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ORIGINAL RESEARCH

RETRACTED ARTICLE: Research on Correlations of miR-196a Expression with Progression and Prognosis of Cutaneous Squamous Cell Carcinoma

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Purpose: This study aimed to investigate the correlation between miR-196a expression and the progression and prognosis of cutaneous squamous cell carcinoma (CSCC).

Patients and Methods: Tissue samples and corresponding paracancerous tissue samples from 117 patients with CSCC were collected. The qRT-PCR analysis was used to detect the expression levels of miR-196a. Kaplan–Meier curve and Cox regression analyses were used to analyze the relationship between miR-196a expression and patients' prognosis. The CCK-8 and transwell assays were used to explore the effects of miR-196a on the abilities of cell proliferation, migration, or invasion.

Results: miR-196a expression was significantly up-regulated in CSCC tissues and cell lines, compared with adjacent normal tissues or cell lines, respectively. High expression of miR-196a was associated with positive lymph node metastasis, high TNM stages, and a lower five-year survival rate. The expression level of miR-196a was up-regulated and the proliferation, migration or invasion ability of cells were significantly increased according

Conclusion: miR-196a is highly expressed in CSCC, thus affecting the occurrence and development of CSCC. More importantly, miR-196a was shown to have potential as a prognostic marker for CSCC.

Keywords: miR-196a, progression, prognosis, cutaneous squamous cell carcinoma

Introduction

Cutaneous squamous cell carcinoma (CSCC), also known as epidermoid carcinoma, is the second most common skin malignancy incidence rate below basal cell carcinoma.[1,2] The malignancy and metastasis rate of CSCC are higher than basal cell carcinoma. The majority of CSCC can be induced by long-term sunlight, such as solar keratosis, burn, posttraumatic scar and chronic inflammatory ulcer.[3,4] In recent years, the incidence rate of CSCC is increasing. It has been reported that patients with a history of CSCC can develop skin tumors of the same tissue type at the same time or again.[5] The risk of recurrence is high and seriously affects human health.[6] The risk of skin cancer is increased in the population with fair skin, old age, more than 30 years of sun exposure, genetic susceptibility factors, and long-term adverse stimulation.[7,8] Surgery is the cornerstone of the treatment of CSCC, and radiotherapy, as well as systemic treatments, are sometimes also implemented.[9] Now, more and more scientists are devoted to finding CSCC-specific indicators to effectively evaluate the prognosis of cancer patients and to provide a new approach for the treatment of CSCC.

MicroRNAs (miRNAs) are a class of small non-coding single-stranded RNA molecules, about 22 nucleotides in length, which are characterized by not being converted into proteins, but by performing their functions in different ways.[10,11] miRNAs are involved in a range of physiological processes, including growth, development, differentiation, and apoptosis. Studies have indicated that about 50% of miRNA are located in tumor gene-related regions on

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chromosomes, and are often accompanied by abnormal miRNA expression in tumors.[12,13] The research about miRNA and CSCC showed that many miRNAs were abnormally expressed in CSCC, such as miR-135b, miR-424, and miR-196a with up-regulated expression, while miR-378, miR-145, and miR-140-3p showed a down-regulated trend.[14] But, there has been no clear report on correlations of miR-196a expression with progression and prognosis of CSCC.

In this paper, we studied the expression of miR-196a in CSCC and analyzed the association between miR-196a expression and CSCC prognosis. Meanwhile, the significance of miR-196a in CSCC cell function was further explored.

Patients and Methods

Patients and Tissue Samples

The CSCC tumor tissues and corresponding adjacent normal tissues from 117 patients with CSCC admitted to Weifang People's Hospital were collected during March 2011 and March 2015. All collected samples were immediately placed in liquid nitrogen and stored at −80°C for use. None of the patients in the study received other treatments before Surgery, including chemotherapy, radiation, and immunotherapy. The clinical characteristics of the patients were collected for further study. All patients were required to sign written informed consent. This study was approved by the Medical Ethics Committee of Weifang People's Hospital (20110146) and conducted in accordance with the Declaration of Helsinki. All patients were followed up for 5 years to investigate the significance of miR-196a on the prognosis of patients.

Cell Culture and Transfection

Four CSCC cell lines (A431, SCC13, HSC-1, and SCL-1) and one human normal skin cell line (HaCaT) were obtained from the Cell Repository, Chinese Academy of Sciences (Shanghai, China). All cell lines were cultured in DMEM (Gibco, Grand Island, NY) containing 10% fetal bovine serum (FBS; Thermo Fisher Scientific, Waltham, USA) and the cultural atmosphere was at 37°C with CO_2.

The CSCC cells were seeded in six-well plates. Then miR-196a mimic, miR-196a inhibitor, and the negative controls (NC) were respectively transfected into cells, and refer to the manufacturers' introduction of Lipofectamine 2000 (Thermo Fisher Scientific, Waltham, MA, USA) for detailed procedures of cell transfection.

RNA Extraction and Quantitative Real-Time PCR

Total RNA was extracted by RNA extraction kit, and the concentration of RNA was determined by NanoDrop 2000 (Thermo Fisher Scientific, Waltham, USA). RNA extraction kit was TRIzol reagent (Thermo Fisher Scientific, Waltham, MA, USA). TaqMan miRNA reverse transcription kit (Thermo Fisher Scientific) was used to reverse-transcribe of total RNA into cDNA. Real-time quantitative PCR (qRT-PCR) was performed using the SYBR-Green I Master mix kit (Invitrogen; Thermo Fisher Scientific, Waltham, USA) on an ABI 7500 Fast Real-Time PCR (Applied Biosystems, Inc., Foster, CA, USA). The relative expression level of miR-196a was calculated by the $2^{-\Delta\Delta Ct}$ method and normalized to U6.

Cell Proliferation Assay

Cell viability was assessed by a cell proliferation assay using Cell Counting Kit-8 (CCK-8, Dojindo Laboratories, Kumamoto, Japan). The cells were inoculated in 96-well plates, mixed gently, placed in 37°C, 5% CO_2 incubator for conventional culture, and CCK-8 reagent was added at 0, 24 h, 48 h, and 72 h, respectively. Finally, the 96-well plate was placed on an ultraviolet spectrophotometer to detect the OD value at 450 nm.

Cell Migration and Invasion Assays

The ability of cell invasion and migration was mainly evaluated by Transwell assays using chambers with 8 μm pore polycarbonate filters (Corning, NY, USA). For cell invasion assay, the upper chamber should be precoated with Matrigel (BD, USA), whereas cell migration assay is not required. The other steps in both migration and invasion assays were the same. The density of A431 cells and SCL-1 cells was 4×10^4 cells/well. The CSCC cells were scattered in a serum-free medium and placed in the upper chamber. Then 500 μL medium containing 10% FBS was added to the lower chamber to ensure no air bubbles between the lower complete medium and the Transwell chamber. It was incubated in an incubator

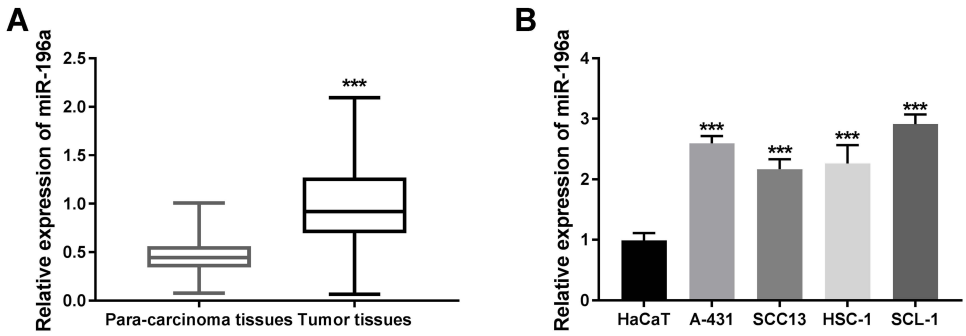

Figure 1 The expression of miR-196a was increased in CSCC tissues and cell lines. (**A**) The expression levels of miR-196a in 117 pairs of CSCC tissue samples and para-carcinoma tissues were detected using qRT-PCR. ***$P < 0.001$ (**B**) The expression levels of miR-196a in 4 CSCC cell lines were meas[illegible]RT-PCR. ***$P < 0.001$.

for 12 h. After being rinsed, the Transwell compartment was wiped with a cotton swab to e[illegible]minate un-m[illegible]grated or un-invaded cells in the upper chamber. The cells migrated or invaded to the lo[illegible]er chambe[illegible] were [illegible]ixed with 4% paraformaldehyde, stained with 0.1% crystal violet dye at room temperature, [illegible]d out of light fo[illegible]5 min, then dried upside down and counted under an inverted fluorescence microscope.

Statistical Analysis

SPSS 22.0 software (IBM, Armonk, NY, USA) was used for data st[illegible]tistics, and [illegible]raphPad 5.0 (GraphPad Software, Inc., La Jolla, CA, USA) was used as the mapping tool. The Student's *t*-test was used for [illegible]comparison between two groups, and a one-way analysis of variance was used for comparison betw[illegible]en multiple [illegible]roups. Mean ± SD was used to represent all results. Kaplan–Meier curve and Cox regression analysis [illegible]re used to [illegible]investigate the value of miR-196a on the prognosis of CSCC. $P < 0.05$ was considered statis[illegible]lly signifi[illegible]t.

Results

Expression of miR-196a in C[illegible]SCC [illegible]issue[illegible] and Cell Lines

To reveal the expression level of miR-[illegible]6a in [illegible]C[illegible]qRT-PCR was used to detect the expression of miR-196a in CSCC and adjacent normal tissues. Fig[illegible]e 1A s[illegible]ed that the expression level of miR-196a in CSCC tissues was higher than that in normal tissues ($P < 0.0$[illegible]). In the det[illegible]tion of cell lines, it was found that the expression levels of miR-196a in CSCC cell lines (A-431, SCC13, [illegible]C-1, SCL-1) were also significantly higher than that in normal cell lines HaCaT (Figure 1B, $P < 0.001$).

Relationship B[illegible]tw[illegible]en Cl[illegible]nicopathological Characteristics and miR-196a Expression in CSCC P[illegible]ti[illegible]nts

To ana[illegible]ze the r[illegible]ationship [illegible]etween miR-196a expression and the clinicopathological characteristics of patients, CSCC patients [illegible]re [illegible]ivided [illegible]nto two groups according to the median expression of miR-196a, the high expression group (n = 59) and the l[illegible]w expression group (n = 58). As shown in Table 1, the expression level of miR-196a was closely related to lymph node met[illegible]tasis ($P = 0.048$) and TNM staging ($P = 0.006$), but other clinicopathological characteristics showed no significant correlation with miR-196a ($P > 0.05$).

Upregulation of miR-196a is Associated with Poor Prognosis in CSCC Patients

The prognostic significance of miR-196a in CSCC was further analyzed through the Kaplan–Meier survival curve and Cox regression analysis. Kaplan–Meier survival curve was used to study the relationship between miR-196a expression level and 5-year survival of patients, the results showed that the 5-year survival rate in the high miR-196a expression group was significantly lower than that in the low miR-196a expression group ($P = 0.031$, Figure 2). Cox regression analysis was used to investigate prognostic independent factors, and Table 2 showed that miR-196a (HR = 4.367, $P =$

Table 1 Association Between miR-196a Expression and Different Clinical Characteristics of Patients with CSCC

Clinical Characteristics	Cases	miR-196a Expression		*P* values
	n = 117	Low (n = 58)	High (n = 59)	
Age				0.521
≤ 65	47	25	22	
> 65	70	33	37	
Sex				0.916
Male	66	33	33	
Female	51	25	26	
Location				0.522
Head, face	66	31	35	
Arm, others	51	27	24	
Tumor size (cm)				0.31
≤ 5	53	29	24	
> 5	64	29	35	
Differentiation				0.[illegible]9
Well-moderate	50	24	[illegible]	
Poor	67	34	33	
Lymph node metastasis				0.048
Negative	83	46	37	
Positive	34	12	[illegible]2	
TNM stage				0.006
I-II	81	47	34	
III-IV	36	11	25	

0.018), lymph node metastasis (HR = 3.038, $P = 0.025$) and TNM staging (HR = 3.595, $P = 0.020$) were the independent prognostic indicators of CSCC patients.

Upregulation of miR-196a Promotes CSCC Cell Proliferation, Migration, and Invasion

A431 and SCL-1 were transfected with miR-196a mimics or inhibitors to test the tumor cellular functions. For cell proliferation, the results of qRT-PCR showed that miR-196a mimic significantly increased the expression level of miR-196a, but miR-196a inhibitor exerted the opposite effect ($P < 0.01$, Figure 3A). Figure 3B shows the experimental results of CCK-8, the up-regulated expression of miR-196a promoted the proliferation of CSCC cells, while down-regulated expression inhibited the proliferation of CSCC cells ($P < 0.05$).

Transwell assays were conducted to study the effects of miR-196a on cell migration and invasion. The results in Figure 4A and B are shown that miR-196a mimic group showed enhanced cell migration and invasion abilities, while the miR-196a inhibitor group showed weakened migration and invasion abilities, compared with control and NC ($P < 0.001$).

Discussion

Cancer research has always been a hot topic among scientists. At present, the treatment of cancer is mainly surgery, chemotherapy, and radiotherapy, but its prognosis is not satisfactory. miRNA has been proved to play a regulatory role in the growth cycle, apoptosis, tumor invasion and metastasis, and new angiogenesis of tumor cells.[10,15,16] About 50% of miRNA genes are located in tumor gene-related regions on chromosomes and are often accompanied by abnormal miRNA expression in tumors.[17,18] For example, a previous study indicated that miR-139-5p plays a role as a tumor suppressor gene in NSCLC, which is of great significance for the prognosis of NSCLC patients.[19] A study by Tian et al confirmed that microRNA-621 was abnormally low in bladder cancer and inhibited the proliferation and metastasis of cancer cells by inhibiting Wnt /β-catenin signal transduction.[20] For CSCC, it was found that miRNAs play important roles in the pathophysiological process of CSCC development.[21] The abnormal expression of miRNAs in CSCC provides

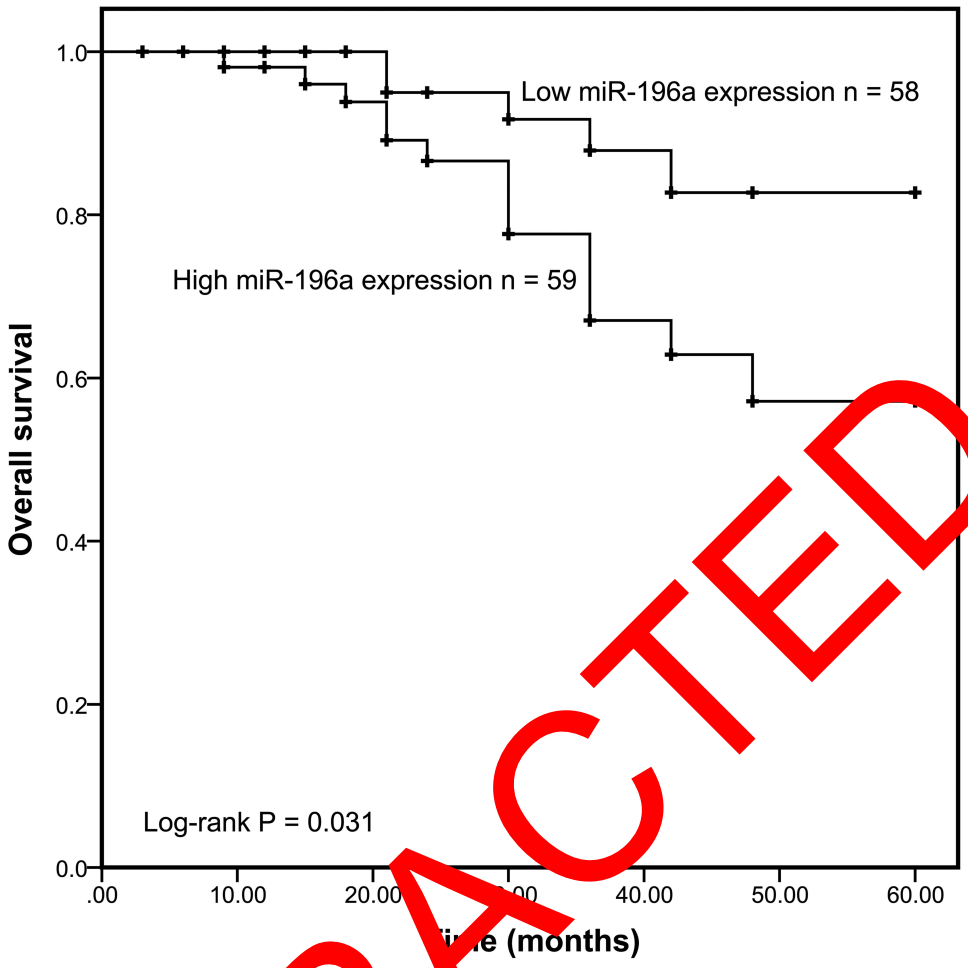

Figure 2 Kaplan–Meier survival curve in relation to the miR-196a expression level in patients with CSCC. Patients with high miR-196a expression exhibited a shorter overall survival time than patients with low miR-196a expression ($P = 0.031$).

a reliable theoretical basis for the prognosis.[23] Wang et al found that low-expressed miR-27a promoted tumor growth and metastasis by targeting EGFR, and miR-27a may play an important role in the process of CSCC.[24] miR-196a is an abnormally expressed miRNA that is common in cancer research. He Xin reported abnormal high expression of miR-196a in colorectal cancer.[25] Zhang et al found that miR-196a plays a key role in glioma susceptibility.[26] Therefore, it is very necessary to study the role of miR-196a in CSCC.

Table 2 Multivariate Cox Analysis of Factors for Survival of CSCC Patients

Variables	Multivariate Cox Analysis		
	HR	95% CI	*P*-value
miR-196a	4.367	1.282–14.874	0.018
Age	2.355	0.841–6.595	0.103
Sex	0.410	0.139–1.210	0.106
Location	0.451	0.162–1.256	0.128
Tumor size	0.672	0.230–1.964	0.468
Differentiation	1.519	0.585–4.327	0.363
Lymph node metastasis	3.038	1.150–8.027	0.025
TNM stage	3.595	1.222–10.582	0.020

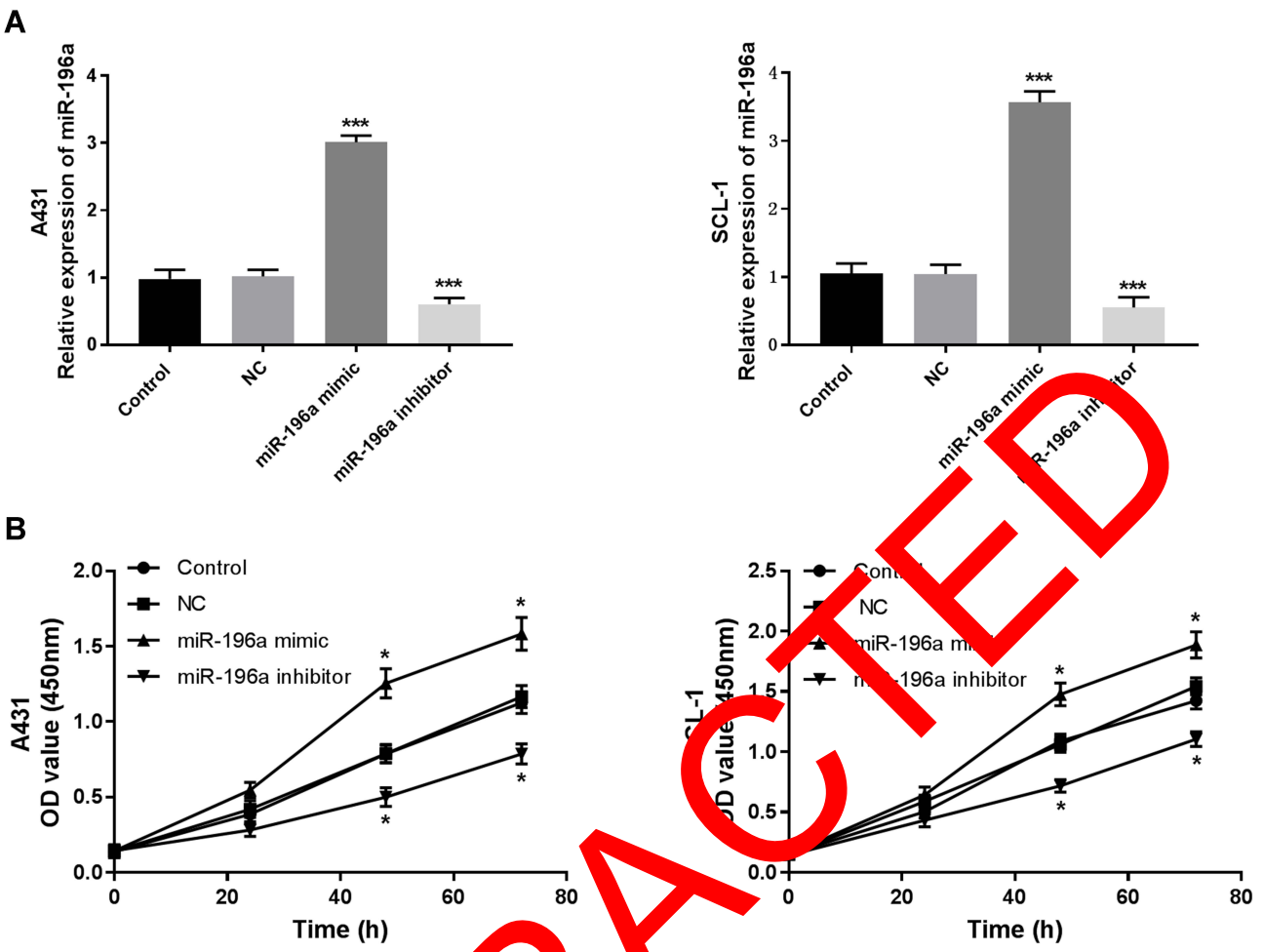

Figure 3 Effects of miR-196a expression levels on prolifer[illegible]n in A431 [illegible]d SCL-1 ce[illegible] (**A**) the expression level of miR-196a was analyzed by qRT-PCR after transient transfection with miR-196a mimic/inhibitor/ NC. (**B**) The [illegible]-8 as[illegible]ed to study cell proliferation. Increased expression of miR-196a accelerated cell proliferative abilities, while knockdown of miR-196a [illegible] 0.05, [illegible] 0.001.

In the current study, it w[illegible] found that [illegible]R-196a was highly expressed in CSCC tissues and CSCC cell lines. The high expression of miR-196 [illegible] CSCC tissues was related to positive lymph node metastasis and high TNM stage. The above results suggest that mi[illegible]196a [illegible]xpression may be involved in the development of CSCC. Moreover, patients with high miR-196a expressi[illegible] had [illegible]orse pr[illegible]nosis than patients with low miR-196a expression. Cox regression analysis results revealed that [illegible]iR-1[illegible]a exp[illegible]si[illegible], lymph node metastasis, and TNM stage may be independent prognostic risk predictors [illegible] CSCC, which implied that miR-196a expression may be a prognostic marker in CSCC. miR-196a is up-regulated in [illegible] other cancers. In thyroid carcinoma, miR-196a was also up-regulated, and the prognosis of patients with up-regulated [illegible]iR-196a was tended poor, miR-196a is an independent prognostic risk factor for thyroid cancer.[27] In gastric cancer, miR-196a is overexpressed and associated with a shorter overall survival time, and miR-196a can be used as a promising new prognostic marker for gastric cancer.[28] Interestingly, miR-196a expression was reduced in melanoma cells compared to healthy melanocytes and mediated the melanoma progression through regulating homeobox B7 (HOX-B7) and bone morphogenetic proteins 4 (BMP4) expression.[29] Thus, given the differences in pathogenesis between CSCC and melanoma, miR-196a may play a different role in the tumor progression, which needs to be further investigated in future studies.

The effects of miR-196a on the proliferation, migration, and invasion of CSCC cells were also explored. In this paper, the upregulated cell lines of miR-196a were successfully constructed to further confirm the effect of miR-196a on CSCC cells. The results showed that the proliferation, migration, and invasion ability of A431 and SCL-1

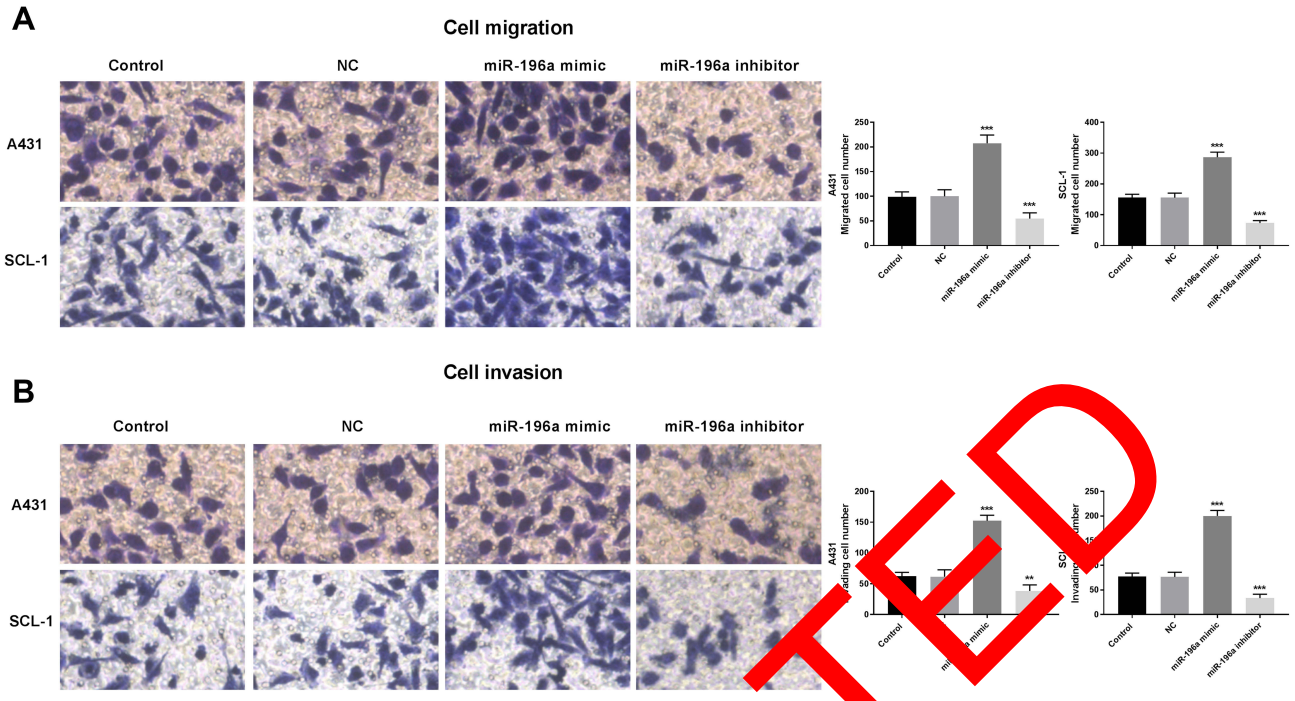

Figure 4 Effects of miR-196a on cell migration and invasion abilities in A431 and SCL-1 cells. (**A**) Cell migration and (**B**) invasion abilities were assessed with Transwell assay. Elevated miR-196a facilitated cell migration and invasion capacities. (magnification 200 ×). $^{**}P < 0.01$, $^{***}P < 0.001$.

were significantly increased after the upregulation of miR-196a expression. It suggested that up-regulation of miR-196a could significantly promote the progression of CSCC. The cellular functions of miR-196a on tumors have been widely reported. For example, in epithelial ovarian cancer, miR-196a may play a role as an oncogenic gene, the high expression of miR-196a is closely related to the poor differentiation of patients, and miR-196a can promote the migration and invasion of epithelial ovarian cancer through its downstream target gene HOXA10.[30] In esophageal squamous carcinoma, miR-196a acts as an oncogene and regulates the proliferation, invasion, and migration of esophageal squamous cell carcinoma cells by targeting ANXA1, which is of great significance for the treatment and prognosis of esophageal squamous cell carcinoma.[31] Similar results have been found in osteosarcomas. miR-196a acts as an oncogene in osteosarcoma to promote tumor cellular functions by targeting HOXA5 and is associated with poor prognosis in osteosarcoma patients.[32]

There are still some shortcomings in this study, for example, the sample size is small, which may make the results biased. On the other hand, the expression of miR-196a was measured in tumor tissue samples. In view of the retrospective study, future studies will also take into account blood samples to further support the clinical value of miR-196a in CSCC in a large scale of samples. Also, the downstream target genes of miR-196a have not been discussed yet, which will be explored in future mechanism studies. For these two problems, CSCC specimens meeting the experimental requirements are also being collected continuously, and further studies will be conducted when the sample size is large enough.

Conclusion

In conclusion, miR-196a was highly expressed in CSCC. The increased expression of miR-196a was closely related to positive lymph node metastasis and high TNM staging in patients with CSCC. The prognosis of CSCC patients with high expression levels of miR-196a was poor. Moreover, miR-196a promoted tumor cell proliferation, migration, and invasion. Therefore, miR-196a may serve as a new therapeutic target for CSCC and provide a new direction for the prognosis of patients.

Disclosure

The authors report no conflicts of interest in this work.

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