Cancer Management and Research

Dovepress

open access to scientific and medical research

Open Access Full Text Article

ORIGINAL RESEARCH

RETRACTED ARTICLE: Regulatory Effect of miR497-5p–*CCNE1* Axis in Triple-Negative Breast Cancer Cells and Its Predictive Value for Early Diagnosis

This article was published in the following Dove Press journal:
Cancer Management and Research

Wei-Wei Liu
Wei-Dong Li
Yan-Ju Zhang
Man-Li Zhang

Breast Center, Cangzhou People's Hospital, Cangzhou 061000, Hebei Province, People's Republic of China

Cancer Management and Research downloaded from https://www.dovepress.com/
For personal use only.

RETRACTED

Objective: To explore the regulatory role of miR497-5p–*CCNE1* axis in triple-negative breast cancer (TNBC) cells and its predictive value for early diagnosis.

Methods: Cancer tissue and adjacent tissue samples were collected from 86 patients with TNBC.RT-PCR was used to detect the expression of miR497-5p and *CCNE1* (target gene) mRNA, determined by biological prediction in tissue and TNBC cells. ROC was used to analyze the diagnostic value of miR497-5p in TNBC. MTT, invasion, and flow cytometry were used to detect the proliferation, invasion, cycle, apoptosis rate, and expression of related proteins of TNBC cells with overexpression of miR497-5p or knockdown of *CCNE1*.

Results: RT-qPCR results showed that miR497-5p levels were significantly downregulated in TNBC tissue and cells, while CCNE1 expression was significantly upregulated, and miR497-5p expression was negatively correlated with that of CCNE1 ($P<0.001$). ROC analysis showed that the AUC of miR497-5p for TNBC was >0.9, which had better diagnostic value. The cell tests revealed that miR497-5p played a role in tumor inhibition, including inhibiting proliferation and invasion of TNBC cells, blocking the cell cycle, and promoting apoptosis. Bioinformatic prediction and subsequent experiments revealed that *CCNE1* was the direct target of miR497-5p. Furthermore, after knocking down the expression of *CCNE1* in TNBC cells, the proliferation and invasion of TNBC cells were significantly inhibited, the cell cycle blocked, and the apoptosis rate significantly increased ($P<0.001$), and expression of the proapoptosis-related proteins Bax and caspase 3 (cleaved) were upregulated, while expression of the antiapoptosis-related protein BCL2 was downregulated ($P<0.001$).

Conclusion: miR497-5p inhibited the proliferation and invasion of TNBC cells by targeting CCNE1, blocked the cell cycle and promoted the apoptosis of TNBC cells, and had better diagnostic value for TNBC. miR497-5p can be used as a new potential target for the treatment of TNBC.

Keywords: miR497-5p, TNBC, CCNE1, proliferation, invasion, apoptosis

Introduction

As one of the most common malignancy tumors, breast carcinoma (BC) is also one of the main causes of cancer-related deaths in women.[1] Triple-negative BC(TNBC) is the most active BC type, has high proliferation and a metastasis phenotype, and manifests as lack of estrogen-receptor and progestin receptor expression, and HER2.[2,3] At present, there is no valid drug for treating TNBC, and it shows aggressive clinical behavior and poor prognosis.[4] Consequently, it is essential to

Correspondence: Man-Li Zhang
Breast Center, Cangzhou People's Hospital, Intersection of Chongqing Road and Jilin North Road, Yunhe District, Cangzhou 061000, Hebei Province, People's Republic of China
Tel +86-135-6645-8334
Email manko8866@126.com

submit your manuscript | www.dovepress.com
DovePress
http://doi.org/10.2147/CMAR.S284277

© 2021 Liu et al. This work is published and licensed by Dove Medical Press Limited. The full terms of this license are available at https://www.dovepress.com/terms.php and incorporate the Creative Commons Attribution – Non Commercial (unported, v3.0) License (http://creativecommons.org/licenses/by-nc/3.0/). By accessing the work you hereby accept the Terms. Non-commercial uses of the work are permitted without any further permission from Dove Medical Press Limited, provided the work is properly attributed. For permission for commercial use of this work, please see paragraphs 4.2 and 5 of our Terms (https://www.dovepress.com/terms.php).

better comprehend the progress of TNBC to promote the diagnosis and treatment of TNBC.

miRNAs are tiny single-stranded nonencoding RNAs with a length of 19–22 nucleotide acids.[5] They can regulate various cell processes (eg, proliferation, migration and metamorphosis) by base-pairing with the 3′UTR of target genes.[6] Studies have shown that abnormal miRNA function is related to the progress of TNBC. For example,[7] miR200c promotes the malignant progress of TNBC through upregulation of PAI2 and polarization of M2-phenotype macrophages. Other studies have shown that miR122-5p promotes TNBC aggression and epithelial–mesenchymal transition by inhibiting *CHMP3* through MAPK signal transduction.[8] Much evidence has indicated that miR497-5p acts on tumor-suppressor genes in various tumors. For example,[9] its overexpression controls the growth, migration, and invasiveness of non–small cell lung carcinoma cells and induces apoptosis by suppressing expression of the *SOX5* gene. Other studies have revealed that it can inhibit the proliferation and growth of liver carcinoma by downregulating IGF1.[10] These results revealed the antitumor activity of miR497-5p in the development of carcinoma. However, there has been no research on the expression and biological function of miR497-5p in TNBC.

CCNE1 is an important factor that can regulate proliferating cells to enter the S and G_1 phases.[11] It has been found that its expression is kept at a high level in TNBC and considered to be bound up with the poor prognosis of patients with TNBC.[12] In this research, we concluded that CCNE1 is a target of miR497-5p, and analyzed its expression and related action in TNBC through the TargetScan website so as to provide more potential targets to diagnose and treat TNBC.

Methods

From January 2019 to December 2019, conjugated TNBC tissue and corresponding adjacent tissue samples were collected from 86 cases newly diagnosed with TNBC in our hospital. All samples were quickly frozen and conserved in liquid nitrogen for subsequent experimental detection. These patients had not received any preoperative therapy. All patients signed the informed-consent form. The research was ratified by the Cangzhou People's Hospital ethics committee. This experiment conformed with the Declaration of Helsinki.

Cell Culture and Transfection

Human TNBC cell strains (MDA-MB231, MDA-MB436, and MDA-MB468) and human normal mammary epithelial cells (MCF10A) were all from the Chinese Academy of Sciences. All cells were developed in DMEM with 10% FBS.Cells were retained in a moist incubator with 5% CO_2 at 37°C. miR497-5p and CCNE1 in cell strains were detected, revealing that the miR497-5p in the MDA-MB 231 and MDA-MB436 cell strains was relatively low, so these strains were selected for transfection and succeeding tests. Cells were transfected with miR497-5p mimics, miR497-5p inhibitor, simulated miRNA negative contrast (miRNC), and *CCNE1* siRNA (si-*CCNE1*) and its negative contrast (GenePharma, Shanghai, China) with a Lipofectamine 2000 kit. Manipulation steps were followed strictly as per kit instructions.

RT-PCR

Total RNA was extracted from tissue with Trizol reagent (Invitrogen, CA, USA). The purity and concentration of RNA were detected through ultraviolet spectrophotometry, and then 5 μg of total RNA was obtained for reverse transcription of cDNA on the basis following the kit instructions. Amplified conditions were PCR parameters of initial denaturation at 94°C for 30 seconds, denaturing at 94°C for 5 seconds, annealing and extension at 60°C for 30 seconds, followed by 40 cycles. U6 was used as internal parameter for miR497-5p, and GAPDH was used as internal parameter for CCNE1. $2^{-\Delta\Delta cq}$ was used to analyze these data.[13] Primer sequences are displayed in Table 1.

Detection of Cell Growth by MTT

After transfection for 48 hours, TNBC cell lines were inoculated into 96-well plates at about 5,000 cells per well. Cell density was 3×104 cells/mL. Cells were then cultivated at 37°C. After culturing for 24, 48, 72, and 96 hours, 10 μL MTT solution was added to each well, then cultivated in the incubator for 4 hours after adding reagents. Then, dimethyl sulfoxide (150 μL) was added and shaken for 10 minutes. Next, absorbance was measured at 490 nm with an enzyme-labeling instrument to test cell growth. This test was repeated three times.

Determination of Cell Invasiveness (Transwell)

After transfection for 24 hours, 3×10^5 cells per well inoculated on a six-well plate. Then, cells were washed with PBS and inoculated in the upper chamber. DMEM (200 μL) was added to the upper chamber. DMEM with 20% FBS (500 mL) was added to the lower chamber. Next, these

RETRACTED

Table 1 Primer sequences

	Upstream 5′–′3	Downstream 5′–′3
miR497-5p	AGCGAAGTTTTGAGCCGATCGGGC	GCCGTGAGTCAGAGGTGGT
U6	CTCGCTTCGGCAGCACA	AACGCTTCACGAATTTGCGT
CCNE1	GCCAGCCTTGGGACAATAATG	CTTGCACGTTGAGTTTGGGT
GAPDH	TGCACCACCAACTGCTTAGC	GGCATGGACTGTGGTCATGAG

were cultivated at 37°C for 48 hours. The cells and substrate that did not pass through the film surface of the upper chamber were scrubbed, washed with PBS three times, immobilized with paraformaldehyde for 10 minutes, and washed through double-steamed water three times. After drying, 0.5% crystal violet was used for staining. Finally, the cell invasiveness was analyzed with microscopy.

Apoptosis Testing

After centrifugation, transfected cells were rinsed through precooled PBSthree times, then immobilized in 70% cold ethanol for one night. Cycles were detected according to the instructions of the manufacturer of the cell-cycle test kit (Leagene Biotechnology, Beijing, China). RNase A liquid solution (100 μL) was added. Cells were resuspended and bathed at 37°C for 30 minutes. After that, 400 μL pro[illegible]m iodide working fluid was put in to wash and resuspe[illegible] the cells for 30 minutes. Next, cell cycles were tested [illegible]t a FACSCalibur FC kit (BD Bioscience[illegible] San [illegible]ose, C[illegible] USA). To detect the apoptosis rate, a[illegible]er kit i[illegible]tructions annexin V–FITC and propidium io[illegible]ide w[illegible]addes in turn and cultivated at ambient temp[illegible]ure in the d[illegible]k for 5 minutes. Then, the FC system w[illegible]s use[illegible]or testing.

Western Blot (WB) Testing

After culturing, ce[illegible] were [illegible]ollected from each group. Total albumin was [illegible]tained [illegible] RIPA l[illegible]is (Beyotime, Shanghai, China). T[illegible]n, pro[illegible]in leve[illegible]e tested with BCA. Next, it was re[illegible]ated to [illegible]g/μL, isolated with 12% SDS-PAGE, then transferred [illegible]VDF film after ionization, dyed in Ponceau working liqui[illegible] immersed in PBST for 5 minutes, and closed with 5% nonfat dried milk for 2 hours. Bax (1:500), BCL2 (1:500), cleaved caspase 3 (1:500), CCNE1 (1:1,000) and β-actin primary antibody (1:1,000) were added and blocked at 4°C for one night. The first antibody was eliminated by washing the film, and HRP-conjugated goat antirabbit secondary antibody (1:1,000) was added, cultivated at 37°C for 1h, and washed three times through PBS for 5 minutes each time. Excess fluid on the film was sucked dry with clogging paper and ECL applied for luminescence and development.

Double Fluorescein–Reporter Enzyme

Double luciferase–reporter gene determination was conducted to determine whether *CCNE1* was the direct target gene of miR497-5p. Reporter plasmids (wild type and mutant) of CCNE1 3′UTR [illegible]uble lucifer[illegible]se were constructed by RiboBio. m[illegible]497-5p [illegible]mimics [illegible]d NC mimics were cotransfected [illegible]o cells with [illegible]*CNE1* wild type and mutant, respective[illegible] wi[illegible] Lipofectamine 2000. After transfection [illegible]r 24 ho[illegible]s, lucif[illegible]ase activity was determined us[illegible]g [illegible]dual lucifer[illegible]reporter gene detection system (Promega, [illegible]adison, WI USA), and the activity of re[illegible]a [illegible]uciferase us[illegible] as a standardized control.

[illegible]tatistical Analysis

SP[illegible]20.0 [illegible]as used to analyse the data. GraphPad Prism 6 [illegible]as used to plot related figures. Quantitative data are expressed as means ± SD and *t*-tests applied. Comparison between groups was conducted with independent-sample *t*-tests. Univariate ANOVA was applied for comparison among multiple groups. LSD *t*-testing was employed for paired comparison afterward. Repeated measurement and ANOVA were applied for expression at various time intervals. Bonferroni analysis was used for post hoc testing. ROC curves were used to analyze the diagnostic value of miR497-5p in TNBC. Pearson's test was applied for correlation analysis. Statistical significance was set at $P<0.05$.

Results

Expression and Diagnostic Value of miR497-5p in TNBC

miR497-5p and *CCNE1* mRNA levels in cancer tissue from TNBC patients were tested by qRT-PCR. Findings revealed that miR497-5p in TNBC tissue and cells was obviously lower than in normal cells, while the *CCNE1* mRNA was obviously greater than that in adjacent tissue and normal cells ($P<0.05$). Correlation analysis revealed that miR497-5p in TNBC tissue was negatively correlated with CCNE1 ($P<0.05$). Analysis of ROC curve revealed

RETRACTED

that the AUC of miR497-5p in TNBC diagnosis was 0.925 (P<0.05), which was of better diagnostic value (Figure 1).

Overexpression of miR497-5p Suppressed Growth and Invasion of TNBC Cells and Induced Cell-Cycle Stagnation and Apoptosis of G_1 Cells

To better comprehend the biological function of miR497-5p, we applied miR497-5p mimics, inhibitor, and miRNC to transiently transfect the TNBC cell strains MDA-MB 231 and MDA-MB436 for further study. After 24 hours, qRT-PCR revealed that miR497-5p was overexpressed or had declined in transfection efficiency. MTT was applied to analyze the effect of miR497-5p on cell proliferation, and showed that overexpression of miR497-5p had obviously suppressed the progression of TNBC cells, while downregulation of miR497-5p had obviously promoted the progression of TNBC cells. As miR497-5p inhibited the progression of TNBC cells, we explored whether this inhibitory effect might be caused by the blocking of a checkpoint in the cell cycle. After transfection for 48 hours, FC was employed to analyse the cell-cycling distribution in TNBC cell lines. It was found th

compared with the miRNC group, the percentage of cells overexpressing miR497-5p in the G_1/G_0 phase had been markedly enhanced (P<0.05), but had had little effect on stage G_2/M, and the percentage of cells in stage S had also declined significantly (P<0.05). In TNBC cell strains transfected with the miR497-5p inhibitor, the G_2/M phase was not obviously affected (P<0.05). It decreased significantly in G_1/G_0 phase (P<0.05), and the percentage of cells in stage S was enhanced (P<0.05). These findings revealed that miR497-5p triggered cell-growth inhibition by blocking tumor cells in stage G_1/G[illegible]. The influence of miR497-5p on TNBC-cell apopto[illegible]s was als[illegible] evaluated. Our data showed that miR424-5p [illegible]mics had [illegible]o signifi-cant influence on the apop[illegible]sis rate ([illegible]gure 2).

Double Fluor[illegible]sce[illegible] Reporter Enzyme

To investigate [illegible]nt mechan[illegible]s o[illegible] miR497-5p in TNBC, bioinformati[illegible] analy[illegible] was carrie[illegible] out to forecast the target gene of miR497-5p. *CCNE1* was determined to be the targe[illegible] gene of miR497-5p. To determine whether the 3'UTR of *CCNE1* could[illegible]e directly targeted by miR497-5p, the lucif[illegible]ase-reporte[illegible] gene was used. Overexpression of miR497[illegible] reduced the luciferase activities of the wild-type

RETRACTED

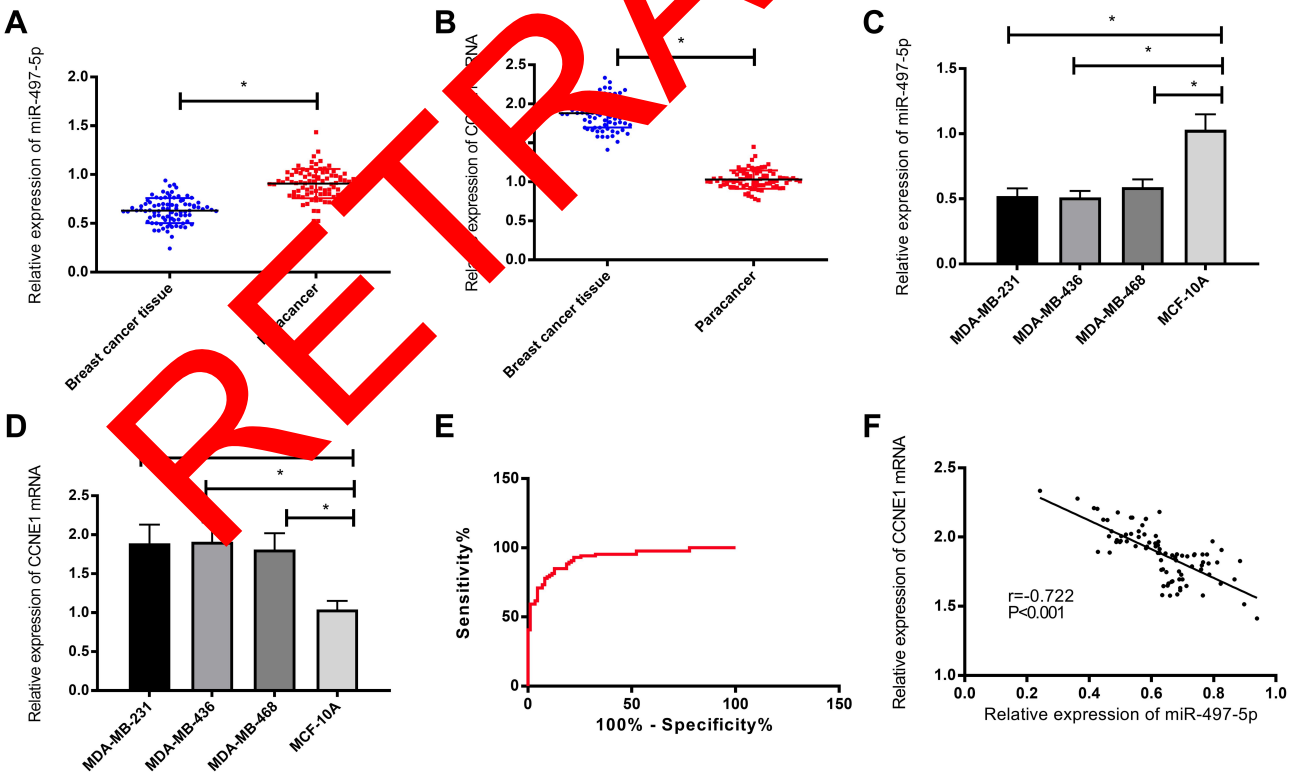


Figure 1 Expression and clinical significance of miR497-5p and *CCNE1* in TNBC. (**A**) Expression of miR497-5p in TNBC tissue; (**B**) expression of *CCNE1* in TNBC tissue; (**C**) expression of miR497-5p in TNBC cells; (**D**) expression of *CCNE1* in TNBC cells. (**E**) ROC of miR497-5p in diagnosis of *TNBC*; (**F**) correlation of miR497-5p with *CCNE1*. *P<0.05.

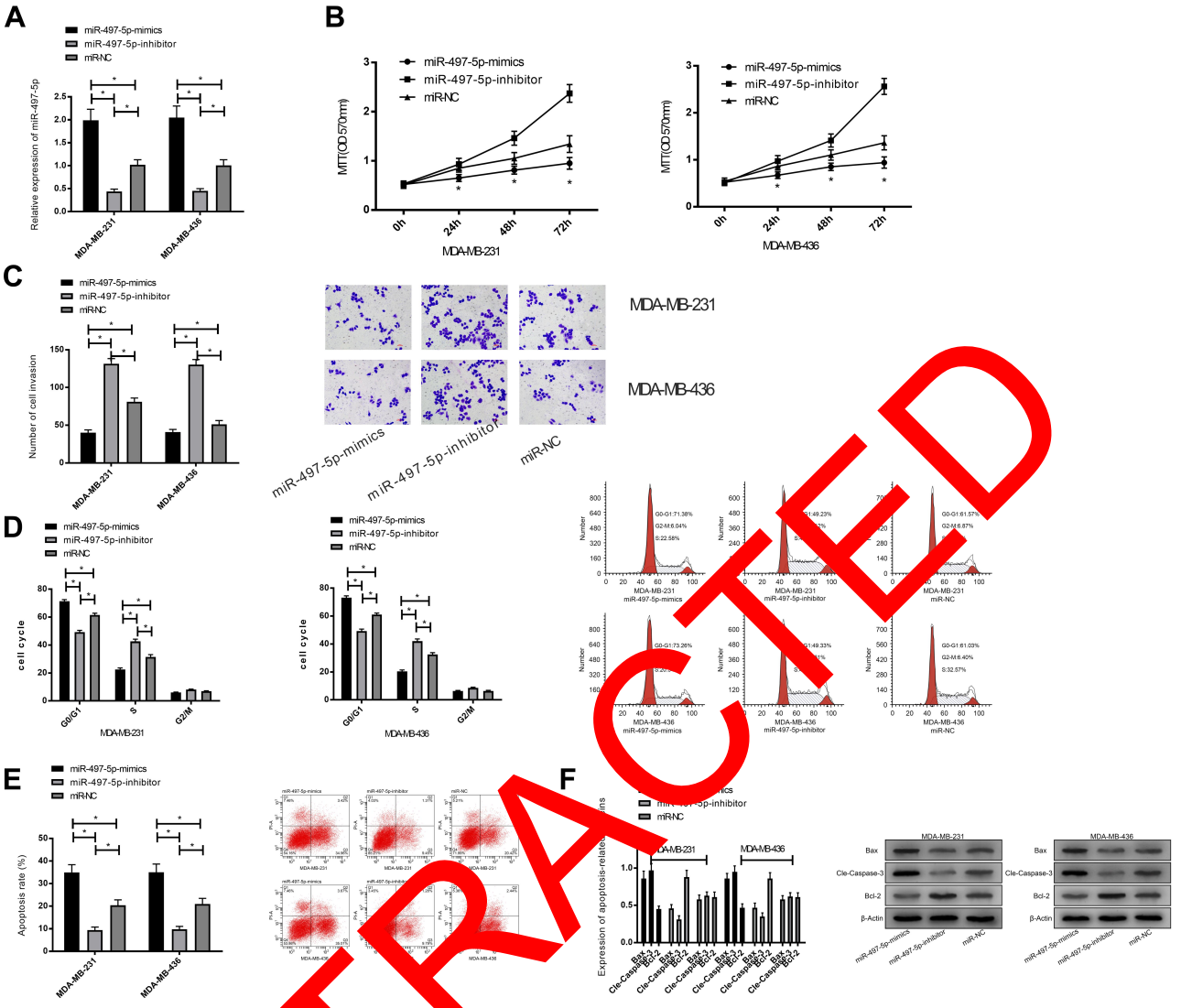


Figure 2 Effects of miR497-5p on proliferation, invasion, apoptosis, and cycle distribution of TNBC cells. (**A**) Levels of miR497-5p in MDA-MB231 and MDA-MB436 cells were analyzed after mimic or inhibitor transfection for 24 hours; (**B**)effect of miR497-5p on proliferation of TNBC cells; (**C**) effect of miR497-5p on invasion of TNBC cells (the scale 50 μm); (**D**) compared with corresponding controls, upregulation of miR497-5p promoted G_1/S transition in MDA-MB231 and MDA-MB436, while down-regulation of miR497-5p promoted G_1/S transition in MDA-MB231 and MDA-MB436 cells; (**E**) effect of miR497-5p on apoptosis of TNBC cells; (**F**) effect of miR497-5p on apoptosis-related proteins in TNBC cells. Data presented as means ± SEM from three independent experiments. *P<0.05.

RETRACTED

CCNE1 3′UTR (P<0.05), but had no influence on the mutant *CCNE1* 3′UTR. Furthermore, WB showed that CCNE1 protein in MDA-MB231 and MDA-MB436 cells transfected with miR497-5p mimics was downregulated, but protein in TNBC cells transfected with miR497-5p-inhibitor, it was obviously enhanced (P<0.05, Figure 3).

Effect of DownRegulation of CCNE1 Expression on Biological Function of TNBC Cells

To verify whether the tumor-inhibition effect of miR497-5p in TNBC was mediated through CCNE1, CCNE1 was knocked down in MDA-MB231 and MDA-MB436 cells. WB analysis revealed that CCNE1 declined in MDA-MB 231 and MDA-MB436 cells after transfection with si-CCNE1 (P<0.05). Following transfection, MTT and cell-invasion tests revealed that si-CCNE1 significantly suppressed the growth and invasion of MDA-MB231 and MDA-MB436 cells, blocked the cell cycle in stage G_1, and facilitated apoptosis (P<0.05). Moreover, WB revealed that knockdown of CCNE1 increased levels of the proapoptosis protein Bax and cleaved caspase 3 expression, while expression of the antiapoptosis protein BCL2 was downregulated (Figure 4).

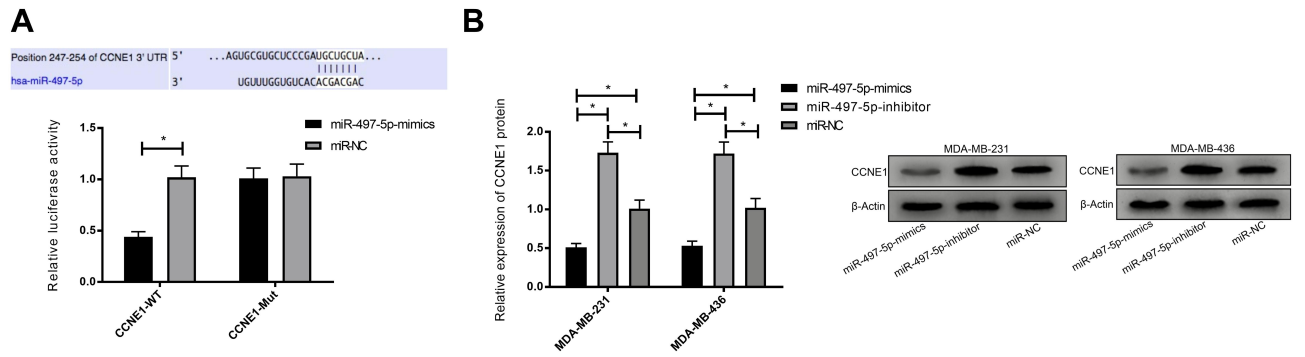
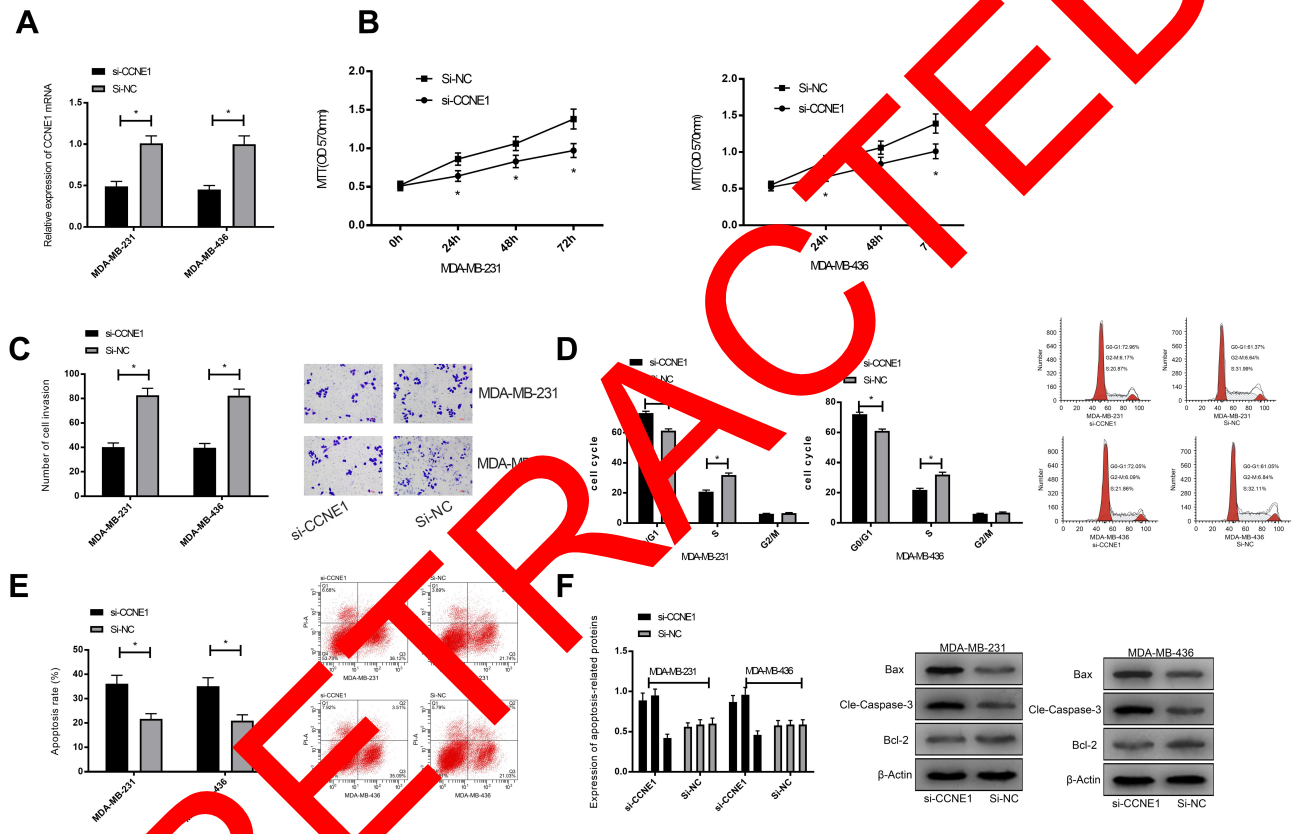


Figure 3 Double fluorescein–reporter enzyme. (**A**) Effect of miR497-5p on *CCNE1* double fluorescein–reporter enzyme activity; (**B**) effect of miR497-5p on CCNE1 protein expression. *P<0.05.



RETRACTED

Figure 4 Effect of downregulating CCNE1 on proliferation, invasion, apoptosis, and cycle distribution of TNBC cells. (**A**) Knockdown efficiency of CCNE1 in TNBC cells; (**B**) effect of downregulating CCNE1 on proliferation of TNBC cells; (**C**) effect of downregulating CCNE1 on invasion of TNBC cells (scale 50 μm); (**D**) compared with corresponding control, downregulation of CCNE1 promoted G_1/S transition in MDA-MB231 and MDA-MB436; (**E**) effect of downregulating CCNE1 on apoptosis of TNBC cells; (**F**) effect of downregulating CCNE1 on apoptosis-related proteins in TNBC cells. Data presented as means ± SEM from three independent experiments. *P<0.05.

Rescue Experiment

MDA-MB231 and MDA-MB436 cells were cotransfected with miR497-5p inhibitor + si-CCNE1. Cell growth, invasiveness, cycle, and apoptosis were detected. The results revealed that growth, invasiveness, cycle, and apoptosis of cells transfected with miR497-5p inhibitor + si-CCNE1 were not different from ells transfected with miRNC, but proliferation and invasion of cells were obviously enhanced compared with cells transfected with si-CCNE1. Cell percentage at the G_1/G_0 stage was significantly decreased, while cells at the S stage were obviously enhanced and apoptosis obviously decreased, indicating that the miR497-5p inhibitor reversed the influence of si-CCNE1 on TNBC cells. WB detection showed that Bax, cleaved caspase 3, and

BCL2 in cells transfected with miR497-5p inhibitor + si-CCNE1 were not different from cells transfected with miRNC, but BCL2 protein expression was obviously higher and Bax and cleaved caspase 3 expression obviously lower than cells transfected with si-CCNE1 (P<0.05, Figure 5).

Discussion

More and more evidence shows that miRNAs play a crucial role in malignant cancer tumors by acting as tumor suppressors or oncogenes.[14] Many miRNAs have been revealed to play a vital role in TNBC. For example, it has been revealed that miR33a can suppress the development of TNBC by directly targeting EZH2 to suppress growth and migration and induce G_1 cell-cycle arrest.[15] However, there are few reports about the function of miR497-5p in TNBC.

In recent years, there have been many reports about the effect of miR497-5p in tumors. For instance, miR497-5p is enhanced in colon carcinoma[16] and it can be a cancer-therapy option for regulating lipid metabolism in the colon. Other studies have revealed that miR497-5p suppresses the proliferation and growth of gastric carcinoma cells by targeting PIK3R1.[17] In our research, miR497-5p in tumor tissue and sera of patients with TNBC was significantly downregulated, and ROC analysis revealed that miR497-5p had better diagnostic value for TNBC. This revealed that miR497-5p was involved in the formation and progression of TNBC. Therefore, we did further cell experiments in vitro. These findings revealed that overexpression of miR497-5p in MDA-MB231 and MDA-MB436 cells obviously inhibited cell proliferation and invasiveness, blocked the G_1 stage, and induced apoptosis. The proapoptotic protein Bax and antiapoptotic protein BCL2 play important roles in apoptosis. Some studies have shown that the mutations that destroy the binding between Bax and BCL2 proteins can induce apoptosis of cancer cells.[18] Our results showed that overexpression of miR497-5p significantly upregulated the expression of Bax and downregulated the expression of BCL2, which was consistent with the change in apoptosis rate. These results strongly indicated that miR497-5p had inhibitory action on TNBC. Studies have also indicated that miR497-5p plays the role of a tumor-suppressor gene.[19,20] Others have revealed that miR497-5p can block the

RETRACTED

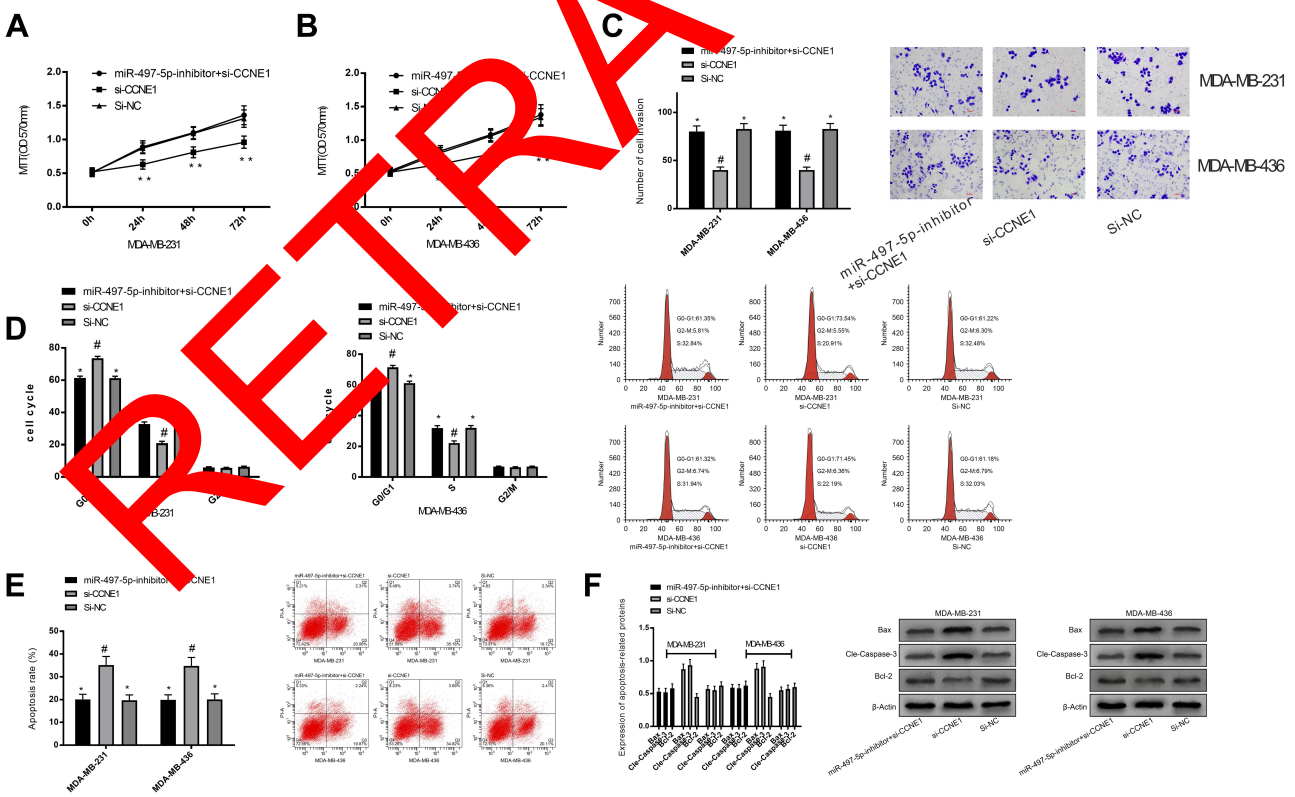


Figure 5 Rescue experiments (**A**, **B**); effect of miR497-5p-inhibitor + si-CCNE1 on proliferation of TNBC cells; (**C**) effect of miR497-5p-inhibitor + si-CCNE1 on invasion of TNBC cells scale 50 μm); (**D**) effect of miR497-5p-inhibitor + si-CCNE1 on cycle of TNBC cells; (**E**) effect of miR497-5p-inhibitor + si-CCNE1 on apoptosis rate of TNBC cells; (**F**) effects of miR497-5p-inhibitor + si-CCNE1 on apoptosis-related proteins in TNBC cells. ** indicates P<0.05, *Compared with #, P<0.01.

cycle of tumor cells and induce apoptosis.[21] Also, *HOXC13-AS* lncRNA can promote the development of BC by inhibiting the expression of miR497-5P, confirming the role of miR497-5P as a tumor suppressor in BC.[22] This is consistent with our research.

As we know, miRNA affects cell function by binding its target gene,[23] and the functional mechanism of miR497-5P in TNBC remains to be further explored. We found that *CCNE1* was one of the targets of miR497-5p through websites. Through luciferase assays, we investigated whether miR497-5p directly targeted *CCNE1* 3′UTR in TNBC cells. In addition, increasing miR497-5p resulted in knockdown of CCNE1 protein, while downregulation of miR195-5p showed an opposite effect. Previous studies have revealed that CCNE1 is a nucleocapsid protein of the cell cycle–regulator family,[24] and plays the role of oncogene in the G_1 and S phases of the cell cycle. In addition,[25,26] evidence has shown that the expression of CCNE1 in other tumors can be regulated by miRNA.

We found that CCNE1 in blood sera and tumor tissue of patients with TNBC was significantly enhanced and that there was a negative correlation between its expression and miR497-5p. We also analyzed the influence of CCNE1 on TNBC cells. Knocking down CCNE1 expression significantly inhibited the growth and invasiveness of MDA-MB231 and MDA-MB436 cells, blocked cells in the G_1 phase, and induced further apoptosis. As a cyclin, CCNE1[27] can catalyze the CDK2 subunit and play a key part in cell-cycle regulation to ensure DNA replication, chromosome separation, and G_1/S-phase transition. This also explained the cell phenotype that we observed in the experiment. Research on CCNE1 in TNBC[28] has revealed that CCNE1 expression is kept at a high level in TNBC and that overexpression of CCNE1 is an early event in the progress of BC. Other research has shown that overexpression of CCNE1 is a specific marker of TNBC.[29] This is consistent with our results. To further verify the combination of miR497-5p with CCNE1, we also conducted rescue experiments. This revealed that the miR497-5p inhibitor reversed the influence of si-CCNE1 on TNBC cells, and further uncovered that miR497-5p affected the development of TNBC by regulating CCNE1.

Conclusion

miR497-5p is obviously declined in TNBC tumor tissue and can be used as a diagnostic marker for HCC patients. Overexpression of miR497-5p can suppress the growth and invasiveness of TNBC cells, block the cell cycle, and induce apoptosis by directly inhibiting the expression of CCNE1, which not only provides new insight into the progress and metastasis of TNBC but also provides a latent target to prevent and treat cancer. However, there are some shortcomings in this study. For example, we did not carry out in vivo experiments to observe whether miR497-5p has the same inhibitory effect on solid tumors, but we will carry out further basic experiments to improve our conclusions in future studies.

Disclosure

The authors report no conflicts of interest in this work.

RETRACTED

References

1. Anastasiadi Z, Lianos G, Ignatiadis E, Ha HV, Mitsis M. Breast cancer in you wome an overview. *Updates Surg*. 2017;69(3):313–317 doi:1 s13304-01 0424-1
2. Li Y, Zhang N, ang H, Yan O. Com ative prognostic analysis for triple-neg reast cancer w taplastic and invasive ductal carcinoma *Clin thol*. 2019;7 (6):418–424. doi:10.1136/jclinpath-2018-205544
3. Yeo , an JL. Breast ca multiple subtypes within a tumor? *Trends Cancer*. 2017;3(11):753–760. doi:10.1016/j.trecan.2017.09.001
4. ng H, Zhou L ang S, et al. Retrospective analysis of concurrent etaxel and epi bicin neoadjuvant versus adjuvant chemotherapy: w h leads to b ter outcomes for different subtype breast cancer patie *Me ine (Baltimore)*. 2018;97(40):e12690. doi:10.1097/MD.0000000000012690
5. Wu L, Li M, et al. Down-regulation of MicroRNA-592 in obesity contributes to hyperglycemia and insulin resistance. *EBioMedicine*. 2019;42:494–503. doi:10.1016/j.ebiom.2019.03.041
6. Trujillo RD, Yue SB, Tang Y, O'Gorman WE, Chen CZ. The potential functions of primary microRNAs in target recognition and repression. *EMBO J*. 2010;29(19):3272–3285. doi:10.1038/emboj.2010.208
7. Meng Z, Zhang R, Wang Y, et al. miR-200c/PAI-2 promotes the progression of triple negative breast cancer via M1/M2 polarization induction of macrophage. *Int Immunopharmacol*. 2020;81:106028. doi:10.1016/j.intimp.2019.106028
8. Wang Z, Wang X. miR-122-5p promotes aggression and epithelial-mesenchymal transition in triple-negative breast cancer by suppressing charged multivesicular body protein 3 through mitogen-activated protein kinase signaling. *J Cell Physiol*. 2020;235(3):2825–2835. doi:10.1002/jcp.29188
9. Li G, Wang K, Wang J, Qin S, Sun X, Ren H. miR-497-5p inhibits tumor cell growth and invasion by targeting SOX5 in non-small-cell lung cancer. *J Cell Biochem*. 2019;120(6):10587–10595.
10. Xu GS, Li ZW, Huang ZP, et al. MiR-497-5p inhibits cell proliferation and metastasis in hepatocellular carcinoma by targeting insulin-like growth factor 1. *Mol Genet Genomic Med*. 2019;7(10):e00860. doi:10.1002/mgg3.860
11. Han Z, Zhang Y, Yang Q, et al. miR-497 and miR-34a retard lung cancer growth by co-inhibiting cyclin E1 (CCNE1). *Oncotarget*. 2015;6(15):13149–13163. doi:10.18632/oncotarget.3693
12. Zhao ZM, Yost SE, Hutchinson KE, et al. CCNE1 amplification is associated with poor prognosis in patients with triple negative breast cancer. *BMC Cancer*. 2019;19(1):96. doi:10.1186/s12885-019-5290-4
13. Wu T, Wang H, Qin F, et al. Expression of zona pellucida B proteins in juvenile rare minnow (Gobiocypris rarus) exposed to 17alpha-ethinylestradiol, 4-nonylphenol and bisphenol A. *Comp Biochem Physiol C Toxicol Pharmacol*. 2012;155(2):259–268. doi:10.1016/j.cbpc.2011.09.005

14. Hosseinahli N, Aghapour M, Duijf PHG, Baradaran B. Treating cancer with microRNA replacement therapy: a literature review. *J Cell Physiol*. 2018;233(8):5574–5588. doi:10.1002/jcp.26514
15. Weihua Z, Guorong Z, Xiaolong C, Weizhan L. MiR-33a functions as a tumor suppressor in triple-negative breast cancer by targeting EZH2. *Cancer Cell Int*. 2020;20:85. doi:10.1186/s12935-020-1160-z
16. Gharib E, Nasri Nasrabadi P, Reza Zali M. miR-497-5p mediates starvation-induced death in colon cancer cells by targeting acyl-CoA synthetase-5 and modulation of lipid metabolism. *J Cell Physiol*. 2020;235(7–8):5570–5589. doi:10.1002/jcp.29488
17. Xia TF, Chen J, Wu K, Zhang J, Yan Q. Long noncoding RNA NEAT1 promotes the growth of gastric cancer cells by regulating miR-497-5p/PIK3R1 axis. *Eur Rev Med Pharmacol Sci*. 2019;23 (16):6914–6926.
18. Raghav PK, Kumar R, Kumar V, Raghava GPS. Docking-based approach for identification of mutations that disrupt binding between Bcl-2 and Bax proteins: inducing apoptosis in cancer cells. *Mol Genet Genomic Med*. 2019;7(11):e910. doi:10.1002/mgg3.910
19. Zhang Y, Zhu Z, Huang S, et al. lncRNA XIST regulates proliferation and migration of hepatocellular carcinoma cells by acting as miR-497-5p molecular sponge and targeting PDCD4. *Cancer Cell Int*. 2019;19:198. doi:10.1186/s12935-019-0909-8
20. Chai L, Kang XJ, Sun ZZ, et al. MiR-497-5p, miR-195-5p and miR-455-3p function as tumor suppressors by targeting hTERT in melanoma A375 cells. *Cancer Manag Res*. 2018;10:989–1003. doi:10.2147/CMAR.S163335
21. Sun Z, Li A, Yu Z, Li X, Guo X, Chen R. MicroRNA-497-5p suppresses tumor cell growth of osteosarcoma by targeting ADP ribosylation factor-like protein 2. *Cancer Biother Radiopharm*. 2017;32(10):371–378. doi:10.1089/cbr.2017.2268
22. Li X, Wang Q, Rui Y, et al. HOXC13-AS promotes breast cancer cell growth through regulating miR-497-5p/PTEN axis. *J Cell Physiol*. 2019;234(12):22343–22351. doi:10.1002/jcp.28800
23. Noorolyai S, Baghbani E, Aghebati Maleki L, et al. Restoration of miR-193a-5p and miR-146 a-5p expression induces G1 arrest in colorectal cancer through targeting of MDM2/p53. *Adv Pharm Bull*. 2019;10(1):130–134. doi:10.15171/apb.2020.017
24. Pils D, Bachmayr-Heyda A, Auer K, et al. Cyclin E1 (CCNE1) as independent positive prognostic factor in advanced stage serous ovarian cancer patients - a study of the OVCAD consortium. *Eur J Cancer*. 2014;50(1):99–110. doi:10.1016/j.ejca.2013.09.011
25. Guo X, Connick MC, Vanderhoof J, Ishak MA, Hartley RS. MicroRNA-16 modulates HuR regulation of cyclin E1 in breast cancer cells. *Int J Mol Sci*. 2015;16(4):7112–7132. doi:10.3390/ijms16047112
26. Shukla K, Sharma AK, Ward A, et al. MicroRNA-30c-2-3p negatively regulates NF-kappaB signaling and cell cycle progression through downregulation of TRADD [illegible]NE1 in breast cancer. *Mol Oncol*. 2015;9(6):1106–1119. [illegible]:10.1016/[illegible]olonc.2015.01.008
27. Au-Yeung G, Lang F, Azar W[illegible]et al. Selective [illegible]rgeting of cyclin E1-amplified high-grade serous o[illegible]ian cancer by cyclin-dependent kinase 2 and AKT [illegible]nibition. *[illegible]in Can[illegible] Res*. 2017;23 (7):1862–1874. doi:10[illegible]158/1078-0432.C[illegible]-1[illegible]0620
28. Lambertini M, Ca[illegible]bell C, G[illegible]er RD, et a[illegible]Dissecting the effect of hormone recep[illegible]r sta[illegible]in[illegible]tients with HER2-positive early breast cancer: expl[illegible]tory analy[illegible]from the [illegible]LTTO (BIG 2-06) randomized clinical [illegible]*Breast Ca[illegible]s Treat*. 2019;177(1):103–114. doi:10[illegible]007/s[illegible]549-019-0528[illegible]
29. Frisa PS, Jacob[illegible]er JW, Blagosklonny MV. Cell cycle-related [illegible]b1 quantifica[illegible]n. *PLoS One*. 2009;4(9):e7064. doi:10.1371/journal.pone.0007064

RETRACTED

Cancer Management and Research

Dovepress

Publish your work in this journal

Cancer Management and Research is an international, peer-reviewed open access journal focusing on cancer research and the optimal use of preventative and integrated treatment interventions to achieve improved outcomes, enhanced survival and quality of life for the cancer patient.

The manuscript management system is completely online and includes a very quick and fair peer-review system, which is all easy to use. Visit http://www.dovepress.com/testimonials.php to read real quotes from published authors.

Submit your manuscript here: https://www.dovepress.com/cancer-management-and-research-journal