OncoTargets and Therapy

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ORIGINAL RESEARCH

RETRACTED ARTICLE: Circular RNA hsa_circ_0023404 promotes proliferation, migration and invasion in non-small cell lung cancer by regulating miR-217/ZEB1 axis

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

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Background: Circular RNAs (circRNAs) have been considered as key regulators of cancer biology. However, the functional role of hsa_circ_0023404 in non-small cell lung cancer (NSCLC) and its regulatory mechanism are still unknown.

Methods: The expression of hsa_circ_0023404, miR-217 and zinc finger E-box-binding homeobox 1 (ZEB1) was evaluated by quantitative real-time polymerase chain reaction. The role of hsa_circ_0023404 in NSCLC progression was determined using cell count kit-8 assay, transwell migration and invasion assay. Luciferase reporter assay was performed to assess the interaction of hsa_circ_0023404, miR-217 and ZEB1 in NSCLC cells.

Results: The expression of hsa_circ_0023404 was upregulated in NSCLC tissues, as well as in NSCLC cell lines. High hsa_circ_0023404 expression predicted short overall survival in NSCLC. Functionally, knockdown of hsa_circ_0023404 inhibited the proliferation, migration and invasion of NSCLC cells. The further molecular mechanism study, hsa_circ_0023404 was shown to interact with miR-217/ZEB1 axis to contribute to the growth of NSCLC cells.

Conclusion: hsa_circ_0023404 promotes the proliferation, migration and invasion of NSCLC cells by regulating miR-217/ZEB1 axis, providing a fresh perspective on circRNAs in NSCLC development.

Keywords: hsa_circ_0023404, microRNA-217, Zinc finger E-box-binding homeobox 1, non-small cell lung cancer

Introduction

Lung cancer is the most prevalent malignant tumor with a high incidence rate and poor prognosis, and non-small cell lung cancer (NSCLC) accounts for approximately 85% of cases.[1] Smoking is widely recognized as a major contributor to NSCLC.[2] Due to the lack of noticeable clinical symptoms and effective screening programs, the majority of NSCLC patients were diagnosed at an advanced stage and have poor prognosis.[3] Metastasis is increasingly regarded as a dominant hindrance toward NSCLC cancer treatment, suggesting that a thorough understanding of the mechanisms that underlie NSCLC metastasis can help to develop an effective therapy for NSCLC.

Circular RNAs (circRNAs) are endogenous, abundant, conserved non-coding RNAs that form a covalently closed continuous loop by back-splicing without 3′-end and 5′-end.[4] This feature confers many properties to circRNAs, many of which have only recently been identified. Due to their unique closed loop structure, circRNAs are resistant to exonuclease-mediated degradation and, as a result, they exhibit higher

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http://doi.org/10.2147/OTT.S201834

stability than most linear RNAs, which makes them an ideal biomarker for diagnostic and therapeutic implications in cancers.[5] circRNAs are capable of interacting with the RNA-binding proteins, thus regulating the expression of target gene.[6] Additionally, circRNAs have been shown to function as sinks for miRNAs, thereby controlling the function of miRNAs.[7] Altered circRNA expression in a number of human cancers has been found, and critical roles of circRNAs in tumorigenesis have been demonstrated. Hsa_circ_0023404, a novel identified circRNA, has been reported to be implicated in tumorigenesis. Hsa_circ_0023404 was highly expressed in NSCLC tissues as compared to their paired adjacent nontumorous tissues. High hsa_circ_0023404 expression in NSCLC was remarkably correlated with regional lymph node involvement, advanced tumor staging and poor prognosis.[8] However, the role of hsa_circ_0023404 in NSCLC and its underlying mechanism are still unclear.

microRNAs (miRNAs) are an extensive category of small (18–25 nucleotides in length), non-coding, single-stranded RNAs that inhibit target gene expression by blocking target mRNA translation or enhancing its degradation through the complementarity between miRNA sequence and target mRNA 3′ untranslated regions (3′UTR).[9,10] miRNAs are recognized as master regulators of various physical and pathological processes, ranging from cell proliferation to tumor development.[11] Recently, miRNA sponge function of circRNA has been documented. Hsa_circ_0023404 functions as a sink for miR-136 to increase matrix metallopreteinases 13 expression and repress extracellular matrix formation, suggesting that hsa_circ_0023404 acts as a miRNA sponge to regulate cell fate decision.[12] However, the molecular function of hsa_circ_0023404 and its potential downstream miRNA target genes in NSCLC pathogenesis have yet to be fully explored.

In this study, we elucidated the role of hsa_circ_0023404 in NSCLC pathogenesis and its regulatory mechanism was also investigated in vitro. Functionally, hsa_circ_0023404 promoted NSCLC cell growth, migration and invasion. Mechanistically, hsa_circ_0023404, through regulating miR-217/zinc finger E-box-binding homeobox 1 (ZEB1) axis, contributed to NSCLC cell growth in vitro.

Materials and methods

Patients and tumor tissues

A total of 36 snap-frozen NSCLC tissues and paired adjacent nontumorous tissues were acquired from patients diagnosed with NSCLC. All patients signed informed consent before this study. This study had acquired the approval from the ethics committee of University-Town Hospital of Chongqing Medical University. The study was performed in accordance with the Declaration of Helsinki and the guidelines of the committee.

Cell culture

Human normal bronchial epithelial (HBE) cells and NSCLC cell lines (A549, H322 and H1299) were purchased from the American Type Culture Collection (ATCC, Rockville, MD), and GLC-82 and PC-A1 cells were obtained from the National Infrastructure of Cell Line Resource (Beijing, China). Cells were incubated in RPMI-1640 (Solarbio, Beijing, China) and dulbecco's modified eagle medium (DMEM; Solarbio) contained 10% fetal bovine serum (FBS; Solarbio) and 1% penicillin/streptomycin (Solarbio) at 37°C and 5% CO_2.

Cells transfection

shRNAs to hsa_circ_0023404 and ZEB1, miR-217 and anti-miR-217 were purchased from GENEWIZ (Jiangsu, China). The hsa-circ_0023404 and ZEB1 expression construct was generated by PCR amplification of has-circ_0023404 and ZEB1 from cDNA of NSCLC cells using the following primers: has-circ_0023404 forward: 5′-GTA CGA ATT CCC ATC CCC TTA TTC AGC-3′, reverse, 3′-CTT CAG TTT CCT CAT CAC TCG AGA CTG-5′; ZEB1 forward: 5′-GTA CGA ATT CFG CCA ATA AGC AAA CGA-3′, reverse, 3′-GTG TAC TAC TTC TGG AAC TCG AGA CTG-5′. pcDNA-circ_0023404 and pcDNA-ZEB1 overexpressing plasmids were constructed by cloning the sequence of has-circ_0023404 or ZEB1 into pcDNA-3.1 vector, respectively. These plasmids were transfected into A549 and H1299 cells using Lipofectamine 2000 (Invitrogen, Carlsbad, CA, USA). At 48 hrs after transfection, cells were harvested for the following study.

Transwell migration and invasion assay

For migration assay, A549 and H1299 cells suspended in serum-free medium were seeded on the top chamber after transfection, and medium contained 10% FBS was added into the lower chamber. For invasion assay, transwell inserts (Fisher Scientific, Waltham, MA, USA) were coated with Matrigel (BD, Franklin Lakes, NJ, USA). After 24 hrs of incubation, cells on the upper surface of the transwell membrane were gently removed using a cotton swab, and cells on the lower surface of the

transwell membrane were fixed with methanol, stained with crystal violet (0.5%; Solarbio) and counted from five randomly selected microscopic fields.

Detection of cell proliferation capacity

A549 and H1299 cells were plated at 2×10^3 cells/well in 96-well plates and grown in medium containing 10% FBS for 24 hrs. After transfection, 10 µl of cell count kit-8 (CCK-8) solution (Beyotime, Shanghai, China) was added into each well and cells were incubated for 2 hrs in a 5% CO_2 incubator at 37°C. The absorbance of each well at 450 nm was read using a spectrophotometer (Bio-Rad, Hercules, CA, USA).

Luciferase reporter assay

The wild-type (WT) sequence of has-circ_0023404 (forward, 5′-GTA CGC TAG CTG GGA GTC TGG AAG-3′; reverse, 3′-ATC TGG TCT CGG GTG GAA ACT CGA GAC TG-5′) and the WT 3′UTR sequence of ZEB1 (forward, 5′-GTA CGC TAG CTG AGA GGC TCC GAG-3′; reverse, 3′-GAA CGC ATG TCT CGA GAC TG-5′) containing the predicted binding site of miR-217 were amplified and subcloned into the pGL3 Basic reporter vectors (Promega, Madison, WI, USA) using the *Nhe* I and *Xho* I restriction sites to generate the pGL3-circ_0023404-WT and pGL3-ZEB1 3′UTR vectors. The site-directed mutagenesis was performed using the QuikChange Lightning kit (Stratagene, La Jolla, CA, USA) to construct the mutant-type (MUT) sequence of has-circ_0023404. A549 and H1299 cells were transfected with pGL3-circ_0023404-WT, pGL3-circ_0023404-MUT or pGL3-ZEB1 3′UTR, together with miR-217, pcDNA-circ_0023404 or matched controls. Cells were collected 48 hrs post transfection and analyzed with Dual-Luciferase Assay System (Promega), in keeping with the manufacturer's instructions.

Quantitative real-time polymerase chain reaction

Trizol reagent (Invitrogen) was applied to isolate total RNA from tissues and cells. cDNA synthesis was conducted using the TaqMan MicroRNA reverse transcription kit (Applied Biosystems, Foster City, CA) for miR-217 and using One Step PrimeScript cDNA kit (Qiagen, Hilden, Germany) for hsa_circ_0023404 and ZEB1. Quantitative real-time polymerase chain reaction (qRT-PCR) was performed in triplicate to determine the expression of hsa_circ_0023404 and ZEB1 with the GeneAmp 7500 system (Applied Biosystems). Meanwhile, TaqMan MicroRNA assay was carried out to evaluate the expression of miR-217. GAPDH was used as the endogenous reference gene for hsa_circ_0023404 and ZEB1, while U6 was employed as the loading control for miR-217. The relative expressions of hsa_circ_0023404, miR-217 and ZEB1 were calculated using the $2^{-\Delta\Delta CT}$ method. Primers for the target genes were listed as follows: has-circ_0023404 forward: 5′-CTG GTG CAG TGG AAG CAG AG-3′, reverse: 5′-CGA CCC TCC ATT GCT CTT CT-3′; miR-217 forward: 5′-ACA CTC CAG CTG GGT ACT GCA TCA CGA ACT G-3′, reverse: 5′-TGG TGT CGT GGA GTC G-3′; ZEB1 forward: 5′-CCC AGG ACA GCA CAG TAA T-3′, reverse: 5′-GAT GGT GTA CTA CTT CTG GAA CC-3′; GAPDH forward: 5′-GGG AAA CTG TG CGT GAT-3′, reverse: 5′-GAG TGG GTG TCG CTG T A-3′; U6 forward: 5′-CGC TTC GGC AGC ACA T ACT A ATT GGA AC-3′, reverse: 5′-GCT TCA A ATT TG G TCA TCC TTG C-3′.

Western blot analysis

Cells were harvested and lysed in RIPA buffer (Beyotime, Shanghai, China). Equal amount of protein was separated on SDS-PAGE and transferred to nitrocellulose membranes (Millipore, Bedford, MA, USA). Then, the membranes were incubated with the primary antibodies anti-ZEB1 (Cell Signaling, San Jose, CA, USA), anti-E-cadherin (Abcam, Cambridge, UK), anti-Vimentin (Abcam, Cambridge, UK), anti-N-cadherin (Abcam, Cambridge, UK) and anti-GAPDH (Santa Cruz Biotechnology, Santa Cruz, CA, USA). ECL substrates were used to visualize protein bands (Millipore).

Statistical analysis

All data were presented as the mean ± standard error of the mean (SEM). Student's *t*-test and One-way ANOVA analysis were utilized to analyze significance, while the log-rank test was applied to analyze the survival data. $P<0.05$ was considered as the limit of statistical significance.

Results

Identification of hsa_circ_0023404 in NSCLC

Initially, we sought to characterize hsa_circ_0023404 in NSCLC tissues using qRT-PCR assay. Hsa_circ_0023404 expression was higher in NSCLC tissues than that in their paired adjacent nontumorous tissues (Figure 1A). A typical feature of circRNAs is resistant to exonuclease-mediated

degradation. We treated total RNA from NSCLC tissues with RNase R and determined the expression of hsa_circ_0023404 and GAPDH in comparison with the untreated samples. The results revealed that hsa_circ_0023404 could resist RNase R, while GAPDH mRNA could be degraded by RNase R (Figure 1B). Furthermore, a marked elevation of hsa_circ_0023404 expression was observed in NSCLC cells, especially in A549 and H1299 cells, compared to HBE cells (Figure 1C). Besides, the overall survival time of NSCLS patients with high hsa_circ_0023404 expression was obviously shorter than those patients with low hsa_circ_0023404 expression, as determined by the Kaplan–Meier survival analysis (Figure 1D).

Knockdown of hsa_circ_0023404 inhibits cell proliferation, migration and invasion in NSCLC cells

Since hsa_circ_0023404 is upregulated in NSCLC, we knocked down hsa_circ_0023404 to investigate its biological role in NSCLC by transfecting A549 and H1299 cells with sh-circ_0023404. Compared to the control, transfection of sh-circ_0023404 remarkably reduced the expression of hsa_circ_0023404 in A549 and H1299 cells (Figure 2A). Downregulation of hsa_circ_0023404 markedly decreased the viability of A549 and H1299 cells, as determined by CCK-8 assay (Figure 2B and C). In parallel, knockdown of hsa_circ_0023404 led to a marked inhibition of cell migration in A549 and H1299 cells (Figure 2D). An inhibitory effect on cell invasion after hsa_circ_0023404 knockdown was also observed in transwell invasion assay (Figure 2E). Additionally, Western blotting analysis was performed to detect epithelial-mesenchymal transition (EMT)-related protein expression in A549 and H1299 cells. The results indicated that the levels of E-cadherin were increased, while the levels of N-cadherin and Vimentin were decreased by hsa_circ_0023404 knockdown in A549 and H1299 cells (Figure 2F, G and H). All these data demonstrated that knockdown of hsa_circ_0023404 inhibits cell proliferation, migration and invasion in NSCLC cells.

Hsa_circ_0023404 upregulates the expression of ZEB1 by sponging miR-217

Bioinformatics analysis predicted that miR-217 was a potential target of hsa_circ_0023404 (Figure 3A). miR-217 or miR-con and the luciferase reporter vectors were co-transfected into A549 and H1299 cells. Compared with the miR-con group, overexpression of miR-217 reduced the relative luciferase activity of the pGL3-circ_0023404-WT reporter vector in A549 and H1299 cells. Transfection of

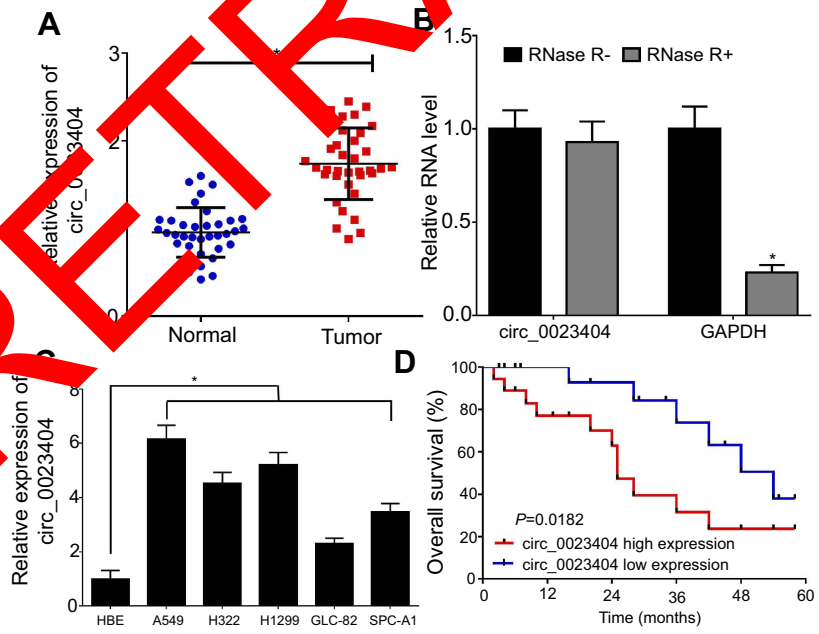

Figure 1 Identification of hsa_circ_0023404 in NSCLC. (**A**) qRT-PCR analysis of hsa_circ_0023404 expression showed increased expression of hsa_circ_0023404 in NSCLC tissues compared to their paired adjacent nontumorous tissues. (**B**) The expression of hsa_circ_0023404 was determined by qRT-PCR after treatment with RNase R. (**C**) qRT-PCR analysis of hsa_circ_0023404 expression showed upregulation of hsa_circ_0023404 in NSCLC cells. (**D**) The Kaplan–Meier survival analysis was used to assess the prognosis of NSCLC patients with different expression level of hsa_circ_0023404. The median of hsa_circ_0023404 expression in NSCLC tissues was used as the cutoff value. *$P < 0.05$; ***$P < 0.001$.

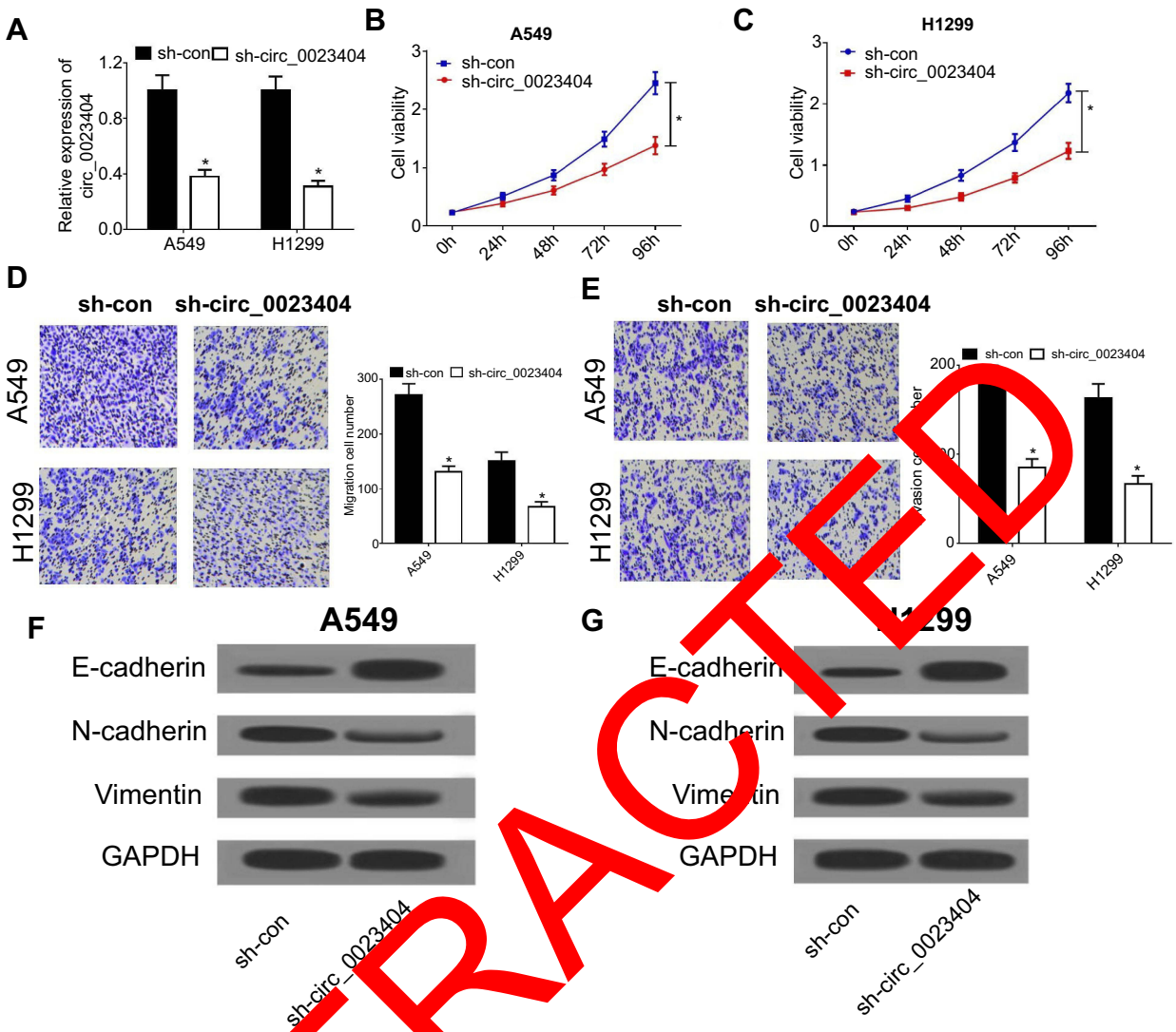

Figure 2 Knockdown of hsa_circ_0023404 inhibited cell proliferation, migration and invasion in NSCLC cells. A549 and H1299 cells were transfected with sh-con or sh-circ_0023404. (**A**) hsa_circ_0023404 level was detected by qRT-PCR in sh-con or sh-circ_0023404 transfected cells. (**B** and **C**) Cell viability was evaluated by CCK-8 assay in sh-con or sh-circ_0023404 transfected cells. (**D**) The migration of A549 and H1299 cells was determined by transwell migration assay after transfection. (**E**) Transwell invasion assay was conducted to analyze the invasion of A549 and H1299 cells transfected with sh-con or sh-circ_0023404. (**F** and **G**) The protein levels of EMT markers (E-cadherin, N-cadherin and Vimentin) were measured by Western blot analysis. *$P < 0.05$.

either miR-217 or miR-219 had no effect on the relative luciferase activity of the pGL3-circ_0023404-MUT reporter vector in A549 and H1299 cells (Figure 3B). Interestingly, when we knocked down hsa_circ_0023404 in A549 and H1299 cells, we observed a pronounced elevation in miR-217 level. Conversely, upregulation of hsa_circ_0023404 decreased the expression of miR-217 in A549 and H1299 cells (Figure 3C). More importantly, ZEB1 was predicted as a target gene of miR-217. Upregulation of miR-217 reduced the relative luciferase activity of the pGL3-ZEB1 3′UTR reporter vector in A549 and H1299 cells, which was strikingly reversed by overexpression of hsa_circ_0023404 (Figure 3D). Introduction of miR-219 mimics dramatically elevated miR-219 expression in A549 and H1299 cells (Figure 3E). In line with this, forced expression of miR-217 obviously decreased the expression of ZEB1 in A549 and H1299 cells. Furthermore, knockdown of hsa_circ_0023404 led to a concomitant decrease in ZEB1 mRNA and protein levels in A549 and H1299 cells, which was markedly blocked by miR-217 silencing (Figure 3F and G). In addition, the expression of ZEB1, as determined by qRT-PCR, was prominently higher in NSCLC tissues than that in paired adjacent nontumorous tissues (Figure 3H). Besides, a positive correlation between ZEB1 and hsa_circ_0023404 expression was noted in NSCLC samples (Figure 3I).

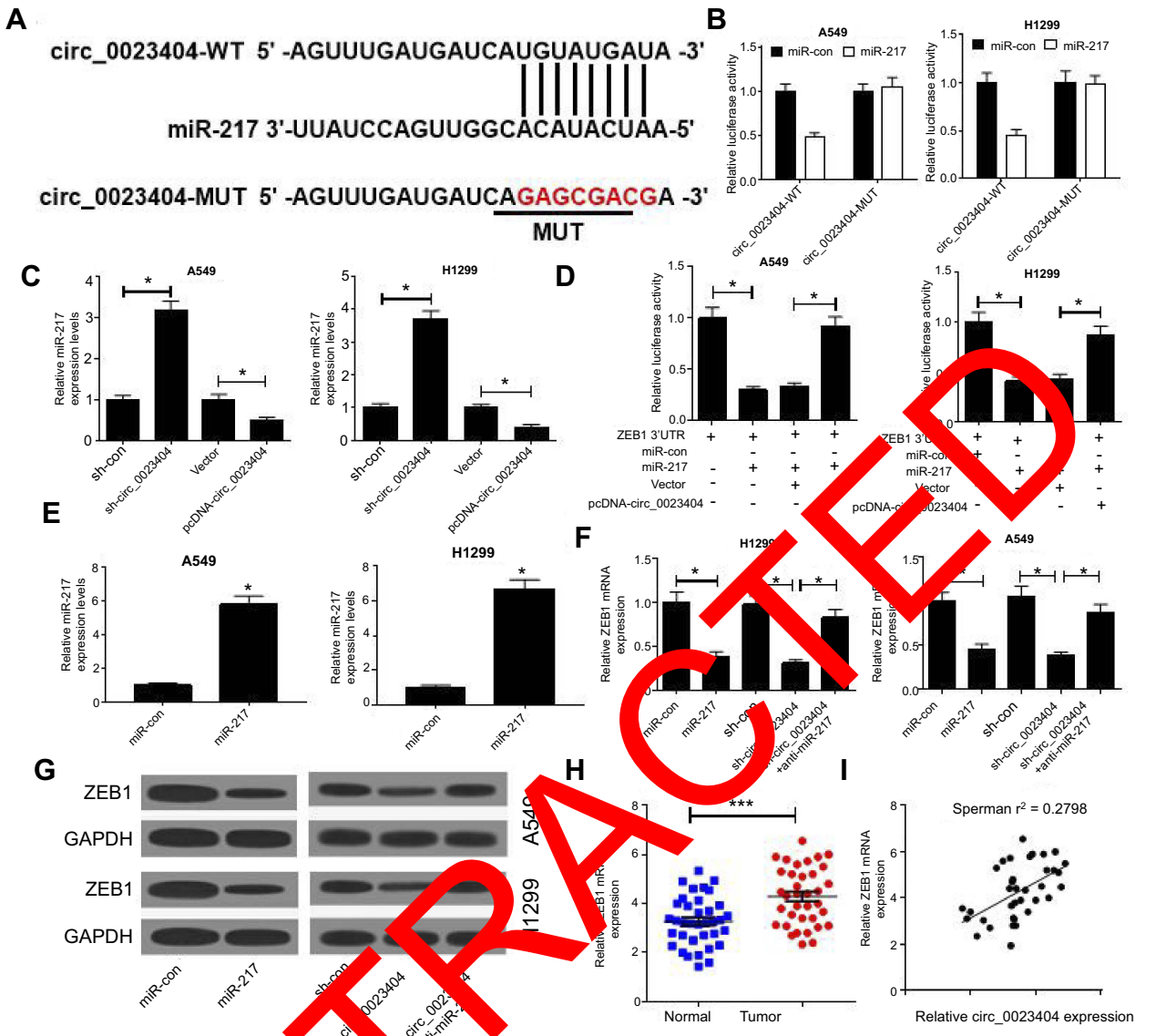

Figure 3 hsa_circ_0023404 upregulates the expression of ZEB1 by sponging miR-217. (**A**) The predicted binding site of miR-217 within the hsa_circ_0023404 3′UTR and the mutated sites were shown. (**B**) miR-217 or miR-con and the luciferase reporter vectors were co-transfected into A549 and H1299 cells. The luciferase activity was determined 48 hrs post transfection. (**C**) The expression of miR-217 was determined in A549 and H129 cells transfected with sh-circ_0023404, pcDNA-circ_0023404 or matched controls. (**D**) miR-217, pcDNA-circ_0023404 or matched controls was transfected into A549 and H1299 cells, together with pGL3-ZEB1 3′UTR. The luciferase activity was evaluated 48 hrs post transfection. (**E**) The miR-217 expression was determined after miR-con or miR-217 mimics transfection. (**F** and **G**) The mRNA and protein levels of ZEB1 were determined after transfection in A549 and H129 cells with miR-217, sh-circ_0023404, anti-miR-217 or matched controls. (**H**) qRT-PCR analysis of ZEB1 expression showed increased expression of ZEB1 in NSCLC tissues. (**I**) Correlation analysis of ZEB1 and hsa_circ_0023404 expression in NSCLC tissues. *$P < 0.05$; ***$P < 0.001$.

Overexpression of ZEB1 blocks the effect of hsa_circ_0023404 knockdown on biological behavior of NSCLC cells

Having shown the positive correlation between ZEB1 and hsa_circ_0023404 expression, we sought to explore whether the regulation of ZEB1 could affect the effect of hsa_circ_0023404 on biological behavior of NSCLC cells. As shown in Figure 4A, knockdown of has-circ_0023404 markedly reduced the mRNA and protein levels of ZEB1 in A549 and H1299 cells, which was obviously reversed by overexpression of ZEB1. CCK-8 assay showed that downregulation of has-circ_0023404 led to a marked reduction in cell viability in A549 and H1299 cells, which was remarkably mitigated by upregulation of ZEB1 (Figure 4B and C). Meanwhile, silencing of has-circ_0023404 inhibited the migration and invasion of A549 and H1299 cells, but these effects could be blocked by ZEB1 overexpression (Figure 4D and E).

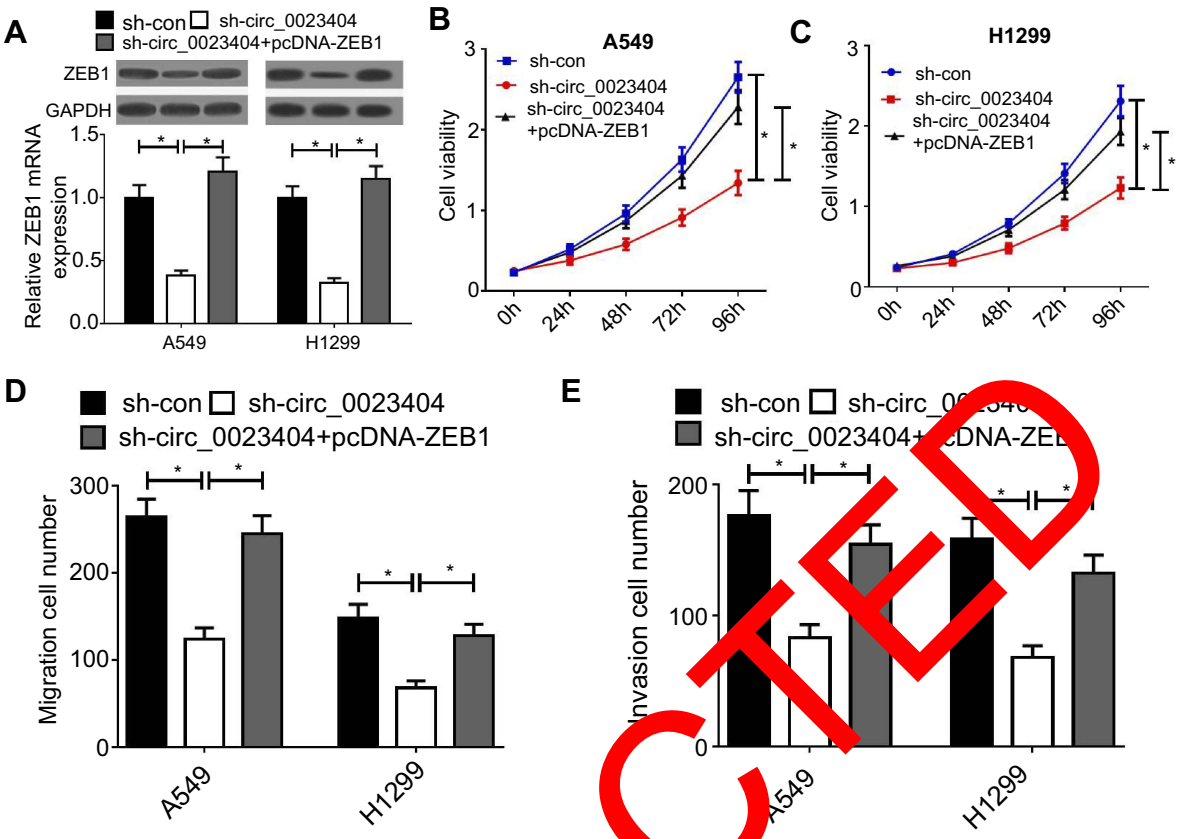

Figure 4 Overexpression of ZEB1 blocks the effect of hsa_circ_0023404 knockdown on biological behavior of NSCLC cells. (**A**) ZEB1 mRNA and protein levels were determined by qRT-PCR and Western blot assays in A549 and H1299 cells transfected with sh-con, sh-circ_0023404 alone or with pcDNA-ZEB1. (**B** and **C**) The viability of A549 and H1299 cells was measured by CCK-8 assay at 24, 48, 72 and 96 h after transfection. (**D**) Cell migration was detected by transwell migration assay in A549 and H1299 cells transfected with sh-con, sh-circ_0023404 alone or with pcDNA-ZEB1. (**E**) Transwell migration assay was carried out in A549 and H1299 cells transfected with sh-con, sh-circ_0023404 alone or with pcDNA-ZEB1. *$P < 0.05$.

Discussion

Previous studies have identified hsa_circ_0023404 as a key regulator in tumorigenesis. Upregulation of hsa_circ_0023404 in cervical cancer is related with poor prognosis. Hsa_circ_0023404 upregulated alpha-globin transcription factor CP2 expression, through targeting miR-136, thus activating yes-associated protein pathway, contributing to cervical cancer development.[13] In esophageal squamous cell carcinoma, hsa_circ_0023404 can be predictive of tumor invasion depth, lymph node metastasis, vascular invasion and poor prognosis. Targeted deletion of hsa_circ_0023404 induced G2/M phase arrest and apoptosis, inhibited cell metastasis and epithelial–mesenchymal transition (EMT) in vitro, as well as suppressed tumor growth *in vivo*.[14] Though a role of hsa_circ_0023404 in tumorigenesis is beginning to be elucidated, hsa_circ_0023404 expression and its regulatory mechanism in NSCLC development are currently uncharacterized. In this study, we found that hsa_circ_0023404 was upregulated in NSCLC, and was negatively associated with the prognosis of NSCLC patients. Functionally, knockdown of hsa_circ_0023404 inhibited the proliferation and metastasis of NSCLC cells, indicating that hsa_circ_0023404 plays an oncogenetic role in the progression of NSCLC and may become a potential prognostic biomarker and a promising therapeutic target in NSCLC.

Dysregulated miRNA expression has been discussed as a major characteristic of malignancies, which acts as a crucial player in the initiation and development of malignancies.[15] miRNAs may serve as tumor suppressor or oncogene to participate in human cancer progression. miR-217 is aberrantly expressed in various cancers and acts as a principal player in tumorigenesis. Previously, gain-of function studies in A549 and SPC-A1 cells and in mice demonstrated the tumor suppressor role of miR-217 in lung cancer.[16] Functional studies in thyroid cancer cell lines showed that miR-217 had a tumor suppressor activity. Overexpression of miR-217 in TPC-1 and SW1736 cells negatively regulated the expression of AKT3, resulting in inhibition of cell proliferation, migration and invasion, indicating miR-217 is an anti-tumor

factor in thyroid cancer.[17] In colorectal cancer cells, miR-217 overexpression impaired mitochondrial membrane potential, activated caspases, externalized phosphatidylserine, as well as induced cell apoptosis through targeting atypical protein kinase c iota type I, BAG family molecular chaperone regulator 3, integrin subunit alpha v and mitogen-activated protein kinase 1.[18] In addition, forced expression of miR-217 in SKOV3 cells, through downregulation of insulin-like growth factor 1 receptor, repressed cell proliferation and metastasis in vitro, as well as inhibited epithelial ovarian tumor growth in vivo.[19] Besides, ectopic expression of miR-217 in HCC1806 and HCC1937 triple negative breast cancer cells revealed miR-217 repressed cell growth and metastasis through targeting Krüppel-like factor 5.[20] These studies indicated that downregulation of miR-217 in cancer cells results in phenotypes important for tumor biology. However, the potential role of miR-217 in hsa_circ_0023404-mediated promotion of NSCLC cell proliferation and metastasis has not yet been explored. In this study, we elucidated the function of and the pathological mechanism of hsa_circ_0023404 during the malignant behavior of NSCLC cells. Our works on the role of hsa_circ_0023404 in NSCLC adds to the growing body of evidence implicating circRNAs-mediated miRNAs regulation in malignancies.

ZEB1, also referred to as δEF-1, belongs to the Zeb family within the zinc finger class of homeodomain transcription factors and is a major inducer of EMT, which confers malignant properties, such as invasion and metastasis on tumor cells.[21] Loss of E-cadherin is recognized as a crucial initial step in EMT process, while ZEB1 is capable of inhibiting the expression of E-cadherin at transcriptional level, thus inducing EMT.[22] Forced expression of ZEB1 induced EMT and enhanced tumorigenesis.[23] Recently, a growing body of evidence has been pointed out that ZEB1 acts as an important player in tumorigenesis. Previous study in NSCLC cell lines revealed that hsa_circ_0020123 promoted cell proliferation and metastasis by upregulating ZEB1 via miR-144, suggesting that the regulatory effect of hsa_circ_0020123 in NSCLC may be mediated by ZEB1.[24] However, whether hsa_circ_0023404-mediated promotion of NSCLC proliferation and metastasis was mediated by ZEB1 is still largely unknown. Downregulation of ZEB1 induced by miR-217 or sh-circ_0023404 was identified in A549 and H1299 cells and a positive correlation between ZEB1 and has-circ_0023404 expression was discovered in NSCLC tissues, suggesting that the promotory effect of has-circ_0023404 on NSCLC progression may be mediated by ZEB1. More importantly, our findings suggested that overexpression of ZEB1 could block has-circ_0023404 silencing-induced promotion of NSCLC cell malignant behavior, indicating that the regulatory effect of has-circ_0023404 in NSCLC is, at least, ZEB1 dependent.

Conclusion

In summary, our findings suggest that hsa_circ_0023404 exerts a tumor-promoting role in NSCLC progression. Our study highlights a mechanism by which hsa_circ_0023404 promotes NSCLC cell growth and metastasis. Targeting hsa_circ_0023404 as a potential therapeutic approach might be used for NSCLC treatment.

Disclosure

The authors report no conflicts of interest in this work.

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