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ORIGINAL RESEARCH

RETRACTED ARTICLE: MicroRNA-155-3p promotes breast cancer progression through down-regulating CADM1

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Background/purpose: Cell adhesion molecule 1 (CADM1) functions as a tumor suppressor and has been identified to be frequently inactivated in breast cancer, and closely associated with patients' poor prognosis and advanced TNM stage. However, the mechanisms underlying CADM1 in breast cancer progression remains incompletely clear. miR-155, a predicted modulator of CADM1 was reported to be overexpressed in breast cancer, and its high expression level was closely related to the malignant progression of breast cancer. The present study aimed to explore whether miR-155-3p could modulate CADM1 expression and then involved in the progression of breast cancer.

Methods: The expression patterns of miR-155-3p in breast cancer tissues and cell lines were determined by RT-PCR technology. The relationship between CADM1 and miR-155-3p were determined by the luciferase gene reporter and Western Blot (WB) assays. Cell proliferation, apoptosis rates and tumorigenesis were determined by CCK-8, flow cytometry and in vivo xenotransplanation experiments, respectively.

Results: miR-155-3p was up-regulated in breast cancer tissues and cells when compared to the adjacent normal tissues and normal breast MCF 10A cells. The mRNA and protein levels of CADM1 showed opposite expression patterns to that of miR-155-3p expression detected, and miR-155-3p could negatively regulate CADM1 expression in breast cancer MCF-7 cells. Moreover, gain-of-function assay showed that overexpression of miR-155-3p promoted cell proliferation, tumorigenesis and repressed cell apoptosis, but these effects were all significantly impaired when the cells were simultaneously transfected with OE-CADM1, the overexpressing vector of CADM1.

Conclusion: This study revealed that miR-155-3p could accelerate the progression of breast cancer via down-regulation of CADM1 expression.

Keywords: miR-155-3p, CADM1, breast cancer

Introduction

Breast cancer is the second most frequent tumor among all kinds of cancers and accounts for the leading type of tumor in women, with an increasing incidence every year worldwide.[1] Although advances in oncological therapy have improved the survival rates of breast cancer patients, a large number of patients still suffer postsurgical pain, as well as tumor progression and metastasis.[2] Overall, the prognosis for patients with breast cancer still remains dim.[3] Therefore, new therapeutic strategies are urgently needed to be explored to shed light on molecular mechanisms underlying breast cancer progression.

Cell adhesion molecule 1 (CADM1), also known as TSLC1 (tumor suppressor in lung cancer 1), was first found to function as a tumor suppressor in non-small

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cell lung cancer cells in 2001.[4] CADM genes exert a protect role against malignant conversion and metastasis through maintenanceof epithelia. CADM1 is frequently lost in invasive lung adenocarcinoma lesions when compared with those non-invasive lung adenocarcinoma lesions.[5] In recent years, accumulated evidences have confirmed that CADM1 is always inactivated in breast cancer, and its inactivation closely associated with patients' poor prognosis and advanced progression.[6–8] For example, a study published by Saito et al[8] reported that 76.9% (160/208) of primary invasive breast cancer tissues showed CADM1 negative expression, and lack of CADM1 expression in these cases was associated with advanced tumor stage, suggesting a vital role of CADM1 plays in breast cancer. However, the mechanisms underlying CADM1 in breast cancer still remains largely unclear.

MicroRNAs (miRNAs) are a series of small single-stranded non protein coding RNAs (20–25 nucleotides) and serve as primary negative regulators of 60% of all human protein coding genes at post-transcriptional level.[9–11] MiRNAs are reported to be involved in multiple physiological processes, such as cell cycle, growth, apoptosis, differentiation and metabolism, and can function as both tumor suppressors and oncogenes.[12] MiR-155 was significantly elevated in breast cancer tissues compared to normal adjoining tissues and the high levels of it displayed a statistical association with the positive lymph node metastasis status, particularly for triple negative breast cancer patients. Conformably, Zheng et al[14] found that miR-155 expression was significantly higher in breast cancer tumor tissues than that in the matched non-tumor tissues, and the high expression levels closely related to lymph node positivity, advanced clinical TNM stage and higher proliferation index. In addition, they also found that knockdown of miR-155 obviously promoted cell apoptosis and reduced cell viability in breast cancer HS578T cells. However, the underlying mechanism of miR-155 in breast cancer is still unknown. Bioinformatics analysis shows that CADM1 is a predicted target of miR-155-3p, but whether CADM1 is under a negative regulation of miR-155-3p in breast cancer remains unknown.

The present study aimed to explore the expression patterns of miR-155-3p and CADM1 in breast cancer, and investigate the relationship between miR-155-3p and CADM1, with the ultimate goal of determination that whether miR-155-3p promotes the progression of breast cancer through down-regulating CADM1 expression.

Materials and methods

Patients and samples obtain

One hundred and twenty-eight paired fresh cancer tissue samples and normal r tissue samples were obtained from patients with breast cancer in Jining No.1 People's Hospital between January 2012 and December 2016. All patients were not subjected to preoperative radiotherapy and/or chemotherapy and all provided written informed consent. The diagnosis and histological grade of each breast cancer were independently determined by two pathologists on the base of WHO classification.[15] Experiments involving human samples were performed in accordance with the Helsinki Declaration and were approved by the ethical committee of Jining Medical University.

Cell culture

Breast cancer cell lines MCF-7, MDA-MB-231 and HCC1937, as well as normal breast cell line MCF 10A were all obtained from American Type Culture Collection (ATCC, Manassas, VA, USA). MCF-7 cells were cultured in Eagle's Minimum Essential Medium (No. 30-2003; ATCC, Manassas, VA, USA), supplemented with 0.01 mg/mL human recombinant insulin and 10% fetal bovine serum (FBS; Gibco, MA, USA). HCC1937 cells were grown in ATCC-formulated RPMI-1640 Medium (No. 30-2001) filling with 10% FBS. MDA-MB-231 cells were cultured in ATCC-formulated Leibovitz's L-15 Medium (No. 30-2008) filling with 10% FBS. MCF 10A were cultured in MEGM Kit (No. CC-3150; Lonza/Clonetics Corporation, CA, USA) with 100 ng/mL cholera toxin (No. C8052; Sigma, MA, USA). All cells were kept in a humidified atmosphere at 37 °C with 5% CO_2.

Cell transfection

Small interfering RNAs (siRNAs) (si-CADM1; No. SR308445, OriGene, Beijing, China) and short hairpin RNA (shRNA) (sh-CADM1; No. TL312210, OriGene) targeting human CADM1 gene were used to down-regulate CADM1 expression. The overexpressing plasmid of CADM1 (OE-CADM1; No. SC115048, OriGene) was used to up-regulate CADM1 expression. To silence and overexpress miR-155-3p, the mimics and inhibitors of miR-155-3p were synthesized by GenePharma (Shanghai, China). Lipofectamine 2000 transfection reagent (Invitrogen, CA, USA) was used for cell transient transfection, referring to manufacturer's instruction.

Mimics-miR-155-3p: 5'-CUCCUACAUAUUAGCAUUAACA-3',

Mimic-NC: 5'-UUCUCCGAACGUGUCACGUTT-3';

Inhibitors-miR-155-3p: 5'-UGUUAAUGCUAAUAUGUAGGAG-3',

Inhibitor-NC: 5'-CAGUACUUUUGUGUAGUACAA-3].

Total RNA isolation and real-time PCR (RT-PCR)

Trizol reagent (Invitrogen) was used to extract the total RNA from breast cancer tissues, adjacent non-tumor tissues and cell lines, conforming to the producer's recommendations. Following reverse transcription with the TaqMan® MicroRNA Reverse Transcription Kit (Applied Biosystems, CA, USA), miR-155-3p and U6 expression patterns were detected by RT-PCR with TaqMan® MicroRNA Assays (Applied Biosystems) in accordance with the manufacturer's directions. The expression patterns of CADM1 and GAPDH were measured with QuantiTect Reverse Transcription Kit and RT-PCR Kit (Qiagen, Beijing noble Ryder Technology Co. LTD, Beijing, China). The mRNA expressions were assessed by relative quantification using the $2^{-\Delta\Delta}$ method. U6 and GAPDH expression levels were used to normalize miR-155-3p and CADM1, respectively. The primers used for this study were listed as follows:

GAPDH-forward (F): 5'-GAGAAG[illegible]GGGC[illegible]A TTT-3',

GAPDH-reverse (R): 5'-[illegible]GATGGCA[illegible]GGACTG TGG-3';

CADM1-F: 5'-CC[illegible]CAGGTGATGC[illegible]CAGAAT-3',

CADM1-R: 5'-[illegible]TCCTC[illegible]GGGGGATCGGTAT-3';

U6-F: 5'-CTCGC[illegible]GGCAC[illegible]ACA-3',

U6-R: 5'-AA[illegible]GCT[illegible]ACG[illegible]ATTTGCGT-3'.

Western blot analysis (WB)

Total proteins from tissue samples and cells were obtained with RIPA lysis buffer (Beyotime Biotechnology, Jiangsu, China). After centrifugation, proteins in the supernatant were degenerated at 100 °C for 10min and quantified using a BCA kit (ThermoFisher Scientific, MA, USA). Then, the proteins were separated by 10% sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and transferred to polyvinylidine difluoride filter (PVDF) membrane (Millipore, MA, USA). After blocking with 10% nonfat milk in PBS diluted with TBST (Tris Buffered Saline Tween-20), the membranes were probed with the following antibodies, including CADM1 (No. C2121, Sigma-Aldrich, MO, USA), cleaved caspase3 (No. 9664, Cell Signaling Technology, MA, USA), caspase3 (No. 9662, Cell Signaling Technology), Bax (No. 2774, Cell Signaling Technology), Bcl-2 (No. 15071, Cell Signaling Technology) and GAPDH (Santa Cruz Biotechnology, CA, USA), followed by HRP-linked secondary antibodies (Thermo Fisher Scientific). The western signaling were enhanced by ECL detection (Millipore) and detected by Gel imaging system (Thermo Fisher Scientific).The western bands were quantified by ImageJ software after background subtraction.

Cell Counting Kit-8 assay (CCK-8)

Cell proliferation was detected using Cell Counting Kit-8 assay (CCK-8). Briefly, different transfected MCF-7 cells (mimic-NC, mimics, inhibitor-NC, inhibitors, inhibitor-NC + si-CADM1, inhibitors + si-CADM1, mimic-NC + OE-CADM1, mimics + OE-CADM1) were plated in a 96-well plate at a density of 200 cells/well. After 1, 2, 3, 4 and 5 days of the treatment, the medium was replaced with 10 μL CCK-8 reagent and 100 μL fresh culture medium for another 3 h, respectively. Light absorbance at 450 nm was measured with a microplate reader.

Flow cytometry

The effects of miR-155-3p/CADM1 axis on the apoptosis of MCF-7 cells was assessed by flow cytometry with Annexin V (FITC)/PI Apoptosis Detection Kits (BD Biosciences, USA) according to the manufacturer's instructions. After 48 h of cell transfections, MCF-7 cells were collected and washed with PBS, followed by incubation with the Annexin V-FITC and PI solution. The fluorescent signal was measured by flow cytometry within 1 h of the staining. FITC-/PI- quadrant represents living cells, FITC+/PI- represents early apoptotic cells and FITC+/PI+ represents late apoptotic cells.

Luciferase report assay

The 3′ UTR sequence of CADM1 mRNA (wild type, WT) and the mutated sequence within the binding sites among miR-155-3p and CADM1 (mutated type, MT) were inserted into the pmiR-GLO dual-luciferase vector (Promega, WI, USA). Subsequently, cells were co-transfected with mimics or mimic-NC together with WT or MT. After 48 h of the transfections, cells were collected and submitted to a dual-luciferase reporter gene assay system

(Promega). Renilla luciferase activity was used as an internal control.

In vivo model establishment and treatment

All procedures referring to animal experiments in this study were performed in accordance with the principles and procedures of the National Institutes of Health Guide for the Care and Use of Laboratory Animals and were approved by the ethical committee of Jining Medical University. Four-week-old male BALB/c nude mice (20–22 g) were purchased from Shanghai SLAC Laboratory Animal Co, Ltd. (Shanghai, China). The mice were fed in separate cages in a pathogen-free environment, under a 12 h-light/dark cycle.

MCF-7 cells transfected with control, mimics, mimic + CADM1, inhibitors and inhibitor + sh-CADM1 were resuspended with 200 μL PBS and then subcutaneously injected into BALB/c mice (n=10 for each group). The mice were euthanized 21 days post-injection. Then the tumors were took out and the weights were recorded.

Statistics

All data are presented as mean ± the standard deviation (SD). Differences between groups were evaluated by SPSS 17.0 software. Specifically, student's *t*-test or one-way ANOVA test was executed to compare the differences between two groups or more. A log rank with Kaplan-Meier survival analysis was performed to assess the overall survival (OS) of breast cancer patients with high/low expression of miR-155-3p. A *P*-value<0.05 was considered statistically significant.

Results

miR-155-3p is highly expressed in breast cancer tissues and cells

To explore the effects of miR-155-3p on the occurrence and development of breast cancer, we first determined its expression levels in breast cancer tissues and cells through RT-PCR. The results showed that miR-155-3p had a higher expression pattern in breast cancer tissues than that of the adjacent non-tumor tissues (Figure 1A). Likewise, miR-155-3p expression was obviously increased in breast cancer cell lines (HCC1937, MDA-MD-231 and MCF-7) as compared to the normal breast MCF 10A cells (Figure 1B), and we chose MCF-7 cells for further study. These results suggested that miR-155-3p was overexpressed in breast cancer, and it might function as an oncogene in breast cancer progression.

High expression of miR-155-3p is closely associated with patients' advanced progression and poor prognosis

Then, we analyzed the association between miR-155-3p expression levels and breast cancer patients' progression and prognosis. Eighty-five breast cancer patients with miR-155-3p high expression and forty-three patients with miR-155-3p low expression were chosen for our study. From the statistical analysis results listed in Table 1, it

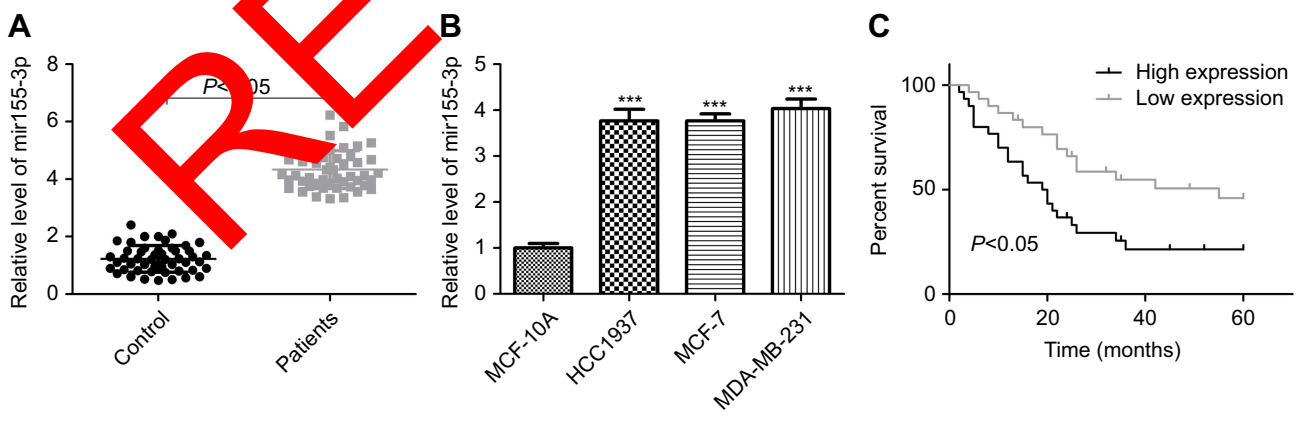

Figure 1 miR-155-3p expression was elevated in breast cancer tissues and cells. (**A**) RT-PCR was performed to evaluate miR-155-3p expression in 40 matched breast cancer tissues and its adjacent normal tissues (n=40; *P*<0.05, tumor group vs control group). (**B**) RT-PCR analysis of the mRNA level of miR-155-3p in normal breast cell line MCF 10A and breast cancer HCC1973, MCF-7 and MDA-MB-231 cell lines (n=3; ***P<0.001, HCC1973/MCF-7/MDA-MB-231 group vs MCF 10A group). (**C**) OS was used to evaluate the association between miR-155-3p expression levels with breast cancer patients' prognosis.

Table 1 Relationship between miR-155-3p expression pattern and clinical clinicopathologic features of breast cancer patients

Features	Total (n)	High expression	Low expression	*P*-values
Age (years)				0.114
≤50	56	33	23	
>50	72	52	20	
Tumor size (cm)				0.266
≤3.0	48	29	19	
>3.0	80	56	24	
LN metastasis				0.027
Negative	53	25	28	
Positive	75	50	25	
PR expression				0.663
Negative	63	43	20	
Positive	65	42	23	
ER expression				0.475
Negative	51	32	19	
Positive	77	53	24	
HER-2 expression				0.461
Negative	45	28	17	
Positive	83	57	26	
TNM				0.001
I-II	47	21	26	
III-IV	81	64	17	

Abbreviations: LN, lymph node; ER, estrogen receptor; PR, progesterone receptor; EPR-2, epidermal growth factor receptor.

indicated that high expression of miR-155-3p was closely associated with the high incidence of LN (lymph node) metastasis (P=0.027) and advanced TNM stage (P=0.001). Moreover, OS was calculated as the time from diagnosis to the date of death or last contact and was used to evaluate the association between miR-155-3p expression levels and patients' prognosis. The results revealed that patients with high expression of miR-155-3p always showed a shorter OS than that in patients with low expression of miR-155-3p (Figure 1C).

Overexpression of miR-155-3p promotes cell proliferation and inhibits cell apoptosis in breast cancer

Next, we explored the function of miR-155-3p in the proliferation and apoptosis of MCF-7 cells. Up-regulation of miR-155-3p viamiR-155-3p mimic transfection obviously increased the expression of miR-155-3p, and vice versa (Figure 2A). Compared with the mimic-NC (negative control) group, MCF-7 cells with miR-155-3p mimic transfection showed a significant increase in cell proliferation, and knockdown of miR-155-3p with inhibitors transfection induced an opposite result (Figure 2B). Moreover, up-regulation of miR-155-3p significantly repressed cell apoptosis from 11.43% to 5.32% (total early and late apoptosis), and down-regulation of miR-155-3p apparently promoted cell apoptosis from 10.95% to17.64% (total early and late apoptosis) as compared with that in the control group (Figure 2C and D). These data revealed that miR-155-3p served as an oncogene in the progression of breast cancer.

miR-155-3p negatively modulates CADM1 expression in breast cancer

Moreover, we explored the underlying mechanism of miR-155-3p in breast cancer development and determined whether CADM1 took part in this process. First, we assessed the expression level of CADM1 in breast cancer tissues and cells. RT-PCR and WB analysis results showed that the mRNA and protein expression levels of CADM1 were reduced in breast cancer tissues when compared to the adjacent normal tissues (Figure 3A and B). Similarly, the mRNA and protein levels of CADM1 in breast MCF-7, HCC1937 and MDA-MB-231 cells were obviously lower than that in MCF 10A, a normal breast cell line (Figure 3C and D). Up-regulation of miR-155-3p significantly decreased CADM1 expression and down-regulation of miR-155-3p increased CADM1 expression not only in mRNA level but also in protein level (Figure 3E and F). Furthermore, luciferase report assay showed that the luciferase activity of CADM1 WT vector was obviously decreased when MCF-7 cells were transfected with miR-155-3p mimics as compared with mimic-NC group, whereas this effect was abrogated when the binding sites were mutated (Figure 3G). Taken together, these results showed that CADM1 under the negative regulation of miR-155-3p was lowly expression in breast cancer tissues and cells.

miR-155-3p accelerates the progression of breast cancer through down-regulation of CADM1 expression

To explore whether CADM1 takes part in miR-155-3p-mediated acceleration in breast cancer progression,

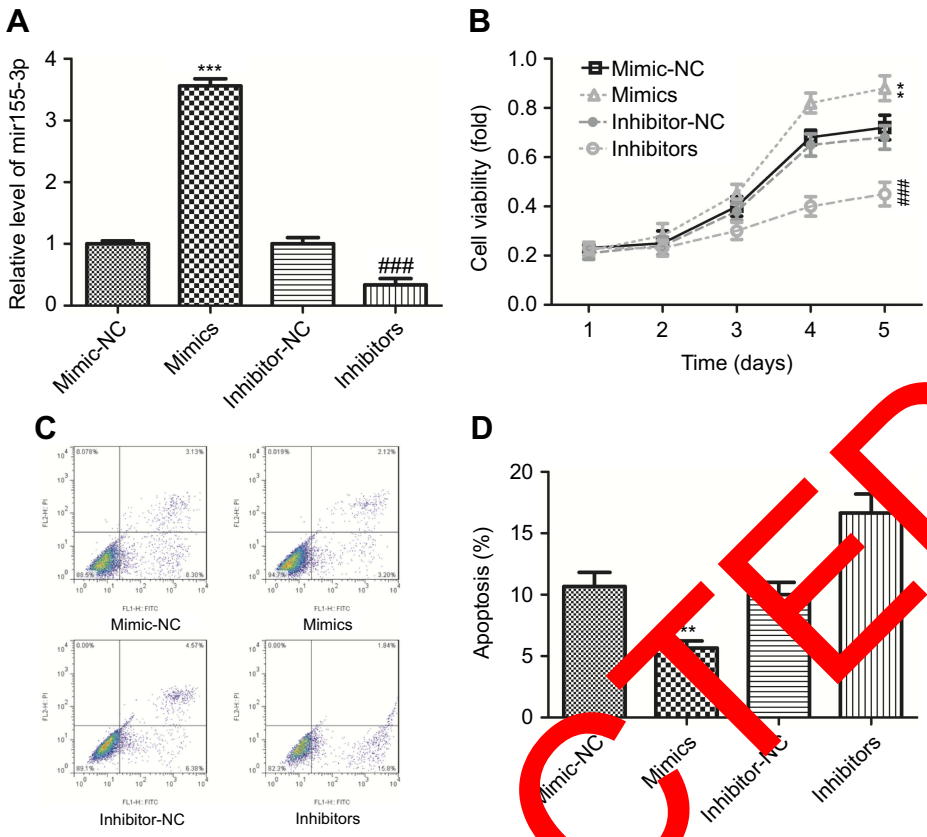

Figure 2 Up-regulation of miR-155-3p promoted cell proliferation and inhibited cell apoptosis in breast cancer MCF-7 cells. (**A**) RT-PCR analysis of the transfected efficiencies after MCF-7 cells were transfected with miR-155-3p mimic, inhibitor or their controls. (**B**) CCK-8 analysis the proliferation of MCF-78 cells after the cells were transfected with miR-155-3p mimic, inhibitor or their controls. (**C–D**) Flow cytometry with annexin V-(FITC)/PI staining used to determine cell apoptosis after MCF-7 cells were treated with miR-155-3p mimic, inhibitor or their controls (right lower quadrant represent early apoptosis cells and right upper represent late apoptosis cells). (n=3, $^{**}P<0.01$, $^{***}P<0.001$, mimic group vs mimic-NC group; $^{\#}P<0.05$, $^{\#\#\#}P<0.001$, inhibitor group vs inhibitor-NC group).

CADM1 overexpressing plasmid and siRNAs were recruited. siRNA-1 targeting CADM1 gene showed the best knockdown efficiency among the three siRNAs, and OE-CADM1 transfection significantly increased CADM1 expression as compared to the control group (Figure 4A and B). Knockdown of miR-155-3p obviously enhanced MCF-7 cell proliferation, whereas CADM1 knockdown promoted cell growth and impaired miR-155-3p inhibitor role in proliferation inhibition (Figure 4C). Cell apoptosis rate was significantly increased when miR-155-3p was knocked down, whereas CADM1 downregulation induced an opposite result and weakened miR-155-3p inhibitor-mediated cell apoptosis promotion (Figure 4E). In addition, si-CADM1 transfection significantly rescued miR-155-3p inhibitors-mediated increases in the relative expression levels of cleaved caspases3/caspase3 and Bax/Bcl-2 (Figure 4G and I). Consistently, both proliferation promotion and apoptosis repression roles of miR-155-3p mimics were terminated when the cells were transfected with miR-155-3p mimic and OE-CADM1 at the same time (Figure 4D and F), as well as the reductions of the relative expression of cleaved caspases3/caspase3 (Figure 4H) and Bax/Bcl-2 (Figure 4J). Moreover, up-regulation of miR-155-3p promoted cell tumorigenesis and down-regulation of it repressed tumorigenesis, and the roles of miR-155-3p up-regulation or down-regulation played in tumorigenesis were significantly abolished when CADM1 and miR-155-3p were simultaneously up-regulated or down-regulated (Figure 5). Taken together, these data demonstrated that miR-155-3p promoted breast cancer progression via down-regulation of CADM1 expression.

Discussion

CADM1 has been identified as a tumor suppressor in breast cancer, and its low expression level closely associates with patients' advanced clinical and pathological characteristics and poor prognosis,[6–8,16] suggesting that CADM1 might be regarded as an effective target for breast cancer treatment. CADM1 is a target of many miRNAs, such as miR-1246,[17]

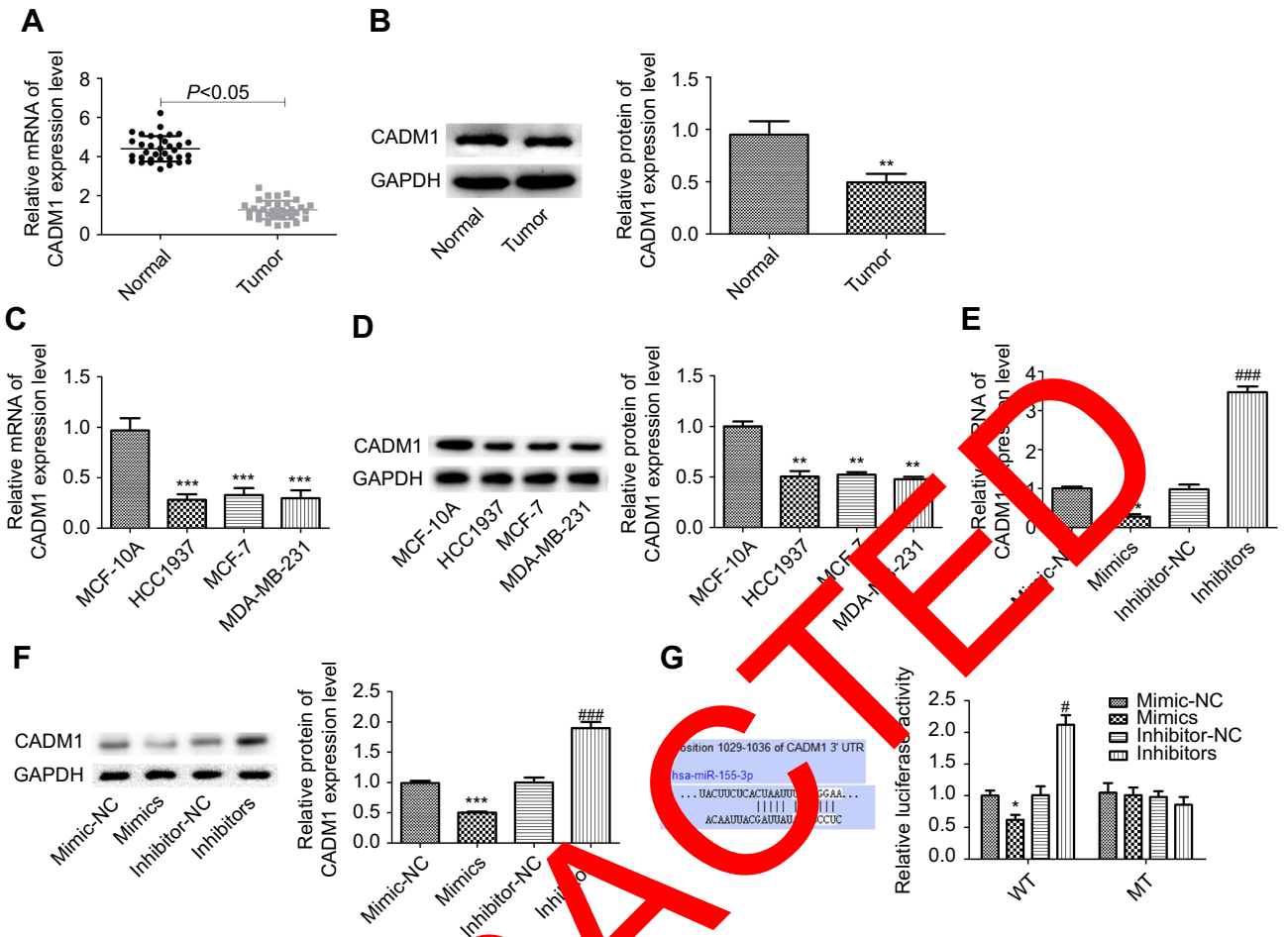

Figure 3 miR-155-3p down-regulated CADM1 expressi in breast cancer cells. (**A–B**) RT-PCR and WB analysis of the mRNA and protein levels of CADM1 in 30 paired breast cancer tissues and adjacent non-tumor tissues, the repre ve WB figur was shown in 3B (n=30; *P<0.05, **P<0.01, tumor group vs control group). (**C–D**) RT-PCR and WB analysis of the mRNA and protein l vels CADM in bre er HCC1973, MCF-7 and MDA-MB-231 cell lines (n=3; **P<0.01, ***P<0.001, HCC1973/MCF-7/MDA-MB-231 group vs MCF 10A grou (**E–F**) RT- and WB analysis of the mRNA and protein levels of CADM1 after MCF-7 cells were transfected with miR-155-3p mimics, inhibitors or their controls 3, ***P<0.001, nics group vs mimic-NC group; ###P<0.001, inhibitors group vs inhibitor-NC group). (**G**) The luciferase activity of CADM1 promoter after trans tion MCF-7 cells wi iR-155-3p MT (mutation) or WT (wild type) (n=3, *P<0.05, mimics groups vs mimic-NC group; #P<0.05, inhibitors group vs inhibitor-NC g oup).

miR-10b,[18] miR-2 [illegible] miR- 4[20] and miR-375.[20] The present study explored t lationshi between CADM1 and miR-155-3 The xpres ns miR-155-3p and CADM1 were i estigated n 40 mat ed primary breast cancer tissues and r ponding ormal tissues. High expression of miR-155-3p s observed in breast cancer tissues while low expression of C DM1 was observed, which indicated that there might be a possible interaction between miR-155-3p and CADM1 in breast cancer. It was further confirmed in the following WB analysis and luciferase report assay, which showed that miR-155-3p negatively regulated CADM1 expression in breast cancer MCF-7 cells.

Multiple clinical and pathological factors are used to classify breast cancer patients so as to evaluate patients' prognosis and determine the best treatment options, including age, tumor size, LN metastasis, lymphovascular invasion, nuclear grade, expression pattern of estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (HER-2).[6,21,22] In the current study, we found that high expression level of miR-155-3p showed a positive association with patients' LN metastasis (P=0.001) and advanced TNM stage, but had no significant influence in the expression levels of PR, ER and HER-2. In addition, the prognosis analysis indicated that patients with miR-155-3p high expression had a shorter OS than that of patients with miR-155-3p low expression. Our findings were consistent with previous studies.[14,23,24]

Zuo et al[25] reported that inhibition of miR-155 could significantly repress proliferation of breast cancer MDA-

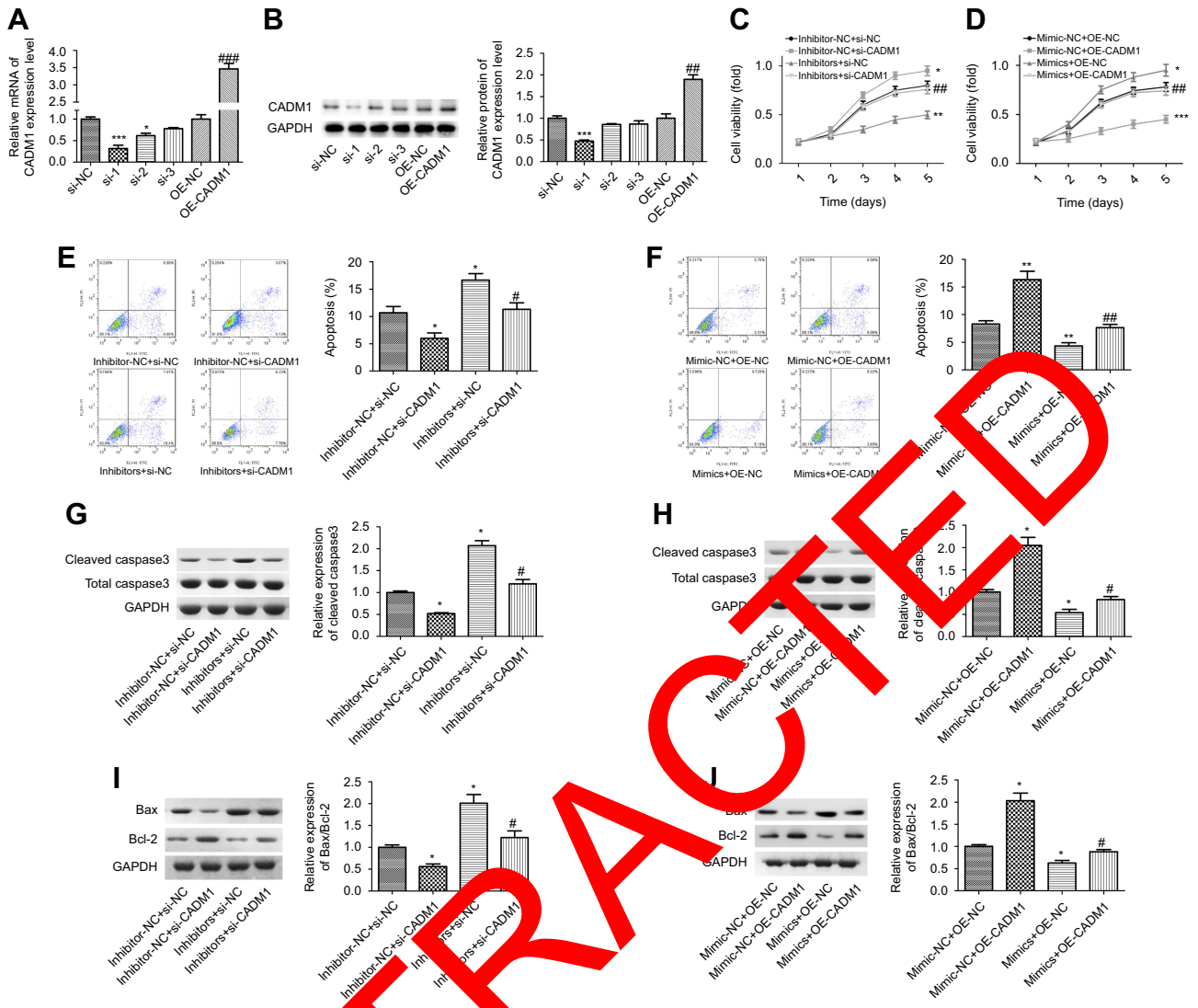

Figure 4 Detection of the effects of miR-155-3p/CADM1 on the proliferation and apoptosis of MCF-7 cells. (**A–B**) The transfection efficiency of siRNAs and over-expressing plasmid targeting to human CADM1 gene was detected by RT-PCR and WB (n=3, *P<0.05, ***P<0.001, si-1/si-2 group vs si-NC group; ###P<0.01, P<0.001, OE-CADM1 group vs OE-NC group). (**C**) CCK-8 was used to assess cell proliferation after MCF-7 cells were transfected with inhibitor-NC + si-NC, inhibitors + si-NC, inhibitor-NC + si-CADM1 and inhibitors + si-CADM1, respectively (n=3, *P<0.05, ***P<0.001, inhibitors + si-NC group or inhibitor-NC + si-CADM1group vs inhibitor-NC + si-NC group; ###P<0.01, inhibitor + si-CADM1 group vs inhibitors + si-NC group). (**D**) CCK-8 was used to assess cell proliferation after MCF-7 cells were transfected with mimic-NC + OE-NC, mimics + OE-NC, mimic-NC + OE-CADM1 and mimics + OE-CADM1 (n=3, *P<0.05, ***P<0.001, mimics + OE-NC group or mimic-NC + OE-CADM1 group vs mimic-NC + OE-NC group; ###P<0.01, mimics + OE-CADM1 group vs mimics + OE-NC group). (**E**) Flow cytometry was used to assess cell apoptosis after MCF-7 cells were transfected with inhibitor-NC + si-NC, inhibitors + si-NC, inhibitor-NC + si-CADM1 and inhibitors + si-CADM1, respectively (n=3, *P<0.05, inhibitors + si-NC group or inhibitor-NC + si-CADM1group vs inhibitor-NC + si-NC group; #P<0.05, inhibitor + si-CADM1 group vs inhibitors + si-NC group). (**F**) Flow cytometry was used to assess cell apoptosis after MCF-7 cells were transfected with mimic-NC + OE-NC, mimics + OE-NC, mimic-NC + OE-CADM1 and mimics + OE-CADM1 (n=3, **P<0.01, mimics + OE-NC group or mimic-NC + OE-CADM1 group vs mimic-NC + OE-NC group; ###P<0.01, mimics + OE-CADM1 group vs mimics + OE-NC group). (**G–J**) WB technology was applied to detect the expressions of cleaved caspase3, total caspase3, Bcl-2 and Bax after cells were transfected with different vectors (n=3, *P<0.05, #P<0.05).

MB-231 cells in vivo and in vitro, and miR-155 expression levels strongly correlated with cells' stem-like properties. Wang et al[26] revealed that up-regulation of miR-155-5p promoted cell proliferation and reduced bufalin-induced apoptosis in triple-negative breast cancer cells. In this study, we revealed that up-regulation of miR-155-3p significantly promoted the proliferation and tumorigenesis and repressed apoptosis of breast cancer MCF-7 cells, but these effects were all broke up when CADM1 was over-expressed, indicating that miR-155-3p promoted the progression of breast cancer in a CADM1-inexistent manner.

However, there are several limitations in our study. CADM1/TSLC1, as a membrane-spanning glycoprotein pertaining to the superfamily of immunoglobulin cell adhesion molecules, has been proved that its depletion accounts for a

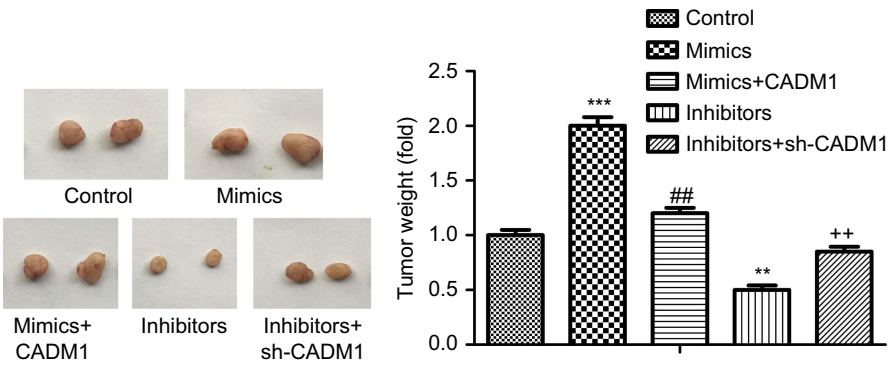

Figure 5 In vivo xenograft assay analysis of the tumor-forming potential. MCF-7 cells were stably transfected control, miR-155-3[illegible]mics, [illegible]R-155-3p mimics + OE-CADM1, miR-155-3p inhibitors and miR-155-3p inhibitors + sh-CADM1, then the cells were subcutaneously injected into the [illegible]nks of mice ([illegible]0/group). (**P<0.01, ***P<0.001, mimic/inhibitor group vs control group; ##P<0.01, mimics+CADM1 group vs mimics group; ++P<0.01, inhibitors + [illegible]ADM1 group vs [illegible]ibitors group).

main reason for cancer cell invasion and metastasis.[27,28] Besides, miR-155 was reported to induce drug resistance in breast cancer.[29] However, whether miR-155-3p can enhance cell migration and invasion, as well as induce drug resistance through down-regulating CADM1 expression in breast cancer is not illuminated in the current study. We intend to reveal it thoroughly in the further study.

In conclusion, this study reveals a strong correlation between miR-155-3p high expression and breast cancer patients' LN metastasis and TNM stage. We first il[illegible]a that overexpression of miR-155-3p negatively reg[illegible]ates CADM1 expression and then promotes the adv[illegible]ed prog[illegible]sion of breast cancer. MiR-155-3p/CADM[illegible]axis m[illegible]ght ser[illegible] as a novel biomarker to predict the prog[illegible]ssion a[illegible]prognosi[illegible] of breast cancer, as well as a potent t[illegible]rapeu[illegible]rget for breast cancer treatment.

Disclosure

The authors have de[illegible]red that no compe[illegible]ng interest exists in this work.

Refere[illegible]ces

1. Sieger[illegible] Naisha[illegible] Jemal A. Cancer statistics, 2013. *CA Cancer J Clin*. 2[illegible](1):11–30. doi:10.3322/caac.21166
2. Miller KD, [illegible]gel RL, Lin CC, et al. Cancer treatment and survivorship statistics, [illegible]016. *CA Cancer J Clin*. 2016;66(4):271–289. doi:10.3322/caac.21349
3. Krop IE, Kim SB, Gonzalez-Martin A, et al. Trastuzumab emtansine versus treatment of physician's choice for pretreated HER2-positive advanced breast cancer (TH3RESA): a randomised, open-label, phase 3 trial. *Lancet Oncol*. 2014;15(7):689–699. doi:10.1016/S1470-2045(14)70178-0
4. Kuramochi M, Fukuhara H, Nobukuni T, et al. TSLC1 is a tumor-suppressor gene in human non-small-cell lung cancer. *Nat Genet*. 2001;27(4):427–430. doi:10.1038/86934
5. Goto A, Niki T, Chi-Pin L, et al. Loss of TSLC1 expression in lung adenocarcinoma: relationships with histological subtypes, sex and prognostic significance. *Cancer Sci*. 2005;96(8):480–486. doi:10.1111/j.1349-7006.2005.00075.x
6. Takahashi Y, Iwai M[illegible]kawai T, [illegible]t al. A[illegible]r[illegible] expression of tumor suppressors CADM[illegible]and 4.1B[illegible]n invasive [illegible]sions of primary breast cancer. *Breast [illegible]ancer*. 201[illegible]19(3):242–[illegible]52. doi:10.1007/s12282-011-0272-7
7. Wikman[illegible]Vestphal L, Sc[illegible]id [illegible]et al. Loss of CADM1 expression is as[illegible]iated [illegible]h poor prog[illegible]sis and brain metastasis in breast cancer patients. [illegible]*cotarget*. 2014;5(10):3076–3087. doi:10.18632/[illegible]rget.1832
8. Saito M, Goto A, Abe [illegible], et al. Decreased expression of CADM1 and CADM4 a[illegible]associated with advanced stage breast cancer. *Oncol Lett*. 2018;1[illegible]2):2401–2406. doi:10.3892/ol.2017.7536
9. Shukla GC, Singh J, Barik S. MicroRNAs: processing, Maturation, [illegible]t R[illegible]cognition and Regulatory Functions. *Mol Cell Pharmacol*. 2011;3(3):83–92.
10. [illegible]tel DP. MicroRNAs: target recognition and regulatory functions. *Cell*. 2009;136(2):215–233. doi:10.1016/j.cell.2009.01.002
11. Friedman RC, Farh KK, Burge CB, Bartel DP. Most mammalian mRNAs are conserved targets of microRNAs. *Genome Res*. 2009;19(1):92–105. doi:10.1101/gr.082701.108
12. Croce CM. Causes and consequences of microRNA dysregulation in cancer. *Nat Rev Genet*. 2009;10(10):704–714. doi:10.1038/nrg2634
13. Chernyy V, Pustylnyak V, Kozlov V, Gulyaeva L. Increased expression of miR-155 and miR-222 is associated with lymph node positive status. *J Cancer*. 2018;9(1):135–140. doi:10.7150/jca.22181
14. Zheng SR, Guo GL, Zhang W, et al. Clinical significance of miR-155 expression in breast cancer and effects of miR-155 ASO on cell viability and apoptosis. *Oncol Rep*. 2012;27(4):1149–1155. doi:10.3892/or.2012.1634
15. Singletary SE, Allred C, Ashley P, et al. Staging system for breast cancer: revisions for the 6th edition of the AJCC Cancer Staging Manual. *Surg Clin North Am*. 2003;83(4):803–819. doi:10.1016/S0039-6109(03)00034-3
16. Zhu Z, Teng Z, van Duijnhoven FJB, et al. Interactions between RASA2, CADM1, HIF1AN gene polymorphisms and body fatness with breast cancer: a population-based case-control study in China. *Oncotarget*. 2017;8(58):98258–98269. doi:10.18632/oncotarget.21530
17. Sun Z, Meng C, Wang S, et al. MicroRNA-1246 enhances migration and invasion through CADM1 in hepatocellular carcinoma. *BMC Cancer*. 2014;14:616.
18. Li QJ, Zhou L, Yang F, et al. MicroRNA-10b promotes migration and invasion through CADM1 in human hepatocellular carcinoma cells. *Tumour Biol*. 2012;33(5):1455–1465. doi:10.1007/s13277-012-0396-1
19. Zheng G, Li N, Jia X, et al. MYCN-mediated miR-21 overexpression enhances chemo-resistance via targeting CADM1 in tongue cancer. *J Mol Med (Berl)*. 2016;94(10):1129–1141. doi:10.1007/s00109-016-1417-0

20. Ishimura M, Sakuraiyageta M, Maruyama T, et al. Involvement of miR-214 and miR-375 in Malignant Features of Non-Small-Cell Lung Cancer by Down-Regulating CADM1. *J Cancer Ther*. 2012;3(4):379–387.
21. Arslan UY, Oksuzoglu B, Aksoy S, et al. Breast cancer subtypes and outcomes of central nervous system metastases. *Breast*. 2011;20(6):562–567. doi:10.1016/j.breast.2011.07.017
22. Harrell JC, Prat A, Parker JS, et al. Genomic analysis identifies unique signatures predictive of brain, lung, and liver relapse. *Breast Cancer Res Treat*. 2012;132(2):523–535. doi:10.1007/s10549-011-1619-7
23. Mattiske S, Suetani RJ, Neilsen PM, Callen DF. The oncogenic role of miR-155 in breast cancer. *Cancer Epidemiol Biomarkers Prev*. 2012;21(8):1236–1243.
24. Wang J, Wu J. Role of miR-155 in breast cancer. *Front Biosci (Landmark Ed)*. 2012;17:2350–2355.
25. Zuo J, Yu Y, Zhu M, et al. Inhibition of miR-155, a therapeutic target for breast cancer, prevented in cancer stem cell formation. *Cancer Biomark*. 2018;21(2):383–392. doi:10.3233/CBM-170642
26. Wang Q, Li C, Zhu Z, et al. miR-155-5p antagonizes the apoptotic effect of bufalin in triple-negative breast cancer cells. *Anticancer Drugs*. 2016;27(1):9–16. doi:10.1097/CAD.0000000000000296
27. Nakahata S, Morishita K. CADM1/TSLC1 is a novel cell surface marker for adult T-cell leukemia/lymphoma. *J Clin Exp Hematop*. 2012;52(1):17–22.
28. Liang QL, Chen GQ, Li ZY, Wang BR. Function and histopathology of a cell adhesion molecule TSLC1 in cancer. *Cancer Invest*. 2011;29(2):107–112.
29. Yu DD, Lv MM, Chen WX, et al. Role of miR-155 in drug resistance of breast cancer. *Tumour Biol*. 2015;36(3):1395–1401. doi:10.1007/s13277-015-3263-z

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