

RETRACTED ARTICLE: MicroRNA-211 promotes non-small-cell lung cancer proliferation and invasion by targeting MxA

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Abstract: Recent studies have shown that microRNAs play a pivotal role in the pathogenesis of cancer. In our current study, the expression levels of microRNA-211 (miR-211) were measured in human non-small-cell lung cancer (NSCLC) tissues and cell lines. We found that miR-211 expression levels were increased in NSCLC tissues and cell lines and that the overexpression of miR-211 promotes cell proliferation and invasion. Using bioinformatics, we demonstrated that miR-211 binds to the 3'-untranslated region of MxA and overexpression of miR-211 suppresses the expression of MxA at both the transcriptional and translational levels in NSCLC cell lines. Furthermore, knockdown of MxA increased the proliferation and invasion of NSCLC cell lines in vitro. High levels of miR-211 expression were associated with a shorter survival time in patients with NSCLC. Taken together, these results suggest that miR-211 promotes tumor proliferation and invasion by regulating MxA expression in NSCLC. This study provides insights into molecular mechanisms of miR-211-mediated tumorigenesis and oncogenesis.

Keywords: miR-211, MxA, non-small-cell lung cancer, proliferation, invasion

Introduction

Lung cancer is the leading cause of cancer-related death worldwide as of 2014, with a 5-year survival rate of only 16%.¹ The prevalence of lung cancer differs among females and males.² In 2012, ~1.8 million people were diagnosed with lung cancer, resulting in 1.6 million deaths worldwide.² Importantly, non-small-cell lung cancer (NSCLC) accounts for ~85% of all lung cancers. The vast majority of lung cancer cases are due to long-term tobacco smoking,³ while other risk factors include specific gene mutations and exposure to radon gas, asbestos, and other forms of air pollution.⁴ Because of the decreased use of tobacco, the rates of lung cancer mortality and morbidity in western countries have decreased over the last several years.^{5,6} However, in China, the rates of lung cancer mortality and morbidity have increased due to excessive tobacco use and air pollution.⁷ Although new targeted drugs have recently emerged, including epidermal growth factor receptor and anaplastic lymphoma kinase inhibitors, the overall survival of patients with lung cancer remains low due to the early recurrence and metastasis.⁸ Therefore, it is crucial to discover novel biomarkers that can accurately predict the prognosis of NSCLC patients and to find new targets for the treatment of this disease.

MicroRNAs (miRNAs) are the short noncoding RNAs of 21–23 nucleotides in length, which can bind to the 3'-untranslated region (UTR) of target mRNAs, resulting in the translational repression or degradation of mRNA. To date, >2,500 mature miRNAs have been identified in humans.⁹ These miRNAs participate in a variety of biological processes including embryonic development and cellular proliferation, differentiation,

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and apoptosis.^{10,11} A number of studies have suggested that the abnormal expression of miRNAs is associated with the progression of a variety of human cancers, such as breast cancer, gastric cancer, lung cancer, and hepatocellular carcinoma, and that these miRNAs can be used as potential cancer biomarkers.^{12,13} For example, microRNA-211 (miR-211) is located on intron 6 of the *Trpm1* gene at 15q13-q14, a locus that is frequently lost in many neoplasms.¹⁴ Unfortunately, the expression pattern and role of miR-211 in tumorigenesis is not well understood. miR-211 expression levels were found to be elevated in breast cancer cells, and the overexpression of miR-211 promoted cellular proliferation by downregulating the expression of several tumor suppressor genes.¹⁵ In contrast, miR-211 was downregulated in cells derived from gastric, hepatocellular carcinoma, and epithelial ovarian tumors, suggesting that it can also be a tumor suppressor.^{16–19} In NSCLC, a recent report showed that miR-211 was overexpressed in cancer cells, eliciting the possibility that miR-211 represents a potential therapeutic target.²⁰ However, the underlying molecular mechanisms whereby miR-211 regulates NSCLC development are poorly understood.

MxA is a 76 kDa cytoplasmic protein that is strongly induced by Interferon and contains a typical guanosinetriphosphate-binding motif.²¹ It has been well established that MxA functions as tumor suppressor by inhibiting tumor cell motility and invasion.²² Previous study has verified that MxA expression is regulated by miR-211 and miR-204 in breast cancer cells.¹⁵ However, it has not yet been determined whether miR-211 can regulate the expression of MxA in NSCLC.

Therefore, we investigated the expression of miR-211 in NSCLC cell lines and tissue specimens using quantitative real-time polymerase chain reaction (qRT-PCR) and we explored the mechanism of miR-211-mediated tumorigenesis and oncogenesis in NSCLC, identifying potential miR-211 target genes. Our study provides the basis for using miR-211 as a novel therapeutic target in NSCLC.

Materials and methods

Patient tissue samples

Paraffin-embedded NSCLC tumor specimens and adjacent noncancerous tissues were collected and stored from 40 patients who underwent surgical resection between September 2008 and October 2010 in the Affiliated Hospital of Guilin Medical College. No patients had previously received chemotherapy, radiotherapy, or other systemic treatments prior to surgery. This study was approved and monitored by the Ethics Committee of the Affiliated Hospital of Guilin Medical College and complied with the Declaration

of Helsinki. Written informed consent was obtained from all recruited patients.

Cell culture

Four human NSCLC cell lines (A549, H1650, SPC-A1, and NCI-H460) and one human bronchial epithelial cell line (16HBE) were obtained from the American Type Culture Collection (ATCC) (Manassas, VA, USA). These cell lines were cultured in Dulbecco's Modified Eagle's Medium (DMEM; Thermo Fisher Scientific, Waltham, MA, USA) supplemented with 10% fetal bovine serum (FBS; Thermo Fisher Scientific), 100 U/mL of penicillin, and 100 U/mL of streptomycin. All cells were incubated at 37°C in a humidified atmosphere containing 5% CO₂.

Cell transfection

An miR-211 mimic (5'-UUCUUUUAUCAUCCUUCGCU-3'), an miR-211 inhibitor (5'-AGGCGAAGGAUGACAAAGGGAA-3'), and a negative control oligonucleotide were designed and synthesized by GenePharma (Shanghai, People's Republic of China). A small interfering RNA (siRNA) against MxA (5'-GATTGCAGAAGGTCAGAGTT-3') was purchased from OriGene (Beijing, People's Republic of China). Transient transfection was performed using Lipofectamine 2000 (Thermo Fisher Scientific) using a final concentration of 50 nM as per manufacturer's instructions. Forty-eight hours after transfection, cells were collected for Western blot and qRT-PCR analyses.

Total RNA isolation and qRT-PCR

Total RNA was extracted from frozen tissues or cells using the TRIzol reagent (Thermo Fisher Scientific) as per manufacturer's instructions. cDNA libraries were synthesized from 5 ng of extracted RNA using a TaqMan miRNA Reverse Transcription Kit (Thermo Fisher Scientific), and the expression levels of miR-211 were determined using an miRNA-specific TaqMan MiRNA Assay Kit. Relative fold changes of miR-211 expression were normalized to U6 snRNA expression. To measure the expression levels of MxA, cDNA was reverse transcribed from total RNA using the PrimeScript™ RT-PCR Kit (Takara, Kusatsu, Japan). qRT-PCR was performed using a SYBR Green PCR Kit (Takara) with a 7500 Fast Real-Time PCR system (Thermo Fisher Scientific) as per manufacturer's instructions. PCR procedures were performed for 40 cycles as follows: denaturation at 95°C for 10 min, 95°C for 15 s, and 60°C for 1 min. The expression levels of MxA mRNA were normalized to glyceraldehyde-3-phosphate dehydrogenase (GAPDH). The relative expression of the tested genes was calculated and normalized

using the $2^{-\Delta\Delta C_t}$ method. The primers used were as follows: MxA: forward: 5'-GAGAGGAACTGTAGGGGAG-3', reverse: 5'-GGAAACATCTGTGAAAGCAA-3'; GAPDH: forward: 5'-AATGGGCAGCCGTTAGGAAA-3', reverse: 5'-TGAAGGGGTCATTGATGGCA-3'.

Western blot analysis

Proteins were extracted from tissues and cell lines using radio immunoprecipitation assay lysis buffer (P0013B; Beyotime Institute of Biotechnology, Haimen, Jiangsu, People's Republic of China). Protein concentrations were measured using a bicinchoninic acid Protein Assay Kit (P0009; Beyotime Institute of Biotechnology). Protein lysates were then separated using 10% sodium dodecyl sulfate polyacrylamide gel electrophoresis and transferred to polyvinylidene difluoride (PVDF) membranes (Bio-Rad Laboratories Inc., Hercules, CA, USA). The membranes were blocked with 5% dry milk at room temperature for 1 h and then incubated with primary anti-MxA (1:1,000, ab207414; Abcam, Cambridge, UK) or anti-GAPDH (1:1,000, ab181602; Abcam) antibodies. After washing, the membrane was incubated with horseradish peroxidase-conjugated anti-rabbit secondary antibodies (1:5,000, ab6721; Abcam). Bands were visualized using an enhanced chemiluminescence detection kit (Pierce; Thermo Fisher Scientific) and a gel imaging system. GAPDH was used as a loading control.

Cellular proliferation

The rate of cellular proliferation was determined by 3-(4,5-dimethyl-2-thiazolyl)-2,5-diphenyl-2-H-tetrazolium bromide (MTT). Briefly, 2×10^3 cells per well were plated in 96-well plates and transfected for 48 h with a final volume of 100 μ L. A total of 20 μ L of 5 mg/mL MTT stock solution was added to each well at selected time points and incubated for another 4 h, after which 150 μ L of dimethyl sulfoxide was added. The optical density was measured and recorded at 490 nm.

Cellular invasion

The rate of cellular invasion was measured using Transwell invasion plates coated with Matrigel (BD Biosciences, San Jose, CA, USA) as per manufacturer's suggestion. Forty-eight hours after transfection, cells were transferred to the upper chambers of Transwell plates containing serum-free DMEM and DMEM containing 10% FBS was added to the lower chambers. The cells were then incubated for 24 h at 37°C, stained with crystal violet, and counted using a light microscope.

Luciferase reporter assay

Cells were seeded in 24-well plates and, then, cotransfected with miR-211 mimic, miR-211 inhibitor, or negative control

miRNA and the mutant (mut) or wild-type 3'-UTR of MxA using Lipofectamine 2000 as per manufacturer's instructions. Forty-eight hours after transfection, the cells were harvested and luciferase activity was measured using a dual luciferase reporter assay system (Promega Corporation, Fitchburg, WI, USA) as per manufacturer's instructions. The primers used to build the wild-type MxA 3'-UTR constructs were as follows: forward: 5'-CTCTCTAGACTCCCACACTCTGTCCAGCCC-3', reverse: 5'-CTCTCTAGACTCTGTCTGCTAGAAATGAG-3'. A Site-Directed Mutagenesis Kit (Yeasen, Shanghai, People's Republic of China) was used to generate the mutant MxA 3'-UTR construct, and the primers used were as follows: forward: 5'-TGTCTTCGTACTGGTTCGCGAT-3', reverse: 5'-GAAAATCGGTACCCAGTCC-3'.

Statistical analysis

Statistical analysis was carried out using the SPSS software Version 19.0 (IBM Corporation, Armonk, NY, USA). Data are presented as mean $\pm$ standard deviation from three separate experiments. Differences between groups were assessed using Student's *t*-test. One-way analysis of variance was used to measure the significance of comparisons between more than two groups. A *P*-value of <0.05 was considered statistically significant for all tests.

Results

miR-211 is upregulated in NSCLC tissues and cell lines

We found elevated expression levels of miR-211 in 28 of the 40 NSCLC tumor samples compared to their corresponding adjacent noncancerous tissues (Figure 1A). As shown in Figure 1B, miR-211 expression levels were 2.9-fold higher in NSCLC tumor samples than in their adjacent noncancerous tissues ($P < 0.05$). The expression levels of miR-211 were also markedly increased in A549 (5.8-fold increase), H1650 (6.6-fold increase), SPC-A1 (5.5-fold increase), and NCI-H460 (4.1-fold increase) cell lines than in human 16HBE bronchial epithelial cells ($P < 0.05$, Figure 1C). Because the expression levels of miR-211 were highest in H1650 and A540 cells among the four NSCLC lines tested, we decided to use them exclusively for further experimentation.

miR-211 promotes the proliferation of NSCLC cells

To investigate the role of miR-211 in the progression of NSCLC, we transfected H1650 and A549 cells with an miR-211 mimic, an miR-211 inhibitor, or a negative control miRNA. The expression levels of miR-211 in miR-211

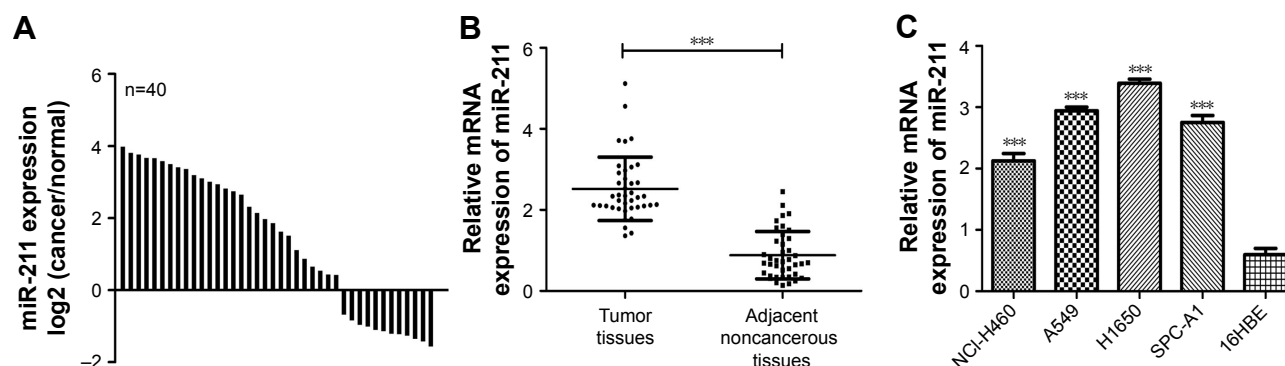


Figure 1 miR-211 is upregulated in NSCLC tumors and cell lines.

Notes: (A) qRT-PCR analysis of miR-211 expression in 40 NSCLC tissues and 40 adjacent noncancerous tissues. (B) The expression of miR-211 in NSCLC tissues was significantly lower than in adjacent noncancerous tissues. (C) Expression levels of miR-211 in four NSCLC cell lines (A549, H1650, SPC-A1, and NCI-H460) compared to one human bronchial epithelial cell line (16HBE) were detected using qRT-PCR analysis. *** $P < 0.001$.

Abbreviations: miR-211, microRNA-211; NSCLC, non-small-cell lung cancer; qRT-PCR, quantitative real-time polymerase chain reaction.

mimic-transfected A549 cells were 2.6-fold higher and 7.8-fold higher than in cells transfected with either a negative control miRNA or an miR-211 inhibitor (Figure 2A). In H1650 cells, the expression levels of miR-211 were 2.2- and 6.4-fold higher after transfection with the miR-211 mimic compared to cells with either a negative control miRNA or an miR-211 inhibitor (Figure 2A). We then investigated the effect of miR-211 on cellular proliferation. As shown in Figure 2B, the rate of proliferation of H1650 and A549 cells transfected with an miR-211 was markedly higher compared to cells transfected with either an miR-211 inhibitor or a negative control miRNA ($P < 0.05$). We also found that the rate of proliferation of NSCLC cell lines was higher compared to human 16HBE bronchial epithelial cells (Figure 2C).

miR-211 promotes the invasion of NSCLC cells

Transfection with an miR-211 mimic significantly increased the invasiveness of A549 cells compared to transfection with an miR-211 inhibitor (344 ± 3 vs 50 ± 8) or a negative control miRNA (344 ± 3 vs 19 ± 11) ($P < 0.05$, Figure 2D). Similarly, it was observed that the invasiveness of miR-211 mimic-transfected H1650 cells was higher than cells transfected with either an miR-211 inhibitor (354 ± 19 vs 64 ± 11) or a negative control miRNA (354 ± 19 vs 149 ± 12) (both $P < 0.05$, Figure 2D).

miR-211 expression levels can be used as a prognostic factor in NSCLC

The clinical significance of miR-211 expression levels in NSCLC was determined by evaluating the correlation

between miR-211 expression levels and clinicopathological features of patients with NSCLC. As presented in Table 1, we found that miR-211 expression levels were closely associated with tobacco smoking status ($P = 0.038$), tumor size ($P = 0.005$), and tumor stage ($P = 0.022$). However, there were no clear associations between miR-211 expression levels and age, gender, or alcohol consumption ($P > 0.05$).

miR-211 expression is associated with poor prognosis in NSCLC

The association between miR-211 expression levels and the overall survival of patients with NSCLC was assessed with a Kaplan–Meier curve and the long-rank test method. As shown in Figure 3, patients with high miR-211 expression levels had shorter 5-year survival rates compared to those with low miR-211 expression levels ($P = 0.019$). We performed univariate and multivariate analyses to identify factors that might influence the overall survival of these patients. We found that miR-211 expression levels ($P = 0.020$), as well as tobacco smoking status ($P = 0.034$), tumor size ($P = 0.036$), and tumor stage ($P = 0.020$), were the independent prognostic predictors of overall survival (Table 2).

MxA expression is regulated by miR-211 in NSCLC cells

Previous study has shown that miR-211 regulates the expression of MxA in breast cancer cells.¹⁵ Therefore, we assessed the expression levels of MxA in NSCLC tissues and cell lines to determine whether MxA is regulated by miR-211 in NSCLC. We aligned the 3'-UTRs of MxA and miR-211 and found that the MxA 3'-UTR contains a conserved putative target site for miR-211 (Figure 4A). To validate MxA

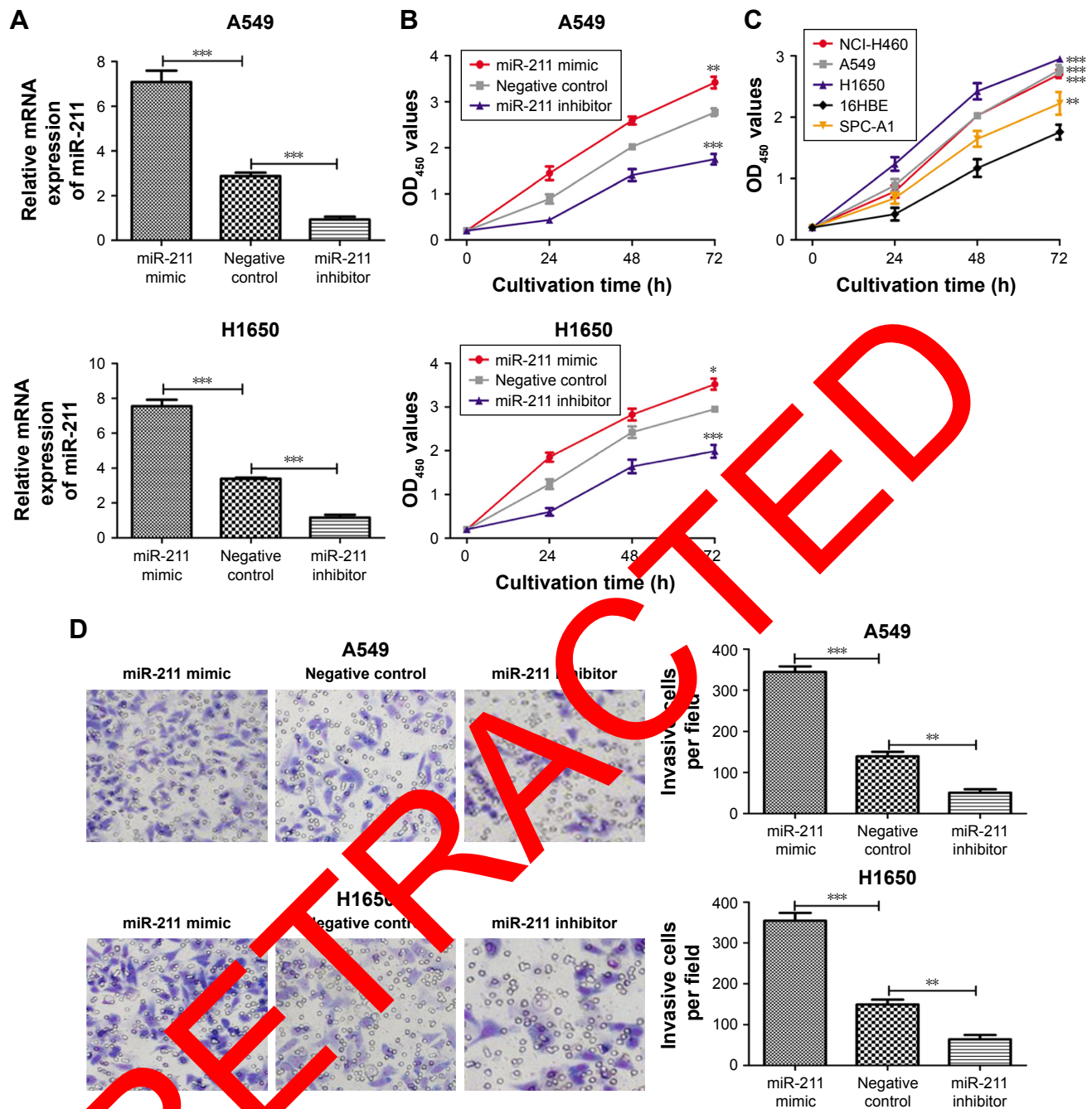


Figure 2 miR-211 promotes proliferation and invasion of NSCLC cells.

Notes: (A) qRT-PCR analysis was used to measure the expression of miR-211 after the transfection of H1650 and A549 cell lines with miR-211 mimic, miR-211 inhibitor, or negative control RNA. (B) MTT assay was used to measure the cell proliferation after the transfection of H1650 and A549 cell lines with miR-211 mimic, miR-211 inhibitor, or negative control RNA. (C) MTT assay was used to measure the cell proliferation of four NSCLC cell lines (A549, H1650, SPC-A1, and NCI-H460) and one human bronchial epithelial cell line (16HBE). (D) Transwell invasion assay demonstrated that overexpression of miR-211 markedly increased the invasive capacity of H1650 and A549 cells compared to the negative control whereas miR-211 inhibitor inhibited NSCLC cell invasion. *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$. OD₄₅₀, optical density at 450 nm.

Abbreviations: miR-211, microRNA-211; miRNA, microRNA; MTT, 3-(4,5-dimethyl-2-thiazolyl)-2,5-diphenyl-2-H-tetrazolium bromide; NSCLC, non-small-cell lung cancer; qRT-PCR, quantitative real-time polymerase chain reaction.

as a direct target of miR-211, we performed a luciferase reporter assay. As expected, an miR-211 mimic reduced the luciferase activity of the wild-type MxA 3'-UTR but not its mut 3'-UTR ($P < 0.05$, Figure 4B). Furthermore, transfection with an miR-211 inhibitor increased the luciferase activity

of the wild-type MxA 3'-UTR but had no effect with the mut MxA 3'-UTR ($P < 0.05$, Figure 4B). Ectopic miR-211 expression repressed MxA protein expression in A549 and H1650 cells (Figure 4C). We found that both the mRNA and protein expression levels of MxA were downregulated in

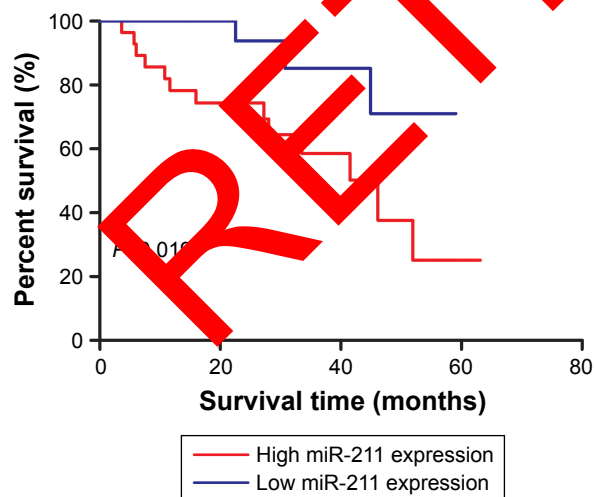
Table I Correlation between miR-211 expression and the clinicopathological parameters

Variables	Number	miR-211 expression ^a		P-value ^b
		Low (n=12)	High (n=28)	
Age (years)				0.293
≥50	22 (55.0%)	7 (17.5%)	15 (37.5%)	
<50	18 (45.0%)	5 (12.5%)	13 (32.5%)	
Gender				0.070
Male	23 (57.5%)	6 (15.0%)	17 (42.5%)	
Female	17 (42.5%)	6 (15.0%)	11 (27.5%)	
Tobacco smoking status				0.038
Nonsmoker	23 (57.5%)	8 (20.0%)	15 (37.5%)	
Smoker	17 (42.5%)	4 (10.0%)	13 (32.5%)	
Tumor size (cm)				0.025
≥5	20 (50.0%)	8 (20.0%)	12 (30.0%)	
<5	20 (50.0%)	4 (10.0%)	16 (40.0%)	
Alcohol drinking status				0.144
Nondrinker	23 (57.5%)	7 (17.5%)	16 (40.0%)	
Drinker	17 (42.5%)	5 (12.5%)	12 (30.0%)	
Tumor stage				0.022
I-II	15 (37.5%)	6 (15.0%)	9 (22.5%)	
III	25 (62.5%)	6 (15.0%)	19 (47.5%)	

Notes: ^aRelative expression of miR-211 was determined using the 2^{-ΔΔCt} method, and the median of 2^{-ΔΔCt} was used to divide all patients into groups based on high expression of miR-211 or low expression of miR-211. ^bχ² test.

Abbreviation: miR-211, microRNA-211.

NSCLC tissues compared with their adjacent noncancerous tissues (Figure 4D and E). Similar results were obtained when comparing the NSCLC cell lines with the human bronchial epithelial cell line (16HBE) (Figure 4F). Furthermore, we found that the expression levels of MxA were inversely correlated with miR-211 in NSCLC patients ($r = -0.85$, $P < 0.05$, Figure 4G).

**Figure 3** miR-211 predicts the prognosis of patients with NSCLC.

Notes: A total of 40 patients were classified into the high miR-211 expression group (n=28) and low miR-211 expression group (n=12). NSCLC patients with high miR-211 expression have a lower 5-year survival rate compared to those with low miR-211 expression.

Abbreviations: miR-211, microRNA-211; NSCLC, non-small-cell lung cancer.

MxA suppresses the proliferation and invasion of NSCLC cells

To determine the role of MxA in NSCLC cellular proliferation and invasion, we silenced the expression of MxA in H1650 and A549 cells. The expression levels of MxA in MxA siRNA-treated cells were significantly decreased compared to untransfected cells (3.2-fold decrease in H1650 cells and 2.7-fold decrease in A549 cells) ($P < 0.05$, Figure 5A). As expected, silencing of MxA expression promoted cellular proliferation and invasion of A549 and H1650 cells (Figure 5B and C). These results suggest that decreased expression levels of MxA recapitulate effects observed with miR-211 overexpression.

Discussion

Recent studies have highlighted a crucial role for miRNAs during tumorigenesis.^{23–29} miR-211 is known to mediate tumorigenesis and oncogenesis and regulates the expression of both tumor suppressor and tumor-promoting genes.^{15–20} Therefore, we investigated the expression pattern of miR-211 and its associated downstream targets in NSCLC. Our results show that miR-211 expression levels were elevated in NSCLC cell lines and tumors. We confirmed that miR-211 overexpression induced NSCLC cell proliferation and invasion. We found that the rates of cellular proliferation and invasion in miR-211 mimic-transfected NSCLC cells were significantly higher compared to cells transfected with an miR-211 inhibitor or a negative control miRNA. Thus, our results suggest that miR-211 promotes the development and progression of NSCLC. We also investigated the clinical significance of miR-211 expression levels in patients with NSCLC and found that miR-211 expression levels were an independent predictor of poor patient prognosis.

We decided to investigate the molecular mechanisms whereby miR-211 promotes the proliferation and invasion of NSCLC cells. Lee et al¹⁵ had previously identified the tumor suppressor MxA as a target of miR-211 in breast cancer cells. We therefore measured the expression levels of MxA in NSCLC tumors and cell lines. We found that the expression levels of MxA were significantly decreased in tumor samples and A549 and H1650 cells compared to noncancerous tissues and 16HBE cells. Furthermore, the expression levels of MxA were reduced in cells treated with an miR-211 mimic. Our results suggest that MxA expression in NSCLC cells is regulated by miR-211.

MxA has been shown to suppress tumor motility, and its expression levels are low in many types of tumors. However, the

Table 2 Univariate and multivariate analyses of factors associated with overall survival

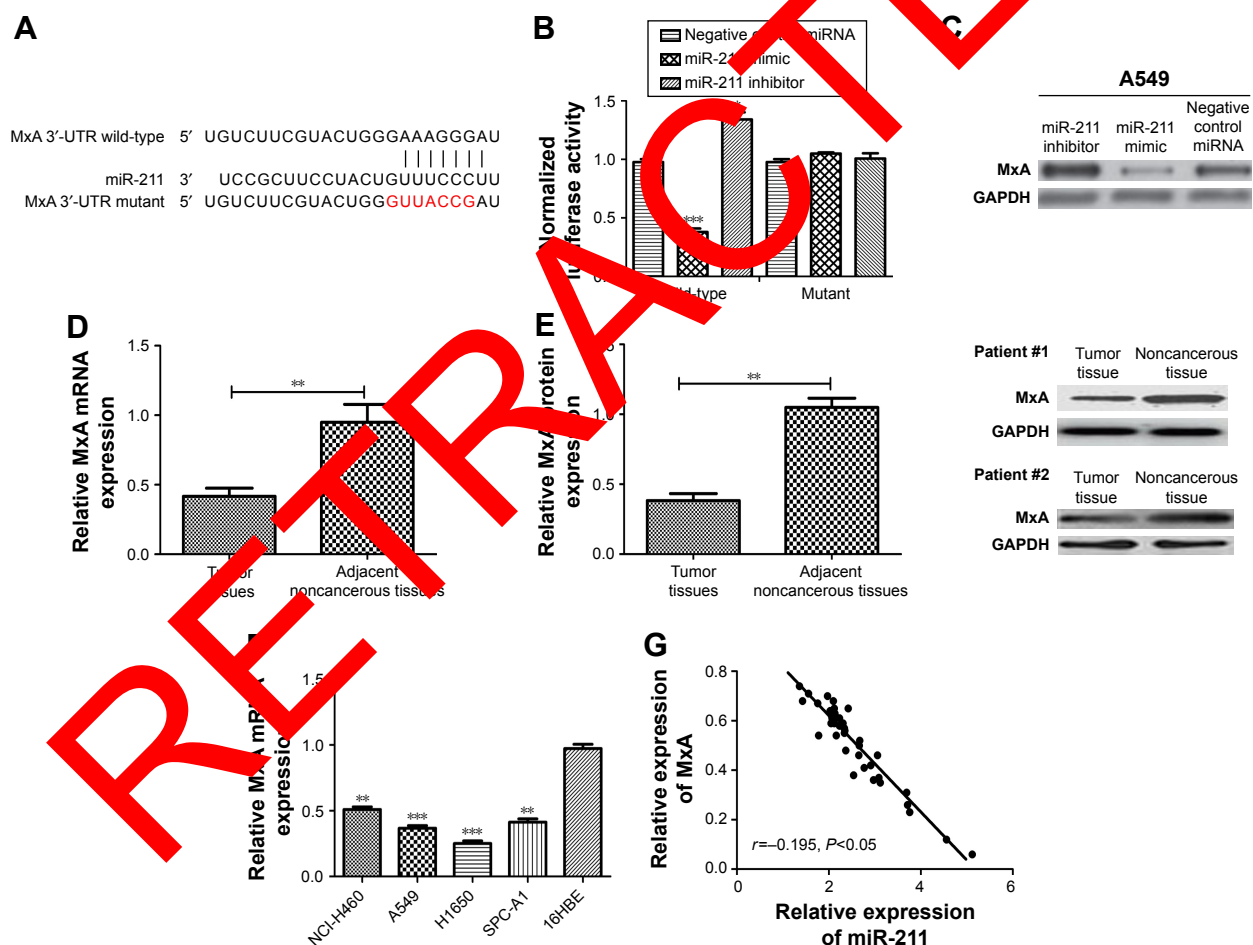
Variables	Univariate analysis		P-value [^]	Multivariate analysis		P-value ^{^^}
	HR	95% CI		HR	95% CI	
miR-211	3.245	1.213–8.685	0.019	3.222	1.204–8.624	0.020
Age	2.224	0.677–7.299	0.188	–	–	–
Gender	2.430	0.779–7.580	0.123	–	–	–
Tobacco smoking status	2.671	1.028–6.941	0.044	2.999	1.085–8.290	0.034
Tumor size (cm)	3.301	1.096–8.381	0.033	2.975	1.076–8.226	0.036
Alcohol drinking status	2.630	0.882–7.844	0.083	–	–	–
Tumor stage	3.183	1.189–8.519	0.021	3.028	1.095–8.373	0.020

Notes: [^]Log-rank test. ^{^^}Cox regression model. – indicates not enrolled in the multivariate analysis.

Abbreviations: CI, confidence interval; HR, hazard ratio; miR-211, microRNA-211.

role of MxA in NSCLC progression remains poorly understood. We showed that silencing of MxA expression significantly increased the proliferation and invasion of NSCLC cells. Therefore, we propose that miR-211 acts as a tumor promoter in NSCLC by regulating MxA expression.

In conclusion, these results suggest that miR-211 is a potential therapeutic target for NSCLC. However, further study using a larger sample of patients is required to confirm the effects of miR-211 expression on patient prognosis and NSCLC tumor development.

**Figure 4** MxA is a direct target of miR-211.

Notes: (A) TargetScan revealed that the 3'-UTR of MxA mRNA contains a putative site that is partially complementary to miR-211. (B) Luciferase activity assay revealed that miR-211 suppressed wild-type MxA 3'-UTR luciferase activity, while it had no effect on mutant MxA 3'-UTR luciferase activity compared to control in A549 cells. (C) Ectopic miR-211 expression inhibited MxA protein expression in A549 cells. (D) qRT-PCR analysis was used to measure the expression of MxA in 40 NSCLC tissues and 40 adjacent noncancerous tissues. (E) Western blot analysis was used to measure the expression of MxA in 40 NSCLC tissues and 40 adjacent noncancerous tissues. (F) qRT-PCR analysis was used to measure the expression of MxA in four NSCLC cell lines (A549, H1650, SPC-A1, and NCI-H460) and one human bronchial epithelial cell line (16HBE). (G) The mRNA expression of MxA correlated inversely with miR-211. *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$.

Abbreviations: miR-211, microRNA-211; miRNA, microRNA; NSCLC, non-small-cell lung cancer; qRT-PCR, quantitative real-time polymerase chain reaction; UTR, untranslated region.

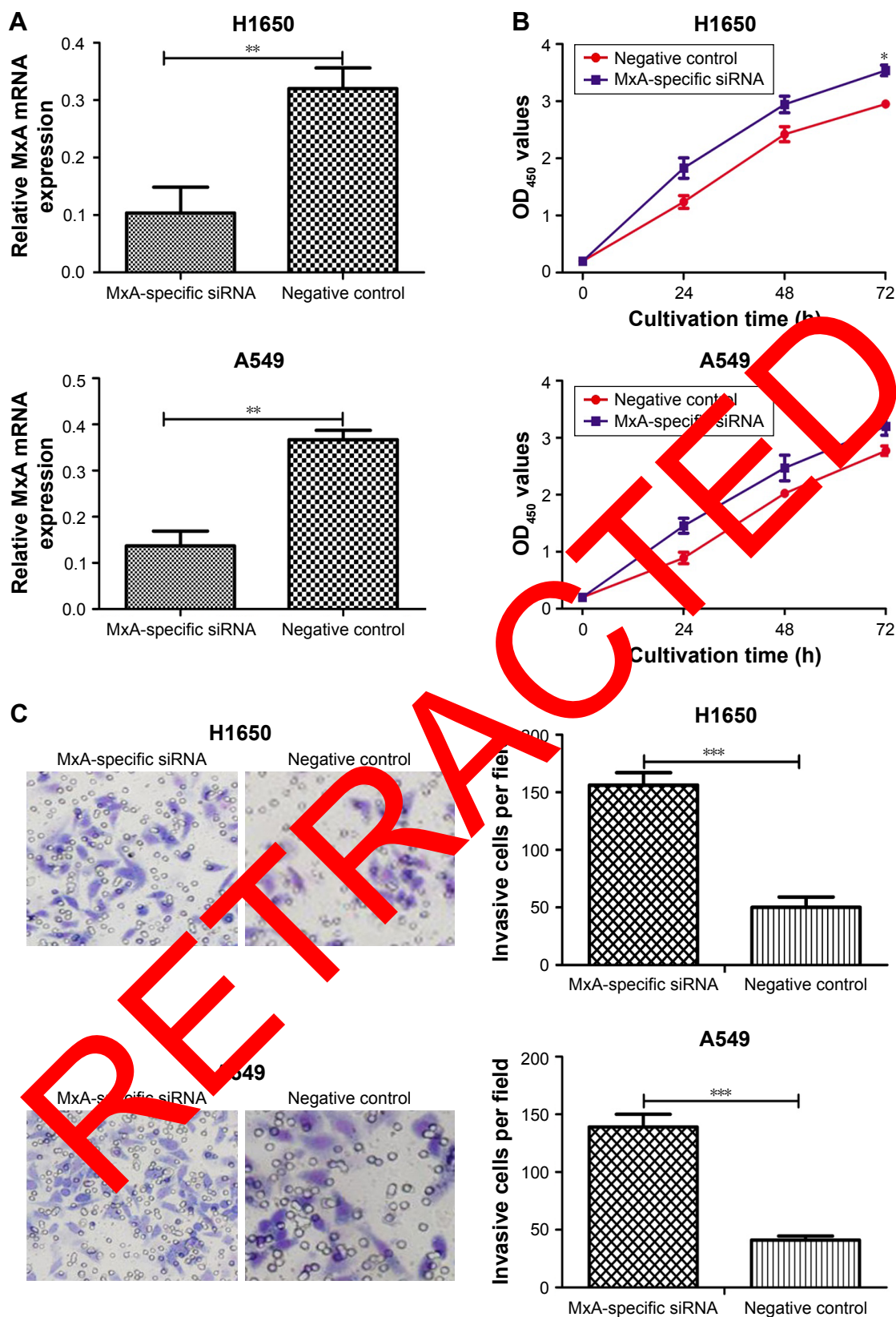


Figure 5 Silencing of MxA promotes the proliferation and invasion of NSCLC cells.

Notes: (A) qRT-PCR analysis was used to measure the expression of MxA in H1650 and A549 cells after MxA-specific siRNA and negative control siRNA transfection. (B) MTT assay was used to measure the cell proliferation in H1650 and A549 cells after MxA-specific siRNA and negative control siRNA transfection. (C) Transwell invasion assay was used to measure the cell invasion in H1650 and A549 cells after MxA-specific siRNA and negative control siRNA transfection. *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$. OD₄₅₀, optical density at 450 nm. Scale bar 50 μ m. Magnification $\times 200$.

Abbreviations: miR-211, microRNA-211; MTT, 3-(4,5-dimethyl-2-thiazolyl)-2,5-diphenyl-2-H-tetrazolium bromide; NSCLC, non-small-cell lung cancer; qRT-PCR, quantitative real-time polymerase chain reaction; siRNA, small interfering RNA.

Conclusion

Our study demonstrates that overexpression of miR-211 promotes proliferation and invasion of NSCLC cells. More importantly, we provided evidence that miR-211 exerts its functional role via inhibiting the expression of MxA in NSCLC. Altogether, these data suggest that manipulation of the level of miR-211 may provide a novel therapy for NSCLC patients in the future.

Author contributions

All authors contributed toward data analysis, drafting and critically revising the paper and agree to be accountable for all aspects of the work.

Disclosure

The authors report no conflicts of interest in this work.

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