ORIGINAL RESEARCH **RETRACTED ARTICLE: MicroRNA-506 regulates** apoptosis in retinoblastoma cells by targeting sirtuin I

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Background: MicroRNAs have been reported to participate the initiation a progression of retinoblastoma (RB), most common malignancy in cheren. refractor mechanisms of chemoresistance and the toxicity of chemotherapid hindered the real ent especially on young children. Novel RB therapies are urgently quired, 2 R-506 is probed to be associated f this mile n RB remains unclear. with the tumorigenesis of various cancers whet the Methods: Here, the impact of miR-506 RB cell survey al in the ro and tumorigenesis in vivo was examined. MiR-506 expression as exprined in hux of RB samples and cell lines as compared with healthy tissues and non-RB cells. U staining and colony formation assay were performed to determine the effector miR-506 on Receil growth. TdT-mediated dUTP nick end labeling (TUNEL) staining d flow cytometry analysis were applied to detect the apoptotic cell number after miR-506 was ownregulated in RB cells. Furthermore, dual-luciferase reporter assay was utilized to confirm direct intraction between miR-506 and SIRT1 gene. regulated in 20 human RB samples from patients as Results: MiR-5 ression wa

WERI-Rb1 and Y79, as compared to that in healthy tissues well as in human B cel⊅ rast, the expression of sirtuin 1 (SIRT1), known as NAD-dependent and non-PR cells. I Jase, regulated in RB samples and cell lines. Aberrant reduced miR-506 deac as dov ression j baired surjual and proliferation of WERI-Rb1 and Y79 cells. The depletion of 506 Apression promoted apoptosis of the two RB cell lines. The results of bioinformh alysis and dual-luciferase assay exhibited that miR-506 targeted the 3'-untranslated matics region of T1 on silencing purpose. The SIRT1 silencing lessened the miR-506 inhibition RB cell proliferation and undermined apoptosis.

slusion: The results provided an insight into the role of miR-506 during RB development and offered potential pharmaceutical strategy for RB diagnosis. Keywords: retinoblastoma, miR-506, apoptosis, SIRT1

Introduction

Retinoblastoma (RB), known as a severe cancer developed in the retina, affects mainly infants and young children under 5 years. The morbidity ratio remains to be ~1:15,000–1:20,000 and responsible for 2–4% of all childhood malignancy.¹ A case report of 2580 based on an epidemiological study was shown in 2015.² Various cellular agents and molecules were recognized to involve in proliferation, apoptosis and tumor cell cycle. It is speculated that genetic and epigenetic mutations occur when oncogenes and tumor suppressor genes induced or suppressed RB progression and carcinogenesis.^{3,4}

MicroRNAs (miRs) are non-coding RNA molecules (length: <22-25 nucleotides) that exert post-transcriptional effects on the specific gene expression.⁵ Increasing

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evidences indicated the essential character of miRs on different cellular processes, including apoptosis. MiR-506 can affect cell growth, differentiation, cancer metastasis and Invasion. Consistently, miR-506 dysregulation investigation has been reported in various cancer-associated studies. The variation of upstream factors accompanied with promoter methylation moderated miR-506 expression.⁶ In human ductal carcinoma cell lines, miR-506 served as a suppressor to alter Vimentin, CD151 and Snai2 gene expression to regulate epithelial-mesenchymal transition.⁷ Similar phenomenon was characterized in HeLa and C33A cells, indicating miR-506 possessed an inhibition property against human cervical cancer.⁸ It was also revealed that miR-506 targeted ETS1 to regulate gastric cancer angiogenesis and cell invasion.⁹ Although miR-506 has been widely investigated in various tumor studies, researchers rarely probed on its role on eye cancer. Wu et al exhibited that miR-506-3p was significantly downregulated in RB tissues and cell lines. Dual-luciferase reporter assay showed that miR-506-3p directly targeted mitosis Gene A (NIMA)-related kinase 6 (NEK6) in RB cells. Enhanced expression of miR-506-3p remarkably suppressed cell proliferation, induced G0/G1 cell cycle phase arrest and apoptosis in RB cells, which were attenuated by NEK6 overexpression using MTT assay, colony formati and flow cytometry analysis.¹⁰ Recent investigation ha demonstrated that knockdown of long-non-codi RNA HOXA11-AS in RB cells suppressed cell prol ration otably. It, furthermore, induced cell cycle arres t G1/G and promoted cell apoptosis. HOXA11 s a com-peting endogenous RNA that inhib expression, which regulated its downstrain taket NEK6 in RB.¹¹ Although the work has evaluated the role of miR-506-3p in RB, the detailed information on miR-506 function during the process is still lacking.

As a nicotinami le adel, e dinucle ade (NAD+)-dependent lysine de cetylan, sirtur 14 (SIRT1) is vital during metabolism inflamm fon and aging. It has been proposed to regulate be remass.¹² In recent cancer research, it is identified that SIM1 served as an oncoprotein or a tumor suppressor upon distinctive circumstances. For instance, it enabled to influence on infiltrating immune lymphocytes.¹³ Furthermore, an altered expression of SIRT1 led to poor prognosis of gastric cancer,¹⁴ breast cancer¹⁵ and soft tissue sarcoma,¹⁶ respectively. Immunohistochemical analysis unraveled a complicated function of SIRT1 in tumorigenesis: 23 of 82 carcinomas demonstrated a lower level of SIRT1 expression in contrast to another 18 cancer cells among the same test group that exhibited an increased expression manner relative to normal colonic mucosa.¹⁷ Additionally, SIRT1 mRNA downregulated in gastric cancer.¹⁸ Here, we examined how miR-506 is involved in RB generation. An upregulated MiR-506 expression was identified among RB cells and the specimens from RB patients. MiR-506 inhibition impaired RB cell proliferation as well as suppressed the tumor growth in vitro and in vivo. The depletion of miR-506 expression caused the induction of apoptosis in RB cells (WERI-Rb1 and Y79). Our results demonstrated that miR-506 suppressed apoptosis via suppressing SIRT1 expression in RB cell lines.

Materials and methods RB samples

Retinal tissues were exected for 20 patients who did not undergo channels and radiation therapy prior to enucleation in the Department of phthalmology at the second Host al Vilin University, China. The patients d 9 female ranged from 0.6 to 9.1 consisted of 11 male years rd (mean, 3.4). Acording to ICRB, the RB patients wer divided interphase I (5 cases), Phase II (9 cases) and Pha III (6 case . The adjacent healthy tissues were set as the ontrol Written informed consent was acquired n each patient guardian. The experimental protocol properties of proved by the Medical Ethics Committee of the Second and the Third Hospital of Jilin University, hina. Patient tissue samples were conducted in accordance with Declaration of Helsinki.

Cell culture

WERI-RB1 and Y79 cell lines were obtained from Chinese Academy of Sciences Cell Bank (Shanghai, China), and then cultured to 70% confluence in RPMI-1640 (Gibco; Thermo Fisher Scientific, Inc., Waltham, MA, USA) supplemented with 10% fetal bovine serum (Hyclone, Logan, UT, USA), 100 U/mL penicillin, as well as 100 mg/mL streptomycin at 37°C under normoxic conditions of 100% humidity, 5% CO₂ and 95% air.

miR-506 and SIRT1 inhibition

The miR-506 inhibitor, NC inhibitor (the scramble control of this inhibitor), SIRT1 siRNA and NC siRNA were obtained from Creative Biogene. Cells were transfected with 2 μ g miR-506/NC inhibitor or 4 μ g SIRT1/NC siRNA with Lipofectamine 2000 transfection reagent (Thermo Fisher). After cell transfection, the mature endogenous miR-506 was inhibited by the miR-506 inhibitor. Sodium

chloride (NaCl; 0.9%) was used for the preparation of miR-506 and NC inhibitors at 10 mg/mL (final concentration).

Cell proliferation measurement

The cell proliferation was examined using cell-light 5-ethynyl-20-deoxyuridine (EdU) Apollo Imaging Kit (RiboBio, China). A fluorescence microscopy was applied for the measurement of the rate of EdU-positive cells.

Western blot analysis

Cell lysates (20 g) was applied to sodium dodecyl sulfate polyacrylamide gel electrophoresis; after protein separation process, polyvinylidene fluoride membranes were utilized for transformation. The membranes were then treated and incubated with primary and secondary antibodies. SIRT1 (ab7343, Abcam, 1:2000) and GAPDH antibodies (ab9485, Abcam, 1:5000) were used for signal detection via Amersham ECL Western Blotting detection system.

RNA extraction and quantitative polymerase chain reaction

Total RNA was extracted with TRIzol reagent using tissues or treated cells, as per the instructions of the facturer. Roche Light-Cycler 480 Real Time PCR s tem (Roche, Switzerland) and SYBR Green were utilized to examine the levels of miR-506 and SIRT / 06 and glyc aldehyde-3-phosphate (GAPDH) performed as a interna control, respectively. The primer sequence re shown as follows: miR-506 F: 5'-GGG 7 TGA G AGG TGT T-3', R: 5'-CAG TGC G G TGG A T-3'; U6 snRNA F: 5'-CTC GCT TCG GCA CA CAT ATA CT-3', R: 5'-ACG CTT CAC GAA TTT CG TGT C-3'; SIRT1 F: 5'-TGA GC T T TCG TGG AGA TAT TTT T-3', R: 5'-CAT G. GGC A G TGG CTC AT-3'; GAPDH P 5'-A T GG CAP CCG TTA GGA AA-3', R: 5'-T A AGC AGT CAN IGA TGG CA-3'. The protocol of que tit ave real-time PCR was designed at 95°C in 20 μ L reaction volume for 10 mins, followed by 40 cycles at 95°C for 15, 60°C for 30 s and 72°C for 30 s. The endogenous reference was used for normalization and the amount of target $(2^{-\Delta\Delta CT})$ was calculated by a calibrator (mean of the controls).

Colony generation assay

Cells were transfected using various reagents. Cells were resuspended in 10% FBS-added DMEM after 2 days of transfection and plated on an 8-mm layer of 0.4% top agar, followed via transferring into 12-well plates with 0.5 mL of 0.5% bottom agar. In fortnight, four regions were randomly chosen from each plate and colonies were quantified.

TdT-mediated dUTP nick end labeling assay

TUNEL assay was applied to examine the apoptosisrelated changes in cells; the nuclei were stained with 4',6-diamidino-2-phenylindole (DAPI, 1:5000; Beyotime, China) and cells were stained using TUNEL fluorescence kit (Roche, Switzerland). The approximate of cells was determined via counting the TUNEL-positive alls under SP8 laser scanning confocal microscope (Leica, Germany).

Analysis of approximation of approximation of approximation of a second second

Apoptotic cell were primined v flow cytometry (FC) assay and the exin V/prividing flow (PI) staining.¹⁹

Dual-luciferative reporter assay

ells that underwent transfection were as follows: miR-06 mimic **SIRT1 WT; NC mimic + SIRT1 WT; miR-**6 mimic + JIRT1 MU; and NC mimic + SIRT1 MU, in WT and SIRT1 MU were synthesized by wh bobio Co. Ltd. (Guangzhou, China). MiR-506 target gene was determined by 3'-untranslated region (UTR) luciferase reporter assay, wherein MU and WT 3'-UTR of SIRT1 were utilized. The reporter luminescence (Rluc) was studied using Renilla luciferase sequence, whereas firefly luciferase sequence was used to examine the calibration luminescence (Luc). Cells were lysed in passive lysing buffer, and Firefly and Renilla luciferase activities were detected via a commercial Dual-Luciferase assay kit (Promega Corp, Madison, WI, USA) according to the manufacturer's instructions. The vectors and miRNA mimic were added into cells and the cells were cultured 24 hrs. Dual-luciferase reporter assay (DLRA) was used for luciferase activity examination.

Animal tests

BALB/c-nu mice (female, five-week-age) were purchased from Vital River (Beijing, China). The suspension of Y79 cells (1×10^6) suspension was loaded in the microliter syringe. Colibri forceps (Storz, SI. Louis, MO) were performed to firmly control the sclera at the limbus area and rotate the globe anteriorly when the animal was appropriately anesthetized. The needle was then manually inserted into mouse sclera and gently rotated until the tip can be viewed through the retina via a stereomicroscope. The tip was inserted advanced slightly further to elevate the retina when the plastic protective sheath hindered over-penetration of the needle and perforation of the neuroretina, With the bevel of the needle facing the globe, 3- to 4-µI injection of cells was injected into the subretinal space. The needle was then guickly withdrawn after the injection and same procedure was repeated at a point 180° opposite to the first injection place on the eye. Typically, two microinjections were conducted into each eye, in the retinal periphery, anterior to the eye's equator. A topical lubricant was placed on the cornea to prevent drying after the procedure. On day 28 after injection, the mice were sacrificed. All animal experiments were performed under the approval of Animal Operating Principal of the Institutional Animal Care and Use Committee in The Second and the Third Hospital of Jilin University, China (regulation guideline: The Legal Administration Documents for Laboratory Animal in People's Republic of China and Beijing Municipality).

Statistical analysis

The data obtained in this study are represented as mean \pm standard deviation (SD). The comparisons between two test groups were examined by one-way actusis of variance (ANOVA), accompanied with the two-liled Student's *t*-test. *P*<0.05 was considered or the tion of the statistically significant at ference between groups.

Results

Expression of miR-506 was upregulated in RB specimens and RB cell lines

MiR-506 expression among RB specimens was examined using qPCR. According to ICRB guidelines, three groups of patients were selected as follows: good, medium and poor prognosis groups. The poor and medium prognosis groups showed a significantly upregulated miR-506 expression manner compared to the good prognosis group and the normal control group (Figure 1A). In addition, WERI-RB1 (RB1) and Y79 cells displayed increased miR-for levens compared with the other tumor cell lines (Ferrer 1B). The ore, miR-506 expression was upregulated in RL ndicating t t the poor prognostic effect is associated with miR-6 ey ession.

Inhibition of miR-5 suppressed tumorigeness of RB humice

To determine how here-506 affects xenograft RB tumor forma on, the Y79 cells at transfected with Adenoviral-506 inhibiton Adenoviral-SIRT1 siRNA, AdenoviralmiF 506 inhibite SIRT1 siRNA and normal Y79 cells miR were sro-inic d into eyes of BALB/c mice, respecely. The tumor growth was daily monitored. MiR-506 evices and SIRT1 mRNA level were confirmed that occurred in mice tumor from each group and that was epleted in mice from miR-506 inhibition or SIRT1 silening group (Figure 2A). These mice were executed on day 28 after injection and then the formed tumors were excised and weighed. The miR-506-silenced tumors developed



Figure I miR-506 expression in RB specimens of patients and RB cell lines (RBI and Y79). (**A**) miR-506 expression in RB specimens from good prognosis (n=5), medium prognosis (n=9), poor prognosis (n=6) and patients with normal volunteer (n=10), as examined using qPCR. (**B**) miR-506 expression was compared between RB cell lines and other cancer cell lines, as examined using qPCR. Data were represented in the form of mean \pm SD. *P<0.05. **Abbreviation:** RB, retinoblastoma.



Figure 2 miR-506 silencing inhibit xenograft tume mation. (A) Expression of miR-506 in the RB specimens of ch group was examine pCR analysis at day 27 sfected wit Adenoviral-miR-306 inhibitor, Adenoviralpost injection. (B) Y79 cells siRNA-SIRTI, Adenoviral-506 inhib siRNA-SIRT I or control cells were injected into eyes of mice (n=10 per gr M were sacrifi d and tumors were weighed at day 28 post-inoculation rs we eighed afte cision from each group. (C) Tumor ata represent the mean \pm SD. *P<0.05 growth curve d ıg 28 DOST-ir RB. reti Abbreviati blastoma.

with a manually slower manner than control group. It displayed a smaller mean tumor volume in contrast to the control group, whereas the silencing of SIRT1 caused a restoration on tumor volume and weight as compared with inhibitor group (Figure 2B and C).

Inhibition of miR-506 suppressed RB cell line proliferation and triggered apoptosis

The influence of miR-506 on RB cells was then investigated. In RB1 and Y79 cells, the miR-506 inhibitor transfection led to a significant reduction in miR-506 level (Figure 3A and B). EdU assay results exhibited a remarkable decrease in the proliferation of these cell types after 24–72 hrs miR-506 inhibitor transfection in contrast to cells from the NC groups (Figure 3C and D). The colony formation assay results demonstrated that the aberrant downregulated expression of miR-506 induced a similar reduction on the colony numbers formed by these two cell types while transfection with NC inhibition presented no effect (Figure 3E and F).

The proliferation of these two DD cells was impaired following with the inhibition miR-5 A speculative that the d role of miR-506 seems to letion of the microRNA exerted a mulator effect g apoptosis in RB cell lines. Both UNEL stain. gure 4A and B) assay results indicated an and FC (Figure and enhancement a apopt is of P 1 and Y79 cell lines with miR inhibitor th cf tion in comparison to that of cells in the groups.

hiR-506 targeted the 3'-UTR of SIRT I

IR-506 was predicted in the Bioinformatics analysis to st the 3 JTR of SIRT1 (Figure 5A). The correlation of mix-506 to 3'-UTR of SIRT1 was investigated using (Figure 5B). The activity of luciferase declined at 50% in cells transfected with the miR-506 mimic fusing to the 3'-UTR of SIRT1 in comparison to the cells in the control groups. Subsequently, we examined the SIRT1 expression in RB specimens and RB cell lines. As exhibited in Figure 5C and D, SIRT1 level in RB cell lines and specimens decreased in contrast to that observed in normal healthy specimens and other cancer cells. The impacts of miR-506 inhibitor on SIRT1 expression between these two RB cell lines were examined by WB and qPCR. Both the protein and mRNA level of SIRT1 enhanced following with the cells that transfected with miR-506 inhibitor (Figure 5E-H). The results indicated that miR-506 targeted the 3'-UTR of SIRT1 gene.

SIRTI silencing counteracted the role of miR-506 on the proliferation and apoptosis of RB cells

To assess whether SIRT1 silencing neutralized the effect of miR-506 on RB cell proliferation and apoptosis, SIRT1 transcription was silenced in the RB1 and Y79 cells. WB and qPCR were used to verify the changes in the expression of SIRT1 (Figure 6A–D). The depletion of SIRT1 expression

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Figure 3 Effect could-506 excession on the coliferation of RB1 and Y79 cells. (A, B) Expression of miR-506 in RB1 and Y79 cells transfected with the miR-506 inhibitor or NC inhibitor examine (1000, (C, D)) Proliferation rate of RB1 and Y79 cells was obtained at 24, 48 and 72 hrs post-transfection using the EdU assay. (E, F) Colony formation assay of R^2 and Y79 cens-transfected with the miR-506 inhibitor or NC inhibitor. The lower panel indicated the number of colonies formed in each group. Data were representeent the form of mean \pm SD. *P<0.05, **P<0.01.

revived the proliferation of the RB1 and Y79 cells repressed by miR-506 inhibition, as shown from the results of EdU assay (Figure 6E and F). Cytometry assay was then performed to examine the apoptosis rate of RB cell lines. Aberrant downregulated expression of SIRT1 caused a visible decreased amount of apoptotic cells corresponding to the transfection with the miR-506 inhibitor (Figure 6G and H). The observable decline of the apoptotic cells subjected to SIRT1 silencing. Previous studies indicated that Bax and p53 induced apoptosis while NF- κ B p65 played an inhibitory role on apoptosis. To further evaluate the mechanism of SIRT1 on apoptosis of RB cell, we examined p53, p65 and Bax expression after transfection. It revealed that inhibition of miR-506 induced the upregulation of both p53 and Bax; however, it led to downregulation of p65. Moreover, the silencing of SIRT1 reversed the effect of miR-506 on the expression of



Figure 4 therrant development of expression of miR-506 enhanced the apoptosis of RB cell lines. (**A**, **B**) TUNEL staining was carried out to examine the number of apoptotic centre of group of an AT79 cells. Magnification, $\times 200$. TUNEL staining cells from each group were displayed in the lower panel. (**C**, **D**) Annexin V-FITC/PI staining and FO the performed to determine the number of apoptotic cells. The upper right quadrant of each plot represents early apoptotic cells and apoptotic rate analysis in RB1 and 79 cells from each group was shown in the lower panel. Data were represented in the form of mean \pm SD. **P*<0.05. **Abbreviations:** RB, insolastoma; TUNEL, TdT-mediated dUTP nick end labeling.

these three proteins (Figure 6I and J). Thus, SIRT1 silencing enabled to reverse the inhibition effect of miR-506 on the proliferation and apoptosis of RB cells.

Discussion

Tumorigenesis is considered as a synergetic intricate process accompanied with several anti-oncogenes and oncogenes. In the present work, an increased miR-506 expression was observed in RB cells and tumor specimens. It also revealed that miR-506 enables to suppress the expression of SIRT1, the key modulator in malignancies. MiR-506 inhibition caused a suppression of cell viability and proliferation. It promoted apoptosis on both RB1 and Y79 cells. Further investigation demonstrated the interaction between miR-506 and the 3'-UTR



K-506. (**A**) Figure 5 SIRTI was a direct targ aphical representation of the conserved miR-506 binding motif at the 3'-UTR of SIRTI. (**B**) Luciferase activity either the wild-type (WT) or mutated (MU) human SIRTI 3'-UTR after miR-506 mimic transfection. The luciferase displayed by the lucifer ructs carr rter co dase. (C, D) qPCR analysis was used to confirm the downregulation during SIRT1 expression in RB specimens and cell activity was normali to the tivity of lac lines. WB (E, F) م qPCR (H) were pe med to examine SIRT1 protein and mRNA expressions, respectively, after transfection of RB1 and Y79 cells with miR-506 hibitor. presented in the form of mean ± SD. *P<0.05. inhibitor and N Abbreviation: R astoma.

of SIRT1 gene, resulting in the abrogation of SIRT1 expression. The knockout of SIRT1 expression neutralized miR-506 on RB cell proliferation. Our findings suggested that miR-506 acted as oncogenic factor by targeting the SIRT1 gene.

The regulating effect of miRNAs on downstream target gene expression has been studied in various cancer types. Multiple target genes downregulated the translation or triggered the cleavage of molecules through the binding of miRs to their 3'-UTR. Therefore, we aimed to examine the expression of miR-506-regulated downstream target genes. Previous research has demonstrated that miR-506 might target different genes, including YAP, ROCK1, CDK4/6-FOXM, IQGAP1 and SPHK1 which mediated various malignancy progressions.^{20–24} It was shown that miR-506 is supposed to target the conservative site of SIRT1 according to bioinformatics analysis. DLRA results further confirmed that 3'-UTR of SIRT1 directly interacted with miR-506 in RB cells. SIRT1 possessed anti-apoptotic



Figure 6 Silencing of SIRTI expression counteracted the effect of miR-506 on RB cell lines. (A–D) Expression of SIRTI was examined in RBI and Y79 cells at both protein and mRNA levels following transfection with different agents. SIRTI i represents interference of SIRTI siRNA, NCi represents transfection with NC siRNA. (E, F) SIRTI silencing recovered the proliferation of RBI and Y79 cells. (G, H) SIRTI silencing eliminated the pro-apoptotic effect of the miR-506 inhibitor. Annexin V-FITC/PI staining and FC were carried out to examine the number of early apoptotic RBI and Y79 cells after 48 hrs of transfection. (I, J) WB was performed to examine the expression of p53, p65 and Bax after 48 hrs of transfection. Results were presented as mean ± SD. *P<0.05, **P<0.01. Abbreviation: RB, retinoblastoma.

property and involved in diverse cellular process including autophagy, proliferation, apoptosis and aging to affect tumorigenesis. It is speculated that the function of miR and SIRT1 interaction varies from the specific tumor-associated oncogenic pathway. For instance, miR-22 acted as an oncogene/tumor-suppressor in prostate cancer and SIRT1 was a target agent to miR-22. Another study showed that SIRT1 overexpression in breast cancer cells induced the downregulated expression of MiR-22.²⁵ The expression of miR-138 in NSCLC declined due to SIRT1 neutralization function on this tumor suppressor gene. AMP-activated protein kinase (AMPK)-mTOR pathway exerted a vital role in adjusting autophagy. MiR-138 reduced SIRT1 expression to undermine the AMPK pathway activity and subsequently promoted the mTOR phosphorylation.²⁶ In prostate cancer, downregulation of miR-221 or miR-222 expression suppressed cell proliferation and migration as well as enhanced apoptosis,²⁷ following with an induced SIRT1 expression. A study implied that downregulation of SIRT1 has the potential to boost migration and reduce cell death,²⁸ suggesting SIRT1 exhibited an inhibitive feature toward the oncogenic activity of miR-221 and miR-222. The escalate manner of SIRT1 expression succeeding miR-506 inhib tion was determined in our study. The knock-down of SIRT1 expression on RB cells recovered the ръ rties of RB cells regulated by miR-506 inhibit in. The bove evidence indicated that miR-506 contributed SSF лану the RB tumorigenesis, modulated by sIRT1.

Conclusion

Our work proposed the function of miR-506 as an RB oncogene during RB programmer. The downregulated miR-506 expression in Kencell line is associated with tumor cell growth in pairmer programmer of its potential role area biogrammer or prognostic agent for RB diagnosis.

Author contributions

All authors contributed to data analysis, drafting and revising the article, gave final approval of the version to be published, and agreed to be accountable for all aspects of the work.

Disclosure

The authors report no conflicts of interest in this work.

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