

MicroRNA-29 targets FGF2 and inhibits the proliferation, migration and invasion of nasopharyngeal carcinoma cells via PI3K/AKT signaling pathway

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Abstract. – **OBJECTIVE:** Studies have indicated that miRNAs may prove essential therapeutic targets for the treatment of cancer. The study was designed to investigate the role and therapeutic potential of miR-29 in nasopharyngeal cancer.

MATERIALS AND METHODS: The quantitative Real-time polymerase chain reaction (qRT-PCR) was used for expression analysis. WST-1 assay was used for cell viability assessment. The 4',6-diamidino-2-phenylindole (DAPI) staining and electron microscopic analysis was used for the detection of apoptosis and autophagy, respectively. Transwell assays were used for cell migration and invasion assay.

RESULTS: It was found that miR-29 is significantly downregulated in nasopharyngeal carcinoma cell lines. Overexpression of miR-29 caused a decrease in the viability of CNE2 nasopharyngeal carcinoma cells via induction of apoptosis and autophagy. Bioinformatics analysis predicted FGF2 to be the target of miR-29 in CNE2 cells, which was also confirmed by luciferase reporter assay. The qRT-PCR results showed that FGF2 and growth factor 2 (FGF2) to be significantly upregulated in the nasopharyngeal carcinoma cell lines. However, miR-29 overexpression in CNE2 cells resulted in post-transcriptional suppression of FGF2 expression. Nonetheless, silencing of FGF2 also caused inhibition of CNE2 cell proliferation via induction of apoptosis and autophagy. Overexpression of FGF2 could reverse the effects of miR-29 overexpression on the proliferation of CNE2 cells. Moreover, overexpression of miR-29 caused a significant decline in the phosphorylation of PI3K and AKT expression cells and inhibits cell migration and invasion of the CNE2 cells. Finally, miR-29 overexpression could also suppress the subcutaneous xenografted tumor growth.

CONCLUSIONS: The findings of the present study indicate the therapeutic implications of miR-29 in nasopharyngeal carcinoma.

Key Words:

MicroRNA, Apoptosis, Autophagy, MiR-29, Nasopharyngeal cancer.

Introduction

Nasopharyngeal cancer is one of the most prevalent malignant tumors in Southeast Asia and Southern China¹. The early stage metastasis of nasopharyngeal carcinoma makes it one of lethal cancers². The five-year survival rate under combined treatment with adjuvant cisplatin chemotherapy and radiotherapy is 50-60%³. The constant relapses and distant metastasis of nasopharyngeal cancer make it difficult to manage with the current treatment strategies⁴. Generally, surgical removal, systemic chemotherapy or radiotherapy is employed for nasopharyngeal carcinoma. However, owing to the severe adverse effects of available drug regimens, the patient's quality of life is drastically impaired⁵. Improvement of prevention through early detection and identification of the therapeutic targets may prove beneficial to curb nasopharyngeal cancer related mortalities⁶. Over the last few decades microRNAs (miRs) have been shown to exhibit therapeutic potential for treating numerous diseases⁷. Consisting of around 20 nucleotides, miRs nearly act in almost all mammalian biological pathways such as apoptosis, proliferation, reg-

ulation of cell cycle and metabolism⁸. The miRs are aberrantly expressed under disease conditions such as cancer⁹. Each miR may modulate the expression of multiple mRNAs and may affect a wide array of processes, many of which are cancer related¹⁰. Among miRs, miR-29 has been shown to be dysregulated in several cancer types and has the potential to act as a therapeutic target for drugs¹¹. MiR-29 has been shown to regulate the apoptosis, tumorigenicity, and prognosis of several types of cancers such as hepatocellular carcinoma¹². The members of miR-29 family have also been shown to regulate the proliferation and invasion of gastric cancer cells¹³. In another study¹⁴, miR-29 has been shown to negatively regulate the EMT regulator N-myc interactor in breast cancer. Furthermore, microRNA-29 has been reported to play a vital role in pathogenesis and progression of osteosarcoma¹⁵. In lung squamous cell carcinoma, miR-29 has been shown to act as a tumor suppressor by targeting LOX2¹⁶. However, the role and therapeutic potential of miR-29 are still unknown in nasopharyngeal cancer. Consistently, the present work was designed to elucidate the role of miR-29 in nasopharyngeal carcinoma and to explore its therapeutic potential. We report that miR-29 is aberrantly downregulated in nasopharyngeal cancer and overexpression of miR-29 suppresses the proliferation of the nasopharyngeal cancer cells by targeting fibroblast growth factor 2 (FGF2) via regulation of PI3K/AKT pathway. To sum up, the present study suggests that miR-29 may prove an essential therapeutic target for nasopharyngeal cancer.

Materials and Methods

Cell Lines and Culture Conditions

The normal nasopharyngeal epithelial cell line (NP460) and nasopharyngeal cancer cell lines (CNE1, CNE2, SUNE1, HK1) were purchased from American Type Culture Collection (ATCC, Manassas, VA, USA). The cell lines were maintained in RPMI-1640 modified Eagle's Medium supplemented with 10% fetal bovine serum (FBS; Thermo Fisher Scientific, Waltham, MA, USA) and antibiotics (100 U/ml penicillin and 100 µg/ml streptomycin), and 2 mM glutamine. The cells were cultured in a CO₂ incubator (Thermo Fisher Scientific, Waltham, MA, USA) at 37°C, 95% humidity and 5% CO₂. All transfections were carried out by Lipofectamine 2000 (Invitrogen, Carlsbad, CA, USA) as per the manufacturer's protocol.

qRT-PCR Analysis

The total RNA from the normal nasopharyngeal cancer cell lines was isolated by TRIzol Reagent (Invitrogen, Carlsbad, CA, USA) following the manufacturer's instructions. The cDNA was synthesized using a reverse transcriptase (Promega, Madison, WI, USA) and amplified with Platinum Super Green qRT-PCR SuperMix-UDG reagent (Invitrogen, Carlsbad, CA, USA) using a real-time detection system (Bio-Rad, Richmond, CA, USA). The reaction mixture consisted of 10 µl containing 1.5 mM MgCl₂, 2.5 units of DNA polymerase, 200 µM dNTPs, 0.2 µM of each primer and 0.5 µg DNA. The reaction conditions were as follows: 95°C for 20 s, followed by 40 cycles of 95°C for 15 s and 58°C for 1 min. The expression was estimated by 2^{-ΔΔCt} method and actin was used as an internal control. The qRT-PCR primers for miR-29 were 5'-CGCCATCCTGGATTAGTAAGAAGGGGC-3' (forward) and 5'-CCGGAATTCAAGGTCAGTG-3' (reverse) and for FGF2 primers were 5'-GGCTTCTTCCTGCGCATCCA-3' (forward) and 5'-GCTCTTAGCAGAC ATTGGAAGA-3' (reverse).

Analysis of Cell Proliferation

The proliferation rate of CNE2 cells was monitored by WST-1 assay. In brief, the CNE2 cells were cultured in 96 well plates at the density of 1 × 10⁵ cells/well. The cells were then transfected with miR-NC or miR-29 mimics and again incubated for 24 h at 37°C. This was followed by the incubation of the cells with WST-1 at 37°C for 4 h. The absorbance was then measured at 450 nm using a Victor 3-microplate reader to determine the proliferation rate at 0, 12, 24, 48 and 96 h time intervals.

Cell Transfection

miR-29 mimics and NC were synthesized by RiboBio (Guangzhou, China). The transfection was carried out by the Lipofectamine 2000 reagent (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's instructions. As the CNE2 cells reached 80%, the appropriate concentrations of miR-29 mimics or NC were transfected into these cells.

Analysis of Cell Death

After transfection with miR-NC or miR-29 mimics, the CNE2 cells were cultured in twenty-four well plates for 24 h at 37°C. The cells were then collected by centrifugation and washed with

PBS. After this, the cells were stained with DAPI for 25 min. The CNE2 cells were then washed with PBS and then observed both by fluorescence and phase contrast microscopy. For annexin V/PI assay, the miR-NC or miR-29 mimics transfected CNE2 cells (5×10^5 cells per well) were incubated for 24 h at 37°C. This was followed by the staining of these cells with annexin V-FITC or PI. The percentage of apoptotic CNE2 cells was determined by flow cytometry.

Electron Microscopy

Autophagy in transfected CNE2 cell was demonstrated by electron microscopy. In brief, the nasopharyngeal CNE2 cancer cells were treated transfected with appropriate constructs and incubated for 24 h. The cells were collected by trypsinization and subjected to washing which was followed by fixation in glutaraldehyde (2%) in phosphate buffer (0.1 M). The cells were then post-fixed in osmium tetroxide (1%). This was followed by the treatment of the cells with ethanol and embedding in resin. Next, the thin section was cut with the help of an ultramicrotome and subjected to electron microscopy.

Transwell Assays

The effects of miR-29 overexpression on the invasion ability of CNE2 cells were determined by transwell chambers with Matrigel. The CNE2 cells were transfected with miR-NC and around 200 μ l cell cultures were placed into the upper chambers and only medium was placed into the bottom wells. After 24 h of incubation, the cells were removed from the upper chamber and the cells that invaded via the chamber were subjected to fixation with 70% ethanol and subsequently stained with crystal violet. Inverted microscope was used to count the number of invaded cells at 200 \times magnification. This procedure was used for cell invasion; however, for the migration assay the inserts were not coated with 50 μ l extracellular matrix.

Target Identification and Dual-Luciferase Reporter Assay

The miR-29 target was identified by TargetScan software (<http://www.targetscan.org>). The miR-29 mimics and NC were co-transfected with the FGF2'-UTR-WT or pGL3-FGF2'-MUT into U87 cells. Dual-luciferase reporter assay (Promega, Madison, WI, USA) was carried out 48 h after transfection. Renilla luciferase was used for normalization.

Western Blotting

The normal and the glioma cell lines were cultured at 37°C for 24 h and then centrifuged at high speed. The cell pellet was washed with PBS and then suspended again in RNeasy lysis buffer. Thereafter, the concentrations of the total proteins were determined and equal concentrations of proteins were loaded on sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) (15%). The samples were transferred to polyvinylidene difluoride (PVDF) membranes and blocking was done using skimmed milk powder. This was followed by membrane incubation with primary antibodies at 4°C for 24 h. Then, the membranes were probed with horseradish peroxidase (HRP) conjugated secondary biotinylated secondary antibodies for 1 h. The membranes were developed and immunoreactive bands observed by ECL-PLUS/Kit as per manufacturer's guidelines.

Statistical Analysis

All the experiments were done in three biological replicates and the values represent the mean of three replicates \pm standard deviation (SD). $p < 0.05$ was considered as significant difference. Student's t -test and Graph Pad prism 7 software (La Jolla, CA, USA) was used for the statistical analysis.

Results

miR-29 is Downregulated in Nasopharyngeal Cancer Cell Lines

Expression of miR-29 was examined in one normal NP460 and four nasopharyngeal carcinomas (CNE1, CNE2, SUNE1, and HK1) cell lines by qRT-PCR (Figure 1A). It was found that miR-29 is downregulated significantly ($p < 0.05$) in all the nasopharyngeal cancer cell lines. Furthermore, miR-29 was found to be downregulated in nasopharyngeal cancer lines by almost 10 fold relative to the normal NP460 cells. Lowest expression of miR-29 was reported in case of CNE2 cell line.

miR-29 Inhibits Proliferation of CNE2 Cells by Induction of Apoptosis and Autophagy

To find out the effects of miR-29 on the proliferation of the nasopharyngeal CNE2 cells, the CNE2 cells were transfected with NC or miR-29 mimics. The overexpression of miR-29 was confirmed by qRT-PCR, which showed about 4.6 fold upregulation of miR-29 in CNE2 cells (Figure 1B).

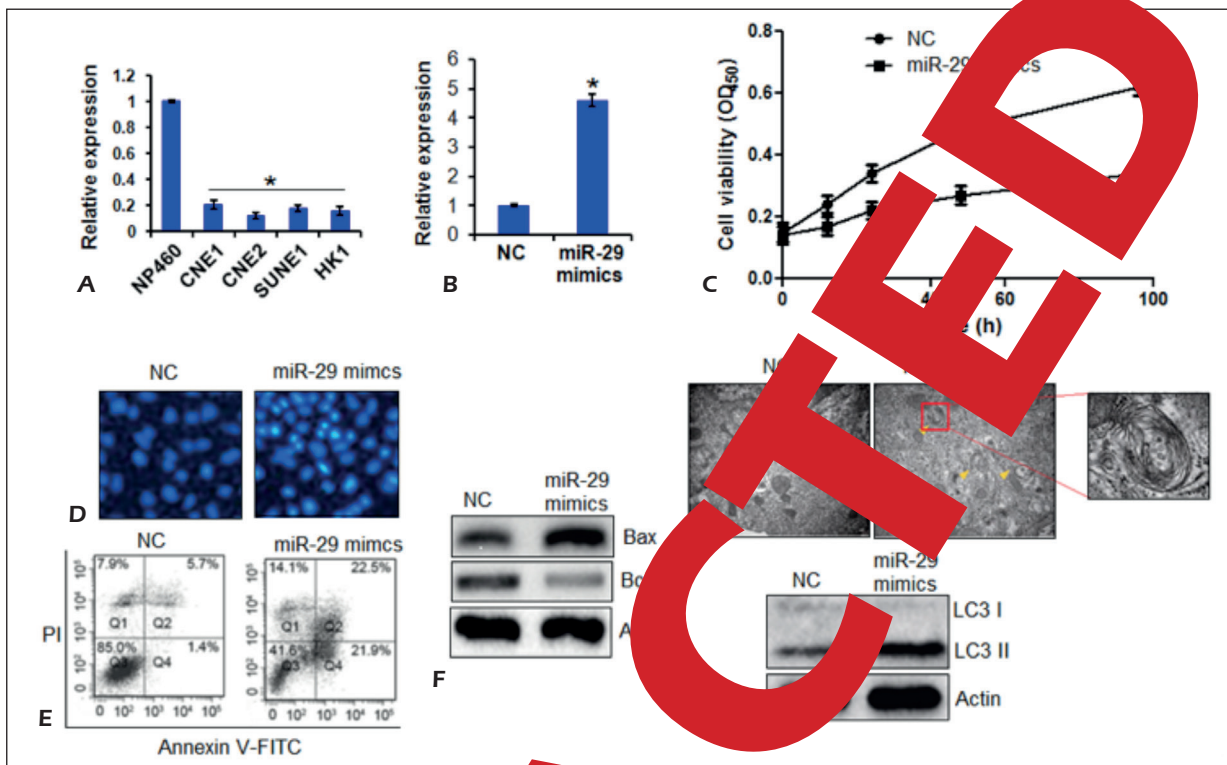


Figure 1. miR-29 inhibits the proliferation of nasopharyngeal cancer cells via induction of apoptosis and autophagy. **A**, qRT-PCR showing the expression of miR-29 in normal nasopharyngeal cancer cell lines **(B)** expression of miR-29 in NC and miR-29 mimics transfected CNE2 cells **(C)** CCK-8 assay showing the viability of the NC and miR-29 mimics transfected CNE2 cells **(D)** DAP staining of the NC and miR-29 mimics transfected CNE2 cells **(E)** Annexin V/PI staining of the NC and miR-29 mimics transfected CNE2 cells **(F)** Expression of Bax and Bcl-2 in NC and miR-29 mimics transfected CNE2 cells **(G)** Electron microscopic images of NC and miR-29 mimics transfected CNE2 cells (Arrow heads depict autophagic vesicles) **(H)** Expression of LC3 I and LC3 II in NC and miR-29 mimics transfected CNE2 cells. The experiments were performed in triplicate and the values represent mean \pm SD (* p < 0.05).

The proliferation rate of the miR-29 mimics' transfected CNE2 cells was monitored at different time intervals. WST-1 assay was found that transfection of miR-29 mimics into the CNE2 cells resulted in a significant decline in the viability of CNE2 cells (Figure 1C). DAPI and annexin V/PI staining of the NC and miR-29 mimics transfected CNE2 cells were performed to observe if miR-29 induces apoptosis in CNE2 cells. The results showed that miR-29 overexpression caused the induction of apoptotic cell death of the CNE2 cells. The CNE2 apoptotic cells increased from 14.1% in the NC to 22.5% in the miR-29 mimics transfected CNE2 cells (Figure 1D). The induction of apoptosis in CNE2 cells was also confirmed by upregulation of Bax and downregulation of Bcl-2 (Figure 1F). Moreover, electron microscopic analysis also showed that overexpression of miR-29 in nasopharyngeal cancer cells resulted in autophagy as evident by the formation of the autophagic

vesicles (Figure 1G). miR-29 overexpression that triggered autophagy was validated by examining the expression of LC3II. As expected, miR-29 overexpression enhanced the expression of LC3 II confirming the induction of autophagy in CNE2 cells (Figure 1H). Taken together, these results indicate that miR-29 overexpression inhibits the CNE2 cell proliferation by via induction of apoptosis and autophagy.

miR-29 Targets FGF2 in CNE2 Nasopharyngeal Cancer Cells

TargetScan analysis of miR-29 revealed FGF2 to be the target of miR-29 (Figure 2A), which was further confirmed by the dual luciferase assay (Figure 2B). Therefore, the expression levels of FGF2 were investigated in all the nasopharyngeal cancer cell lines as well as in the normal cell line. It was found that the expression of FGF2 was significantly upregulat-

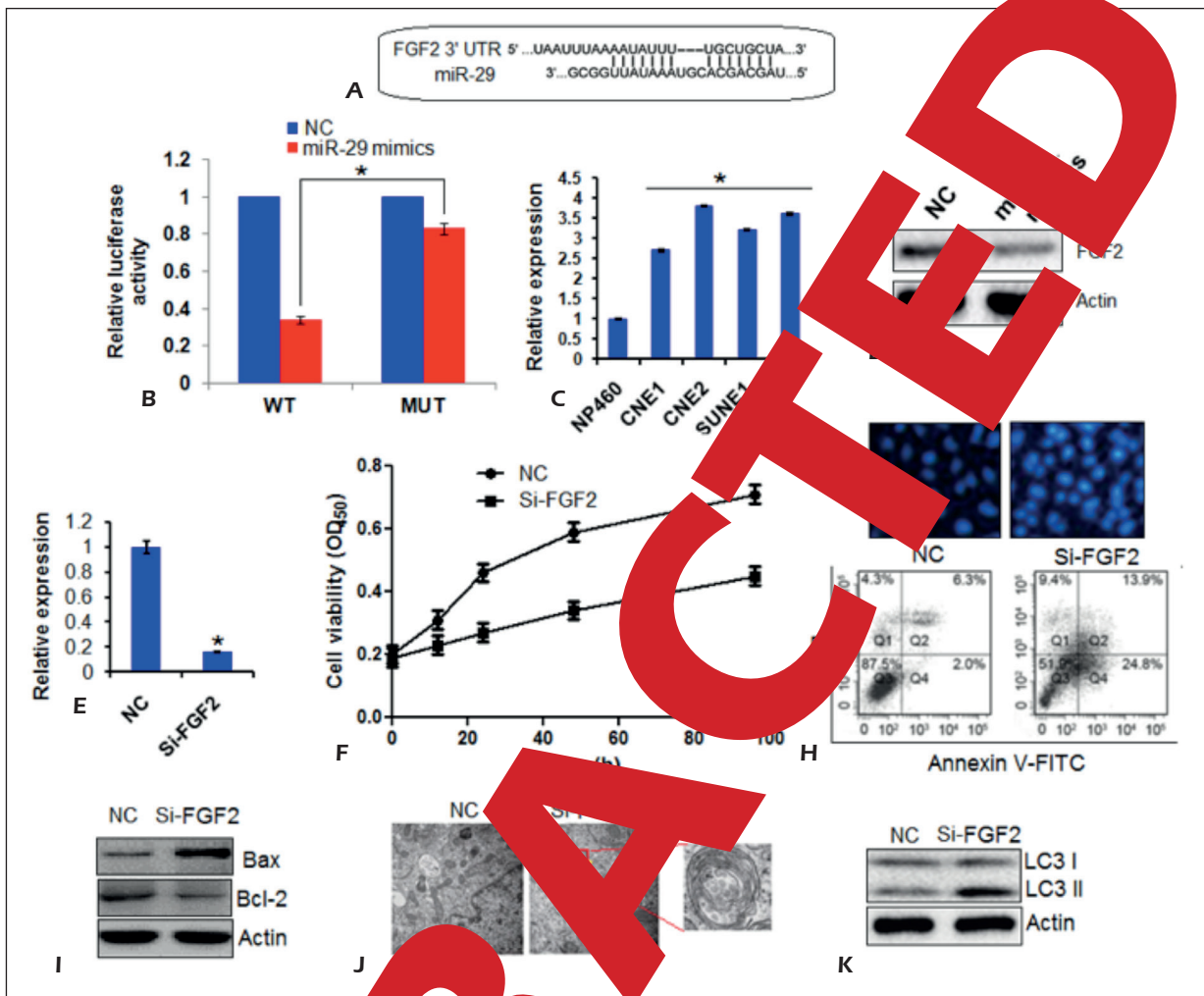


Figure 2. miR-29 exerts its effects through post-transcriptional repression of FGF2. **A**, TargetScan analysis showing FGF2 as the target of mi-29 **(B)** Dual luciferase reporter assays showing the expression of FGF2 in normal NP460 and four different nasopharyngeal cancer cell lines **(D)** Western blot analysis showing the expression of FGF2 in NC and miR-29 mimics transfected CNE2 cells **(E)** expression of FGF2 in NC and Si-FGF2 transfected CNE2 cells **(F)** CCK-8 assay showing the viability of the NC and Si-FGF2 transfected CNE2 cells **(G)** DAPI staining of NC and Si-FGF2 transfected CNE2 cells **(H)** Annexin V/PI staining of the NC and Si-FGF2 transfected CNE2 cells **(I)** Expression of Bax and Bcl-2 in NC and Si-FGF2 transfected CNE2 cells **(J)** Electron microscopic images of NC and Si-FGF2 transfected CNE2 cells (Arrow heads depict autophagic vesicles) **(K)** Expression of LC3 I and LC3 II in NC and Si-FGF2 transfected CNE2 cells. The experiments were performed in triplicate and the values represent mean \pm SD (* $p < 0.05$).

ed (3.6 fold) in the nasopharyngeal cancer cell lines (Figure 2C). However, the expression of FGF2 in CNE2 cells decreased significantly upon miR-29 overexpression (Figure 2D). The effects of the FGF2 on the proliferation rate of the nasopharyngeal cancer cells were also investigated. It was found that the silencing of FGF2 (Figure 2E) had significant ($p < 0.05$) decline in the proliferation of the CNE2 nasopharyngeal cancer cells (Figure 2F). The decline in viability was again found to be due to the induction of apoptosis and autophagy (Figure 2G-K).

FGF2 Reverses Growth Inhibitory Effects of miR-29 on CNE2 Cells

miR-29 overexpression as well FGF2 silencing both inhibited the proliferation of the CNE2 cells through induction of apoptosis and autophagy. We sought to know if FGF2 overexpression could reverse the tumor suppressive effects of miR-29 on CNE2 cells. Interestingly, it was found that FGF2 overexpression in the miR-29 mimics transfected CNE2 cells promoted the proliferation of the CNE2 cells indicative of the inhibitory effects of the miR-29 overexpression are directly via suppression of FGF2 (Figure 3).

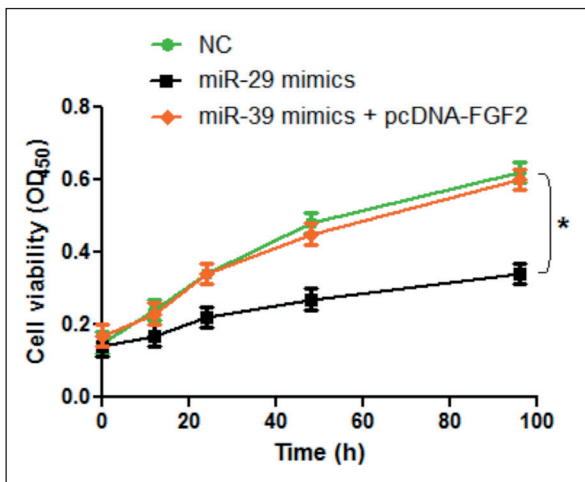


Figure 3. FGF2 overexpression reverses the effects of miR-29 overexpression on the viability of the CNE2 nasopharyngeal carcinoma cells. The experiments were performed in triplicate and the values represent mean \pm SD (* p <0.05).

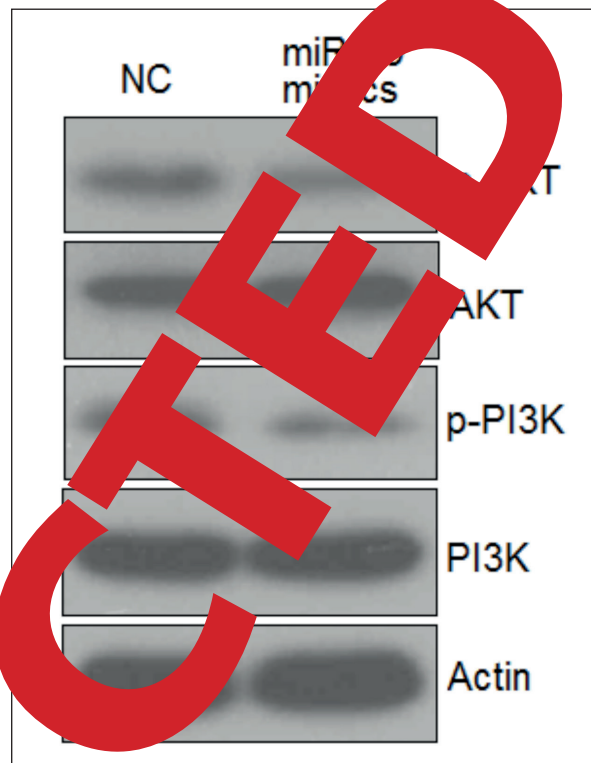


Figure 4. Effect of miR-29 overexpression on the PI3K/AKT pathway in CNE-2 cell lines. The experiments were performed in triplicate.

miR-29 Modulates PI3K/AKT Pathway in CNE2 Cells

This study explored the relation between miR-29 and FGF2 and FGF2 has been shown to regulate the PI3K/AKT signaling pathway. The effects of miR-29 overexpression were investigated on the PI3K/AKT signaling pathway. It was found that miR-29 overexpression inhibited the phosphorylation of both AKT and PI3K (Figure 4).

miR-29 Inhibits the Migration and Invasion of the CNE2 Cells

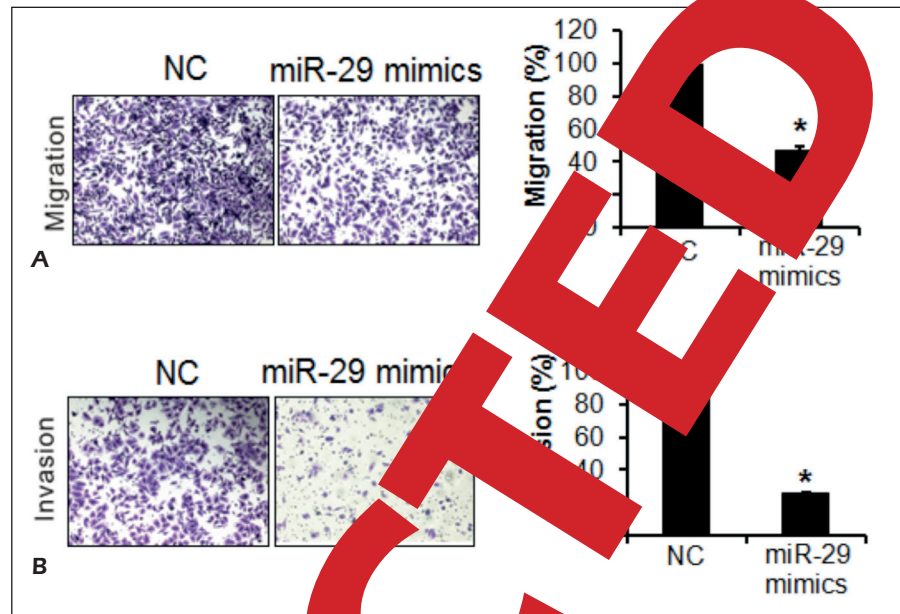
The effects of miR-29 overexpression were also investigated on the migration and invasion of the CNE2 nasopharyngeal cancer cells. It was found that miR-29 overexpression resulted in the suppression of both migration and invasion of the CNE2 cells (Figure 5A and B). The migration of CNE2 cells was inhibited by 57% and the invasion was inhibited by 55%.

Discussion

Nasopharyngeal carcinoma is one of the most common head and neck malignancy¹⁸. The early diagnosis of nasopharyngeal carcinoma, late diagnosis, unavailability of therapeutic targets and the adverse effects of the treatment strategies used for treatment are the main obstacles that

limit its treatment¹⁹. It has been reported that miRNAs control the expression of around thirty percent of the human genes and are involved in a wide array of cellular processes²⁰. Owing to the importance of the miRNAs in cellular and physiological processes, several studies²¹ have revealed the potential of miRNAs as therapeutic targets. Herein, the role and therapeutic potential of the miR-29 were investigated in nasopharyngeal cancer. It was found that miR-29 was aberrantly downregulated in nasopharyngeal cancer cells. Kwon et al²² carried out earlier have indicated that dysregulated expression of miR-29 may be associated with the development of pancreatic cancer. Moreover, miR-29 has been shown to be dysregulated in gastric cancer and in head and neck squamous cell carcinoma^{23,24}. Overexpression of miR-29 in the CNE2 nasopharyngeal cancer cells caused significant reduction in the proliferation of the CNE2 nasopharyngeal cancer cells via induction of apoptosis and autophagy. These results are also supported by previous studies wherein miR-29 has been shown to inhibit the proliferation of gastric cancer and induces apoptosis in hepatocellular carcinoma cells^{12,13}.

Figure 5. Effect of miR-29 overexpression on (A) migration (B) invasion of the CNE2 nasopharyngeal cancer cell lines. The experiments were performed in triplicate and the values represent mean \pm SD (* p <0.05).



Bioinformatics analysis indicated FGF2 to be the potential target of miR-29. Herein, we observed that FGF2 is highly upregulated in nasopharyngeal cancer and miR-29 overexpression of the human nasopharyngeal cancer cells. Overexpression of miR-29 inhibits the proliferation of CNE2 nasopharyngeal cancer cells. Moreover, FGF2 silencing could also inhibit the growth of CNE2 nasopharyngeal cancer cells by inducing apoptosis and autophagy via targeting FGF2 mediated PI3K/AKT pathway. Henceforth, miR-29 may be an essential therapeutic target for the treatment of nasopharyngeal cancer.

Furthermore, FGF2 overexpression was found to reverse the effects of miR-29 overexpression on the proliferation of the CNE2 cells. FGF2, is generally located in the nucleus and/or cytoplasm. It has been shown to be involved in the regulation of cell proliferation and progression several cancer types such as lung and breast cancers to name a few.²⁶ Recently Zhu et al²⁷ showed that FGF2 regulates the PI3K/AKT pathway in nasopharyngeal carcinoma. Therefore the effect of miR-29 overexpression was also investigated on the PI3K/AKT pathway and results showed that miR-29 overexpression led to the inhibition of the phosphorylation of Akt and PI3K. It is important to note that a number of previously carried out studies have shown inhibition of PI3K and Akt phosphorylation with suppression of tumor growth and progression of cancers²⁸. The overexpression of miR-29 also resulted in the inhibition of proliferation and invasion of the CNE2 nasopharyngeal carcinoma suggesting that miR-29 may play a role in the metastasis of the nasopharyngeal carcinoma, which needs to be explored.

Conclusions

We showed that miR-29 is downregulated in the human nasopharyngeal cancer cells. Overexpression of miR-29 inhibits the proliferation of CNE2 nasopharyngeal cancer cells by inducing apoptosis and autophagy via targeting FGF2 mediated PI3K/AKT pathway. Henceforth, miR-29 may be an essential therapeutic target for the treatment of nasopharyngeal cancer.

Conflict of Interests

The authors declare that there are no conflicts of interest.

References

- 1) XIAO X, ZHANG Z, CHANG ET, LIU Z, LIU Q, CAI Y, CHEN G, HUANG QH, XIE SH, CAO SM, SHAO JY. Medical history, medication use, and risk of nasopharyngeal carcinoma. *Am J Epidemiol* 2018; 26: 1-7.
- 2) ZHENG YQ, CUI YR, YANG S, WANG YP, QIU YJ, HU WL. Opa interacting protein 5 promotes metastasis of nasopharyngeal carcinoma cells by promoting EMT via modulation of JAK2/STAT3 signal. *Eur Rev Med Pharmacol Sci* 2019; 23: 613-621.
- 3) CHANG ET, ADAMI HO. The enigmatic epidemiology of nasopharyngeal carcinoma. *Cancer Epidemiol Prev Biomarkers* 2006; 15: 1765-1777.
- 4) HALESAPPA RA, THANKY AH, KUNTEGOWDANAHALLI L, KANAKASETTY GB, DASAPPA L, JACOB L. Epidemiology and outcomes of nasopharyngeal carcinoma: experience from a regional cancer center in Southern India. *South Asian J Cancer* 2017; 6: 122.

- 5) NEWMAN DJ, CRAGG GM. Natural products as sources of new drugs from 1981 to 2014. *J Nat Prod* 2016; 79: 629-661.
- 6) HARVEY AL, EDRADA-EBEL R, QUINN RJ. The re-emergence of natural products for drug discovery in the genomics era. *Nat Rev Drug Discov* 2015; 14: 111.
- 7) CARTHEW RW, SONTHEIMER EJ. Origins and mechanisms of miRNAs and siRNAs. *Cell* 2009; 136: 642-655.
- 8) SLABY O, SVOBODA M, FABIAN P, SMERDOVA T, KNOFLICKOVA D, BEDNARIKOVA M, NENUTIL R, VYZULA R. Altered expression of miR-21, miR-31, miR-24 and miR-145 is related to clinicopathologic features of colorectal cancer. *Oncology* 2007; 72: 397-402.
- 9) TAO J, WU D, XU B, QIAN W, LI P, LU Q, YIN C, ZHANG W. microRNA-133 inhibits cell proliferation, migration and invasion in prostate cancer cells by targeting the epidermal growth factor receptor. *Oncol Rep* 2012; 27: 1967-1975.
- 10) WANG S, LI Q, WANG K, DAI Y, YANG J, XUE S, HAN F, ZHANG Q, LIU J, WU W. Decreased expression of microRNA-31 associates with aggressive tumor progression and poor prognosis in patients with bladder cancer. *Clin Transl Oncol* 2013; 15: 849-854.
- 11) FABBRI M, GARZON R, CIMMINO A, LIU Z, ZANESI N, CALLEGARI E, LIU S, ALDER H, COSTINEAN S, FERNANDEZ-CYMERING C, VOLINIA S. MicroRNA-29 family reverts aberrant methylation in lung cancer by targeting DNA methyltransferases 3A and 3B. *Proc Natl Acad Sci U S A* 2007; 104: 15805-15810.
- 12) XIONG Y, FANG JH, YUN JP, YANG J, ZHANG Y, JIANG Z, ZHUANG SM. Effects of MicroRNA-29 on apoptosis, tumorigenicity, and prognosis of hepatocellular carcinoma. *Hepatology* 2010; 51: 2342-2345.
- 13) LANG N, LIU M, TANG QL, CHEN X, LIU Y. Effects of microRNA-29 family members on proliferation and invasion of gastric cancer cell lines. *Cancer* 2010; 29: 603-610.
- 14) ROSTAS JW, PRUITT HC, METCALE LA, BAILEY SK, BAE S, SINGH KP, DEWITT DJ, RICHARDS WO, TUCKER JA. microRNA-29 negatively regulates EMT regulator N-myc-related factor in breast cancer. *Mol Cancer* 2014; 13: 102.
- 15) ZHANG W, QIAN JX, LIU Y, LIU TD, WANG CF, CHEN JY, WEI XZ, FU C, LI H. MicroRNA-29 plays a central role in osteosarcoma tumorigenesis and progression. *PLoS Biol* 2012; 46: 3000062.
- 16) MIZUNO K, SUGIYAMA T, MATAKI H, MATSUSHITA R, KAMIKAWAJI K, KUMAMOTO T, TAKAHASHI T, GOTO Y, NISHIKAWA R, KATO M, ENOKI H. Tumor suppressive microRNA-29 family targets cell migration and invasion directly targeting CXCL2 in lung squamous cell carcinoma. *Int J Cancer* 2012; 131: 448-450.
- 17) HUA F, LI CH, CHEN XG, LIU XP, LIU Y. miR-29a exerts anticancer activity towards SKNSH neuroblastoma cancer cells by inducing apoptosis and cell cycle arrest, and inhibiting the PI3K/AKT/MEK/ERK cascade. *Int J Mol Med* 2018; 51: 3492.
- 18) LOU F, MA HN, XU L, CHEN Y, LI YB. The polymorphisms of CD14 3'UTR are associated with the binding of miRNAs and associate with nasopharyngeal carcinoma in a Chinese population. *Chin J Pharmacol Sci* 2014; 18: 2444-2452.
- 19) CROOKER K, CHEN R, ANANDH M, HENOLD L, ANANT S, THOMAS S. miRNAs promote natural chemopreventive and chemotherapeutic activity in head and neck cancer. *Cancer Prev Res* 2012; 5: 445-450.
- 20) BUSHARAH M, COHEN SM. miRNAs: functions. *Annu Rev Physiol* 2007; 20: 175-205.
- 21) NAKAMOTO T, CROCE CM. MicroRNAs as therapeutic targets in cancer. *Transl Res* 2011; 157: 210-225.
- 22) SHAN JJ, NABINGER M, WANG Z, SAHU SS, ALLURI RK, ABDUL-SATER Z, YU Z, GORE J, NALEPA G, SAXENA R, KORC M. Pathophysiological role of microRNA-29 in pancreatic cancer. *PLoS One* 2015; 10: 11450.
- 23) GONG J, LI J, LIU Y, LIU C, JIA H, JIANG C, WANG Y, LUO M, ZHANG L, DONG L, SONG W. Characterization of microRNA-29 family expression and investigation of mechanistic roles in gastric cancer. *Cancer* 2013; 35: 497-506.
- 24) KINOSHITA T, NOHATA N, HANAZAWA T, KIKKAWA N, YAMAMOTO N, YOSHINO H, IITSAKO T, ENOKIDA H, NAKAGAWA M, OKAMOTO T, KAWAKAMI N. Tumour-suppressive microRNA-29s inhibit cell migration and invasion by targeting laminin-integrin signalling in head and neck squamous cell carcinoma. *Br J Cancer* 2013; 109: 2636.
- 25) ZHANG L, YU H, BADZIO A, BOYLE TA, SCHILDHAUS HU, LU X, DZIADZIU SZKO R, JASSEM J, VARELLA-GARCIA M, HEASLEY LE, KOWALEWSKI AA. Fibroblast growth factor receptor 1 and related ligands in small-cell lung cancer. *J Thorac Oncol* 2015; 10: 1083-1090.
- 26) SHARPE R, PEARSON A, HERRERA-ABREU MT, JOHNSON D, MACKAY A, WELTI JC, NATRAJAN R, REYNOLDS AR, REIS-FILHO JS, ASHWORTH A, TURNER NC. FGFR signaling promotes the growth of triple-negative and basal-like breast cancer cell lines both in vitro and in vivo. *Clin Cancer Res* 2011; 17: 5275-5286.
- 27) ZHU M, YING J, LIN C, WANG Y, HUANG K, ZHOU Y, TENG H. Baicalin induces apoptotic death of human chondrosarcoma cells through mitochondrial dysfunction and downregulation of the PI3K/Akt/mTOR pathway. *Planta Med* 2019; 85: 360-369.
- 28) HE Q, REN X, CHEN J, LI Y, TANG X, WEN X, YANG X, ZHANG J, WANG Y, MA J, LIU N. miR-16 targets fibroblast growth factor 2 to inhibit NPC cell proliferation and invasion via PI3K/AKT and MAPK signaling pathways. *Oncotarget* 2016; 7: 3047.