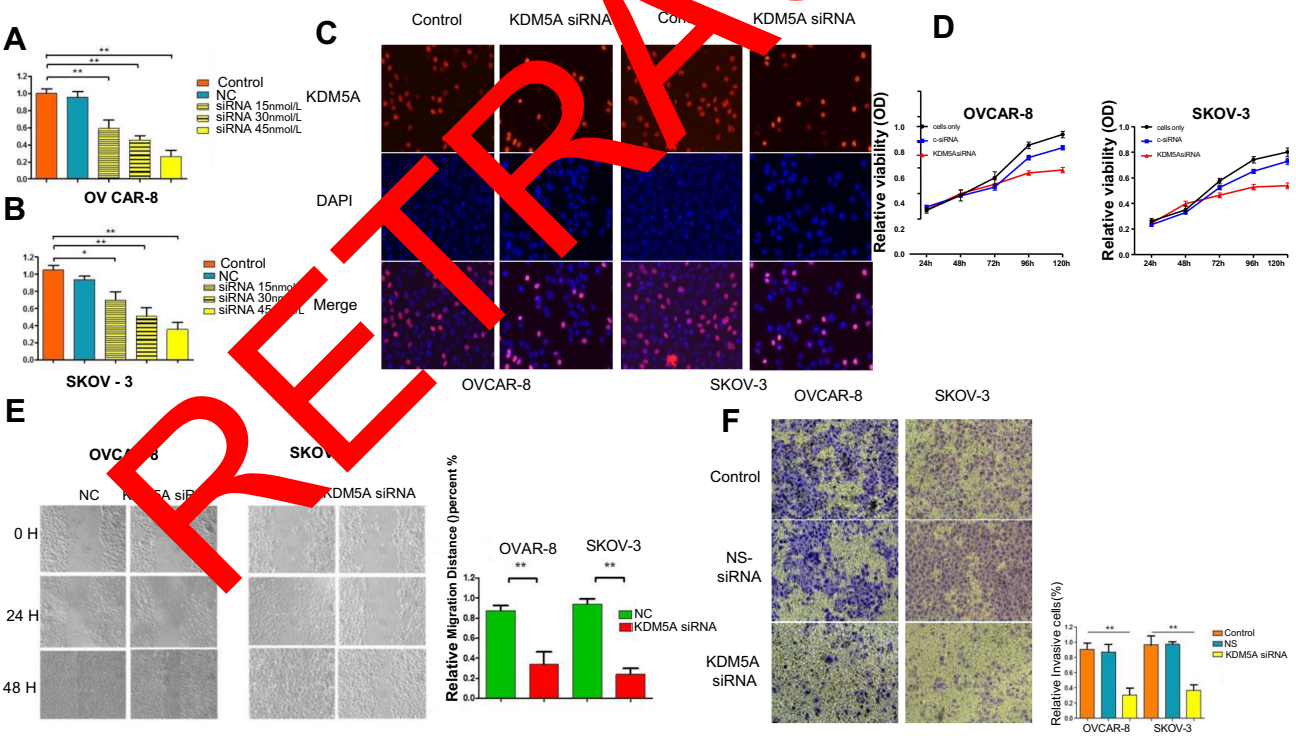

Figure 3 RNAi mediated KDM5A silencing suppresses in vitro ovarian cancer cell proliferation, metastasis and invasion. (**A** and **B**) Dose-dependent KDM5A siRNA downregulated the expression of KDM5A. (**C**) EdU assay showed that treated with KDM5A siRNA could suppress proliferation of OVCAR-8 and SKOV-3 cells. (**D**) Proliferation assays indicated that downregulation of KDM5A inhibited the proliferation capacity of OVCAR-8 and SKOV-3 cells. (**E**) KDM5A silencing caused a remarkable suppression of cell migration in OVCAR-8 and SKOV-3 cells using wound-healing assay. (**F**) The invasiveness of OVCAR-8 and SKOV-3 cells infected with KDM5A siRNA was significantly suppressed according to cell invasion assay.

invasion capacities of ovarian cancer were significantly reduced after miR-421 overexpression (Figure 4A–H).

Key Role of miR-421/KDM5A in Ovarian Cancer Growth and Metastasis in vivo

To further study the oncogenic role of miR-421 partly through the negative regulation of KDM5A, we injected OVCAR-8 cells harboring Lenti-miR-421 or control into the nude mice. Lenti-miR-421 group significantly reduced the tumor weight and volume compared with the control group (Figure 5A–D). This is consistent with the result in vitro. Moreover, IHC staining of xenograft tumors confirmed lower KDM5A and stronger Ki-67 staining in Lenti-miR-421 tumor tissues than in the control group. Besides, the expression of KDM5A was negatively correlated with the expression of miR-421 (Figure 5E).

Discussion

As an important member of KDMs, KDM5A may contribute to tumor development and progression in various ways.[25–28] A recent study in high-stage and high-risk neuroblastomas indicates KDM5A is overexpressed and correlated with poor prognosis. The cancer progression of neuroblastomas is modulated by KDM5A through inhibiting the translation of p53.[25] A recent study reveals that KDM5A is overexpressed in glioblastoma (GB) compared to normal brain tissue. The expression of KDM5A is increasingly accompanied by the development of Temozolomide (TMZ) resistance. GB cell growth can be inhibited efficiently after using TMZ/KDM inhibitor (JIB 04).[29] However, there are few reports on its role in ovarian cancer.

This study evaluated KDM5A expression in ovarian cancer and normal ovarian tissues and revealed that KDM5A expression is significantly elevated in ovarian cancer. Furthermore, high KDM5A expression was significantly associated with poor prognosis of ovarian cancer. We further found that KDM5A was significantly upregulated in ovarian cancer by analyzing TCGA and GEO datasets. After the KDM5A knockdown, the proliferation, migration and invasion capacities of ovarian cancer cells were considerably reduced, suggesting that KDM5A plays an oncogenic role in the progression of ovarian cancer. Consistent with these results, Feng et al[30] found that KDM5A expression was significantly elevated in ovarian

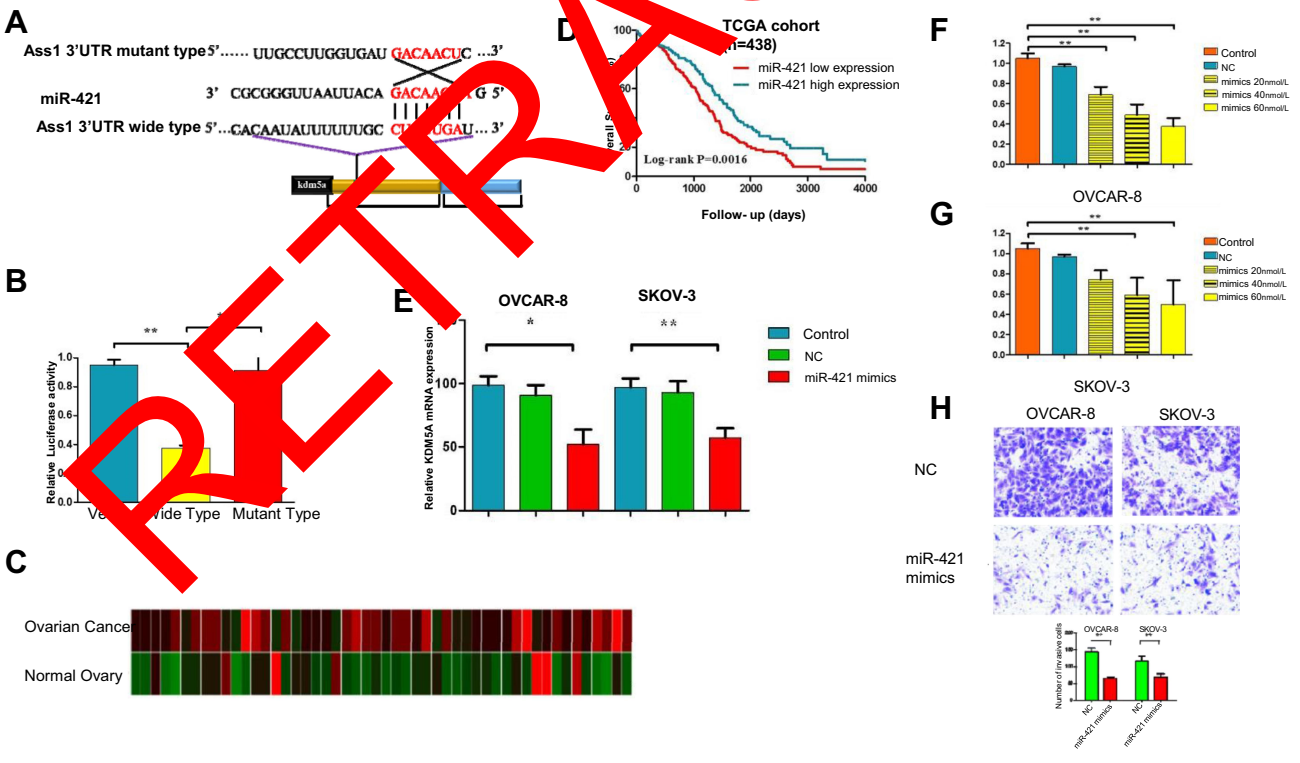

Figure 4 KDM5A as the functional target of miR-421. (**A**) Schematic representation of the miR-421 site in KDM5A 3′-UTR. (**B**) Luciferase assays using KDM5A 3′UTR region with either wide-type miR-421 binding site or mutant binding site after ectopic expression of miR-421. (**C**) Relative expression of miR-421 in normal ovary and ovarian cancer tissues. (**D**) miR-421 expression levels in TCGA BRCA cohort. (**E–G**) The expression of KDM5A mRNA and protein after using miR-421 mimics or NC on in OVCAR-8 and SKOV-3 cells. (**H**) The invasiveness of OVCAR-8 and SKOV-3 cells infected with miR-421 mimics was significantly suppressed according to cell invasion assay.

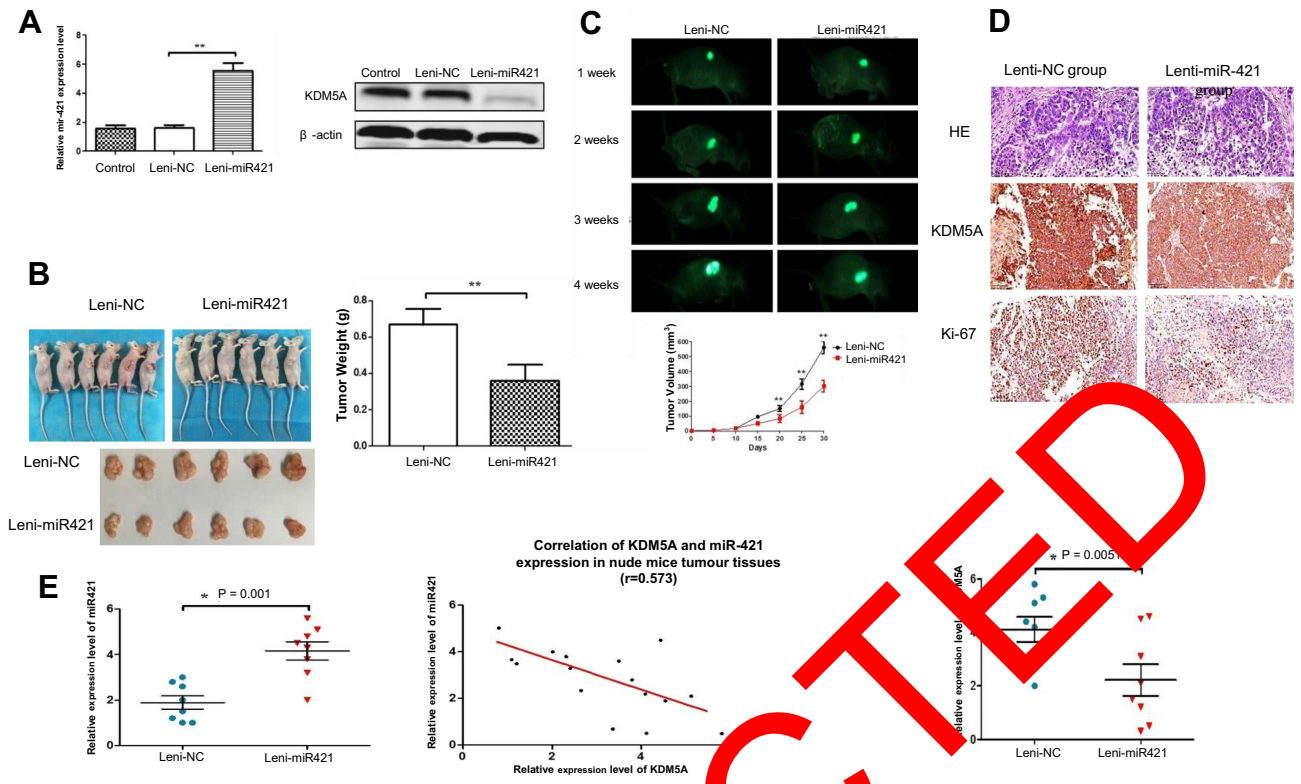

Figure 5 The over-expression of miR-421 suppress KDM5A tumorigenesis in vivo. (**A**) Effect on the expression of miR-421 and KDM5A after transfection of Lenti-NC and lenti-miR-421 in ovarian cancer cells. (**B**) Tumor volume and tumor weight in lenti-miR-421 group were markedly smaller than those of Lenti-mock group. (**C**) Images of tumor formation were performed by a live imaging system detecting the luciferase signal. The luciferase signal of the lenti-miR-421 tumors was lower than that of the Lenti-mock group. (**D**) Sections of xenograft tumors stained with hematoxylin and eosin (H&E) as well as immunohistochemical staining for KDM5A and Ki-67. (**E**) miR-421 expression in relation to the expression levels of KDM5A mRNA.

cancer tissues compared with adjacent normal tumor ovarian tissues. KDM5A expression has been found to be also elevated in ovarian cancer cell lines including SKOV3/PTX cells. In our study, the KDM5A knockdown suggestively reduced the proliferation, migration and invasion capacities of OVCAR-8 and SKOV-3 ovarian cancer cells. Collectively, the results from this and other studies indicate a role of KDM5A as an oncogene.

miRNA is an important regulatory factor of gene expression in a variety of ways from transcriptional regulation to post-translational protein modification and plays a dual role of oncogene or tumor suppressor in ovarian cancer progression. Bioinformatics analysis predicted that miR-421can target KDM5A mRNA. Indeed, by using the luciferase activity assay, we confirmed that the KDM5A 3′-UTR region was a direct target of miR-421. In recent years, miR-421 has been found to be abnormally expressed in tumors including breast cancer, liver cancer, and pancreatic cancer. And its aberrant expression is to be associated with tumor metastasis and poor prognosis.[27,31–34] A recent study reported that the miR-421 expression level in breast cancer tissues was significantly higher than that in adjacent normal breast tissues and that miR-421 promoted cell proliferation and colony formation in vitro.[35] Meanwhile, other studies have shown that miR-421 is down-regulated in cancer tissues and acts as a tumor suppressor. Recently, a study reported that miR-421 is low expressed in glioma tissues and cell lines. Its function as a tumor suppressor in glioma is via MEF2D.[36] There are currently no reports on the role of miR-421 in ovarian cancer. We speculated that miR-421 might exert its effects through KDM5A. Thus, we compared miR-421 expression in ovarian cancer and normal ovarian tissues and found that it was significantly reduced in ovarian cancer tissues. Moreover, the OS of patients with ovarian cancer who had low miR-421 expression was significantly shorter than that of patients with high miR-421 expression. This suggested that miR-421 expression is closely related to the clinical prognosis of patients with ovarian cancer and that miR-421 might be a tumor suppressor. Additionally, miR-421 overexpression in ovarian cancer cells significantly reduced the proliferation, migration, and invasion of these cells, an effect similar to that of KDM5A

inhibition. These results suggested that the miR-421/KDM5A regulatory axis might play a crucial role in the progression of ovarian cancer.

To verify the effect of miR-421/KDM5A on tumor growth in vivo, the effect of miR-421 overexpression on ovarian cancer cell growth was investigated in nude mice. Compared with nude mice transfected with empty capsids, the in vivo proliferation rate of ovarian cancer cells over-expressing miR-421 was significantly reduced. Furthermore, the expression levels of both KDM5A and Ki67 were reduced after overexpression of miR-421, and tumor expression levels of miR-421 and KDM5A were negatively correlated. This indicated that miR-421 targets and negatively regulates KDM5A expression in ovarian cancer, which in turn affects the tumor cell proliferation rate. However, the detailed molecular mechanisms should be further explored.

Conclusion

The role of KDM5A in promoting the proliferation, migration, and invasion of ovarian cancer cells has been well established. Besides, we found that KDM5A is highly expressed in ovarian cancer and is associated with poor clinical prognosis. Our report also showed that miR-421 targeted KDM5A and demonstrated the important role of the miR-421/KDM5A regulatory axis in ovarian cancer. Collectively, this work has provided evidence for an oncogenic role for KDM5A/miR-421 in ovarian cancer progression.

Abbreviations

KDM5A, Lysine specific demethylase 5A; RBP2, Retinoblastoma binding protein 2; JARID1A, jumonji, AT rich interactive domain 1A; Rb, Retinoblastoma binding protein; Jmj, Jumonji; H3K4, Histone 3 Lysine 4; CDKN1B, Cyclin dependent kinase inhibitor 1B; miRNA, MicroRNA, Ribonucleic acid; MTA1, Metastasis Associated 1; GEO, Gene Expression Omnibus; TCGA, The Cancer Genome Atlas; ATCC, American Type Culture Collection; DMEM, Dulbecco's Modified Eagle Medium; FBS, Fetal bovine serum; cDNA, complementary deoxyribonucleic acid; qRT-PCR, Quantitative Reverse Transcription Polymerase Chain Reaction; MTT- 3, (4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide; DMSO, Dimethyl sulphoxide; FIGO, International Federation of Gynecology and Obstetrics, MEF2D, Myocyte Enhancer Factor 2D.

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Disclosure

The authors report no conflicts of interest in this work.

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