Original Article

SYT7 promotes breast cancer cells growth through the PI3K/AKT pathway

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Background: Breast cancer is one of the most malignant tumors in the reproductive system and has a poor prognosis. The aim of this study was to investigate the function and underlying mechanism of synaptotagmin 7 (SYT7) in breast cancer.

Methods: We utilized The Cancer Genome Atlas (TCGA) database and the Kaplan-Meier plotter database to assess the correlation between SYT7 expression and the prognosis of breast cancer patients. The efficacy of SYT7 knockdown was evaluated through reverse transcription-quantitative polymerase chain reaction (RT-qPCR) and Western blotting. Furthermore, we examined the impact of SYT7 on breast cancer cell proliferation and apoptosis using Cell Counting Kit-8 (CCK-8), clone formation assays, and flow cytometry. Through Western blot analysis, we investigated the influence of SYT7 on the expression of apoptosis-related markers and the PI3K/AKT signaling pathway in breast cancer.

Results: The TCGA database data analysis revealed a significant up-regulation of SYT7 expression in breast cancer tissues compared to normal tissues ($P<0.001$). A correlation was observed between SYT7 expression and tumor size ($P=0.009$), as well as estrogen receptor (ER) expression level ($P<0.001$) and progesterone receptor (PR) expression level ($P<0.001$) in breast cancer patients. Analysis of the Kaplan-Meier plotter database indicated that high SYT7 expression was associated with a shorter overall survival (OS) ($P=0.009$). The mRNA expression results indicated higher SYT7 expression in breast cancer tissues compared to adjacent normal tissues ($P=0.005$). CCK-8, clone formation assay, and flow cytometry results demonstrated that SYT7 promoted the proliferation and inhibited the apoptosis of breast cancer cells. Western blot assay confirmed the activation of PI3K/AKT signaling by SYT7.

Conclusions: The findings suggest that SYT7 is highly expressed in breast cancer and that its high expression is linked to clinical characteristics and prognosis. Inhibition of SYT7 through knockdown can suppress proliferation and promote apoptosis of breast cancer cells, making it a potential target for breast cancer diagnosis and treatment.

Keywords: Synaptotagmin 7 (SYT7); breast cancer; PI3K/AKT signal; proliferation; apoptosis

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Introduction

Breast cancer, a prevalent malignancy among females on a global scale, stands as the foremost contributor to cancer-related fatalities in women (1). Currently, the primary approaches to addressing breast cancer revolve around local intervention (surgery and radiotherapy) and systemic intervention. The widespread use of breast cancer screening techniques like B-ultrasound, mammography, and minimally invasive biopsy has significantly enhanced the early detection rate of breast cancer. As a result of the significant prevalence and fatality rate of breast cancer, coupled with limited awareness about the condition among some individuals afflicted by it, breast cancer continues to pose a critical risk to women's well-being. Hence, it is imperative to thoroughly examine the mechanisms that trigger and progress breast cancer to effectively treat individuals suffering from this condition. Furthermore, it is crucial to investigate novel therapeutic targets and potential genes linked to this condition.

By using an analysis of The Cancer Genome Atlas (TCGA) database, we find synaptotagmin 7 (SYT7) displayed a much higher change between paired normal and cancer tissues. We thus chose SYT7 as a candidate gene for the research. Synaptotagmin (SYT) is classified as a secretory vesicle protein, primarily consisting of a transmembrane domain at its N-terminal and a C2 domain (C2A and C2B) at its C-terminal, responsible for Ca^{2+} binding (2-4). SYT is the main Ca^{2+} sensor during synaptic transmission and mediates the regulation of membrane fusion by calcium ions (5,6).

Research findings indicate that the SYT family exhibits an oncogenic function in certain cancer types. According to the investigation conducted by David *et al.*, there is a proposition that the expression levels of SYT witness an augmentation in small cell lung cancer. Additionally, it has been observed that SYT forms an association with syntaxin within the cellular membrane of small cell lung cancer (the type of SYT has not been mentioned though) (7). Jun *et al.* have shown that proto-oncogene lung cancer fusion kinase activates the invasion pathway by phosphorylating extended SYT1 (E-SYT1) (8). SYT1 is up-regulated in colon cancer, and highly expressed SYT1 promotes colon cancer proliferation and inhibits apoptosis (9). Kanda *et al.*'s study demonstrated that SYT7 is a driving factor in the formation of liver metastasis of gastric cancer (10). Based on the investigation conducted by Wang *et al.*, it was discovered that the expression of SYT7 is notably heightened in colorectal cancer, leading to an increase in cell proliferation (11). In the instance of glioma, SYT7 also plays a vital role, as its amplified expression contributes to the proliferation of glioma cells (12). Moreover, SYT13 exhibits higher levels of expression in gastric cancer patients with peritoneal metastasis, thereby promoting enhanced migratory and invasive capabilities in gastric cancer cells (13). Consequently, it can be deduced that SYT7 displays oncogenic characteristics in various types of tumors. The expression levels of SYT7 in breast cancer exhibit variation according to database records. It has been observed that elevated SYT7 expression levels are associated with the prognosis of breast cancer patients.

However, the precise biological function and molecular mechanism of SYT7 in breast cancer are still to be explored and documented. In our present research, we find that SYT7 is overexpressed in breast cancer patients and promotes breast cancer proliferation *in vivo*. We present this article in accordance with the MDAR reporting checklist (available at https://tcr.amegroups.com/article/view/10.21037/tcr-24-7/rc).

Highlight box

Key findings

- Synaptotagmin 7 (SYT7) is upregulated in breast cancer and significantly correlated with clinical outcome.

What is known and what is new?

- SYT family exhibits an oncogenic function in certain cancer types.
- SYT7 plays a potential target for breast cancer.

What is the implication, and what should change now?

- SYT7 promotes breast cancer cells growth through the PI3K/AKT pathway.
- The inhibitors acting on SYT7 in breast cancer need to be investigated.

Methods

Reagent

TRIzol, Lipofectamine™ 2000, and polymerase chain reaction (PCR) primers were purchase from Invitrogen Company (Carlsbad, CA, USA). Cell Counting Kit-8 (CCK-8) was purchased by Beyotime Company (Shanghai, China). The experiment utilized a reverse transcription kit that was bought from Promega (located in Madison, USA). Shanghai Jiying Company (Shanghai, China)

synthesized the small interfering RNA of SYT7 (si-SYT7) as well as its negative control (NC) pair [small interfering RNA (siRNA) NC]. SYT7 (Cat. No. ab121383) antibody was purchased from Abcam (Cambridge, UK). Anti-p-PI3K (Cat. No. sc-12929), anti-caspase 3 (Cat. No. sc-271759), anti-Bcl-xl (Cat. No. sc-8392) and anti-GAPDH (Cat. No. sc-47724) were purchased from Santa Cruz Biotechnology Company (Newark, NJ, USA). Anti-AKT (Cat. No. WL0003b) and anti-cleaved-caspase 9 (Cat. No. WL01838) were purchased from Wanleibio Company (Shenyang, China), anti-cleaved PARP (Cat. No. 9541), anti-Bax (Cat. No. #502), anti-Bcl-2 (Cat. No. #2870), anti-mouse immunoglobulin G (IgG) (Cat. No. 7076), and anti-rabbit IgG (Cat. No. 7074) were purchased from CST (Danforth, MA, USA). Anti-p-AKT (Cat. No. 66444) and anti-goat IgG (Cat. No. SA00001-4) were purchased from Proteintech Group (Wuhan, China).

Cell culture

Control and tumor cells were obtained from the American Type Culture Collection (ATCC; Rockville, MD, USA). All cell lines were cultured in RPMI 1640 medium (Gibco, Grand Island, NY, USA) supplemented with 10% fetal bovine serum (Gibco) at 37 ℃, and MCF-10A was cultured as for formerly described (14).

Tissue sample

The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013). The study was approved by the Biomedical Ethics Committee of the First Affiliated Hospital of Chongqing Medical University (No. 2019-208) and informed consent was taken from all the patients. The tissue samples used in this research were obtained from the Biobank of Molecular Oncology and Epigenetics at the Chongqing Key Laboratory, located within the First Affiliated Hospital of Chongqing Medical University.

Analysis of the correlation of SYT7 and breast cancer

The TCGA database was utilized to acquire the breast cancer's *SYT7* gene expression data for analysis. A study cohort comprising of 1,096 patients diagnosed with breast cancer was examined, alongside 112 normal breast specimens to act as controls. Specifically, the SYT7 expression levels were sorted based on the median, wherein the top 50% constituted the low expression group, while the bottom 50% constituted the high expression group. By comparing these expression levels, discrepancies in SYT7 expression within breast cancer tissues were evaluated. Subsequently, 934 breast cancer patients were selected from the TCGA database, ensuring the availability of complete clinical and pathological information. Based on diverse clinical characteristics (T stage, N stage, M stage, etc.), the patients were divided into various groups. Comparative analyses were then performed to assess the distinctions between these groups and the SYT7 high and low expression groups. To ascertain statistical significance, the Chi-square test was employed and results were deemed significant if $P<0.05$. Additionally, the prognostic disparities of breast cancer patients were analyzed using the Kaplan-Meier plotter online database, considering the diverse expression levels of SYT7.

Extraction of total RNA

The weighed tissue (50 mg) was cut with sterile scissors, and 1 mL Trizol reagent was added to the homogenizer to homogenize. After the tissue is completely dissolved, the suspension was collected, 200 μL chloroform was added and shook vigorously to mix. The mixture was placed for 15 min and centrifuged; the transparent layer was taken and placed in a centrifuge tube, an equal volume of isopropyl alcohol was added, mixed and centrifuged. Next, 75% ice ethanol was added to wash and dry, and Nanodrop-2000 (Foster City, CA, USA) was used to detect RNA concentration and the purity is qualified when it is 1.8–2.0.

Cell culture and transfection

T47D and MCF-7 cells were seeded in a six-well cell culture plate with a density of 4×10^5 per well during the logarithmic growth phase. Once the cells had fully adhered and reached a confluence of 60%, the procedures outlined in the Lipofectamine™ 2000 manual were followed to introduce small interfering RNA (si-SYT7) and its NC group separately. After 48 hours, the cells were collected for subsequent experimentation.

Kaplan-Meier plotter database analysis

The levels of SYT7 expression and its correlation with prognosis were investigated in patients with breast cancer by referring to the Kaplan-Meier plotter database (http://kmplot.com/analysis/).

Reverse transcription-quantitative PCR (RT-qPCR)

For normalization, GAPDH served as the internal control. The following primers were used for RT-qPCR analysis:

SYT7 forward primer: 5-ACTCCATCATCGTGAA CATCATC-3,

Reverse primer: 5-TCGAAGGCG AAGGACTC ATTG-3;

GAPDH forward primer: 5-CCAGCAAGAGCAC AAGAGGAA-3,

Reverse primer: 5'-GGTCTACATGGCAACTC AAGG-3.

Clone formation experiment

MCF-7 cells (200, 400, and 800 cells per well) were planted into six-well plates, and T47D cells were plated in six-well plates. After culturing for 2 weeks, cells were fixed with paraformaldehyde (Beyotime) for 35 min and then stained with crystal violet (Beyotime Institute of Biotechnology, Haimen, China, C0121) for 15 min.

CCK-8 experiment

After transfection, the cells in each group were made into a cell suspension (density: 2×10^4/mL), and 100 µL per well was seeded into a 96-well plate. Three duplicate wells per group were set up, so that the 96-well plate could be cultured routinely in the thermostat. After the cells have completed attachment, CCK-8 solution (10 µL/per well) was added and incubated in the incubator for 2 hours in the dark. Then the optical density (OD) value was measured at 450 nm with a microplate reader. Then, same method was used to measure the OD value of the 96-well plates after culturing for 24, 48, 72, and 96 hours.

Flow cytometry

Cells were collected from each experimental group 48 hours after transfection. The cells were then washed with phosphate-buffered saline (PBS) and centrifuged at a speed of 1,000 rpm for a duration of 5 min. Next, the supernatant was removed and the cells were suspended again using Annexin binding solution. Following the addition of 10 µL of Annexin V-PE, an incubation at room temperature was conducted for 15 min in a dark environment. The assessment of cell apoptosis within each group was conducted using flow cytometry. For the flow cytometry analysis, cells obtained from each experimental group 48 hours post-transfection were subjected to PBS washing and centrifugation at 1,000 rpm for 5 min. Subsequently, the supernatant was discarded and the cells were treated overnight with 75% ice-cold ethanol. The following day, the distribution of the cell cycle was analyzed.

Western blot

After transfection 48 hours, the cells were added Racial and Identity Profiling Act (RIPA) protein lysis, and centrifuge at 4 ℃ to extract the protein. Determine the protein concentration according to the instructions of the bicinchoninic acid (BCA) protein concentration assay kit. After configuring the sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gel, take samples (30 µg per sample) for constant voltage 80 V electrophoresis separation, then transfer to polyvinylidene difluoride (PVDF) membrane at constant current 200 mA in ice bath. For 1 hour, the membranes were obstructed with 5% non-fat dried milk in Tris-buffered saline comprised of 0.05% Tween-20 (TBST). Afterward, incubation with the primary antibodies occurred overnight at 4 ℃. As secondary antibodies, horseradish peroxidase (HRP) anti-rabbit IgG were employed. The utilization of the Bio-Rad enhanced chemiluminescence detection system (located in Hercules, CA, USA) facilitated the analysis of the signals.

Statistical analysis

Each experiment was repeated three times independently. Statistical analysis and data graph creation were conducted using SPSS 22.0 and Graph Pad Prism 8.0 software. A comparison between two groups of independent samples was performed using the unpaired independent samples *t*-test. The correlation between SYT7 expression and clinical pathological characteristics of patients with breast cancer was assessed using the Chi-square test. Survival curves were generated through Kaplan-Meier analysis and compared using the log-rank test. A P value of less than 0.05 was considered indicative of a statistically significant difference.

Results

SYT7 is overexpressed in human breast cancer tissues and associated with clinical outcomes

The TCGA database was utilized to examine the disparity in SYT7 expression between breast cancer tissue and normal

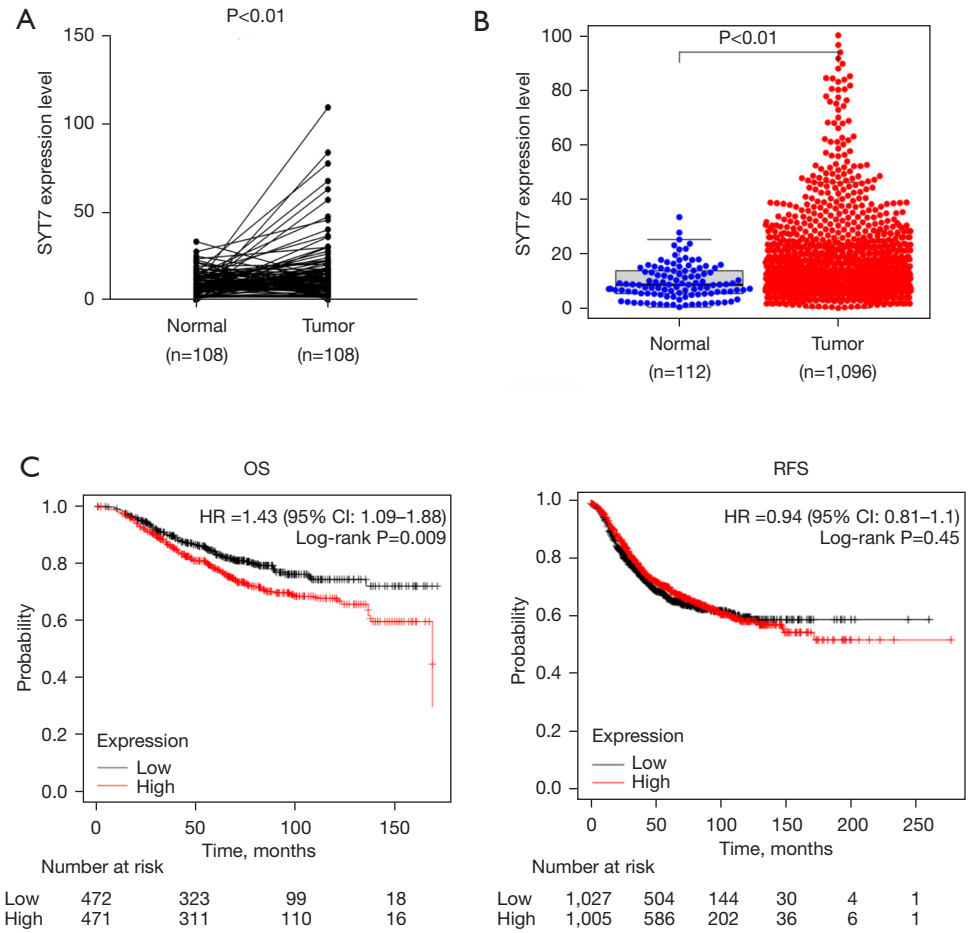

Figure 1 SYT7 is overexpressed in human breast cancer tissues and associated with clinical outcomes. (A) Analysis of SYT7 expression in 108 pairs of matched breast cancer tissues and adjacent tissues using the TCGA database. (B) Analysis of SYT7 expression in 1,096 breast cancer tissues and 112 normal tissues using the TCGA database. (C) Utilizing the Kaplan-Meier plotter database to examine the association between SYT7 expression and OS or RFS. SYT7, synaptotagmin 7; OS, overall survival; RFS, recurrence-free survival; HR, hazard ratio; CI, confidence interval; TCGA, The Cancer Genome Atlas.

breast tissue. The findings indicated a notable up-regulation of SYT7 expression in breast cancer tissue compared to normal breast tissue (*Figure 1A,1B*). An analysis conducted using the Kaplan-Meier plotter online database revealed no statistical variation in recurrence-free survival between the two groups of breast cancer patients categorized based on high and low SYT7 expression. However, a notable distinction in overall survival (OS) between the two groups was observed. Specifically, breast cancer patients with elevated levels of SYT7 expression showcased a poorer prognosis (*Figure 1C*).

Furthermore, the TCGA database was employed to assess the correlation between SYT7 expression levels (*Table 1*). The findings indicated a significant association between high SYT7 expression and tumor size, as well as estrogen receptor (ER) and progesterone receptor (PR) levels.

SYT7 is highly expressed in both breast cancer cells and tissues

Using qPCR, the presence of SYT7 mRNA was identified in various breast cancer cell lines. The findings demonstrated a noteworthy elevation in SYT7 expression levels across multiple breast cancer cell lines compared to normal human breast epithelial cells (*Figure 2A*). Additionally, the mRNA expression analysis of SYT7 in 22 pairs of breast cancer tissues exhibited a substantial increase as compared to the

Table 1 Correlation analysis between SYT7 expression levels and clinicopathological characteristics in 934 breast cancer patients

Characteristic	Number	SYT7 expression		χ^2	P value
		Low (N=467)	High (N=467)		
Age (years)				0.16	0.69
<55	376	191	185		
≥55	558	276	282		
T stage				9.530	0.02
Tx-1	248	132	116		
T2	543	280	263		
T3	116	46	70		
T4	27	9	18		
N stage				1.629	0.65
N0	465	240	225		
N1	299	142	157		
N2	102	49	53		
N3	68	36	32		
M stage				0.29	0.59
Mx-0	920	459	461		
M1	14	8	6		
TNM stage				1.997	0.57
x-I	171	93	78		
II	539	264	275		
III	210	102	108		
IV	14	8	6		
ER				21.967	<0.001
Negative	212	136	76		
Positive	722	331	391		
PR				16.243	<0.001
Negative	310	184	126		
Positive	624	283	341		
Her-2				0.426	0.51
Negative	746	369	377		
Positive	188	98	90		

SYT7, synaptotagmin 7; TNM, tumor, node, metastasis; ER, estrogen receptor; PR, progesterone receptor; Her-2, human epidermal growth factor receptor-2.

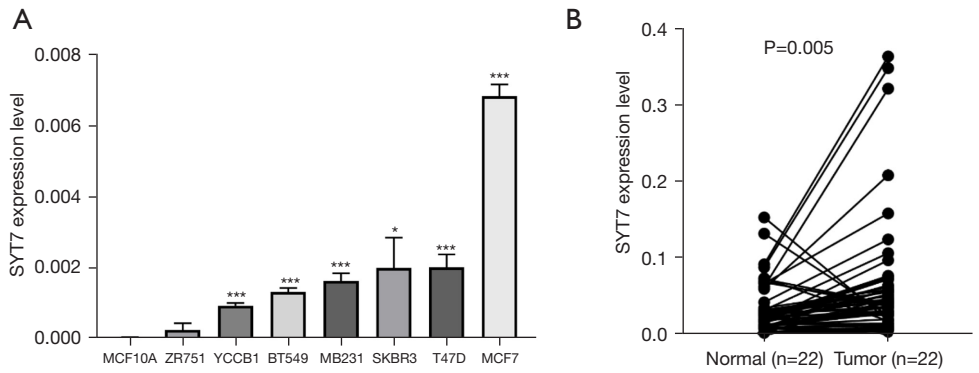

Figure 2 SYT7 is highly expressed in both breast cancer cells and tissues. (A) In our study, qPCR was employed to identify the presence of mRNA of SYT7 in different cell lines of human breast cancer. (B) Additionally, we conducted qPCR analysis to assess the mRNA expression of SYT7 in 22 pairs of human breast cancer tissues and their respective nearby tissues. *, P<0.05 (P=0.02); and ***, P<0.001. SYT7, synaptotagmin 7; qPCR, quantitative polymerase chain reaction.

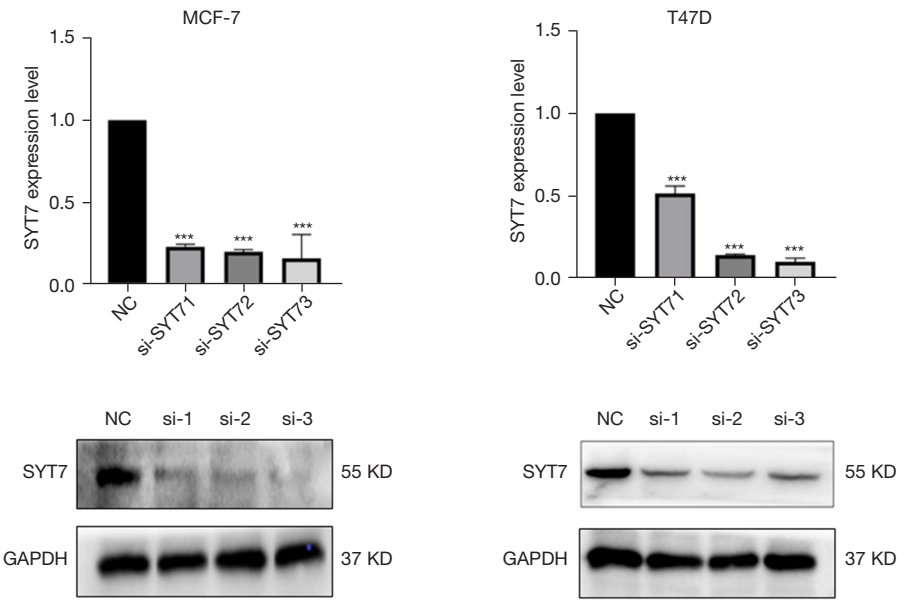

Figure 3 Knockdown efficiency of three SYT7 siRNAs in different breast cancer cells by qPCR and western blot. For all panels, ***, P<0.001. SYT7, synaptotagmin 7; NC, negative control; siRNA, small interfering RNA; qPCR, quantitative polymerase chain reaction.

corresponding adjacent tissues (*Figure 2B*).

Examining the impact of si-SYT7 interference in MCF-7 and T47D cell lines

To evaluate the effects of si-SYT7, we transfected both the MCF-7 and T47D cell lines with si-SYT7 and an NC. We then confirmed the knockdown efficiency at both the transcriptional and protein levels. *Figure 3* illustrates the successful knockdown of SYT7 expression in breast cancer cells compared to the NC group (*Figure 3*).

Knockdown of SYT7 inhibits the proliferation and colony formation of MCF-7 and T47D cells

Through CCK-8 and colony formation experiments, we confirmed that suppressing SYT7 expression inhibited the ability of MCF-7 and T47D breast cancer cells to

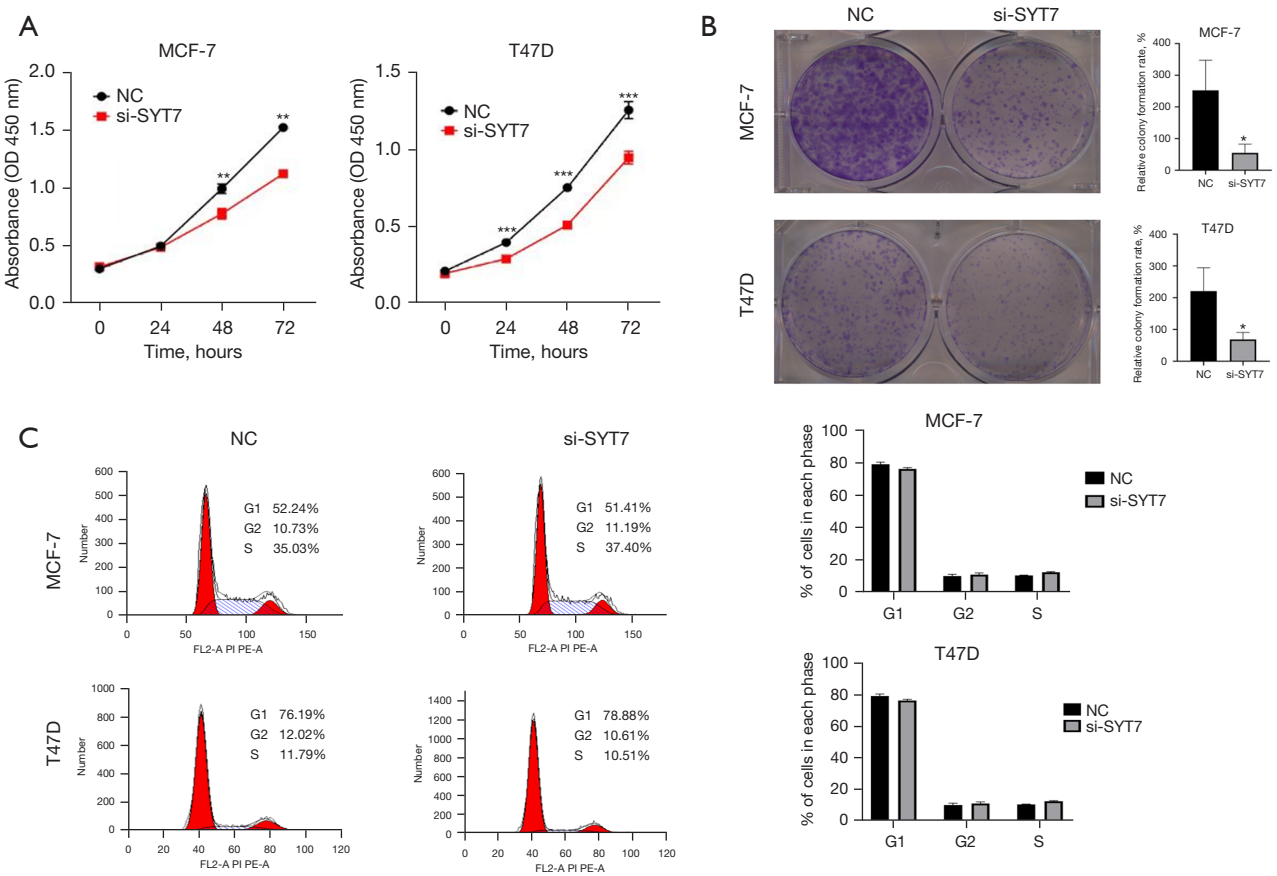

Figure 4 Knockdown of SYT7 inhibited the proliferation and colony formation of MCF-7 and T47D cells. (A) The CCK-8 assay was implemented to evaluate the activity of MCF-7 and T47D cells. (B) In order to assess the cell colony formation, a colony formation experiment was carried out in MCF-7 and T47D cells that were transfected with si-SYT7 (cells were stained with crystal violet staining solution). (C) To quantify the distribution, flow cytometry analysis was conducted. For all panels, *, P<0.05 (P=0.03); **, P<0.01; and ***, P<0.001 (P=0.008). OD, optical density; NC, negative control; SYT7, synaptotagmin 7; CCK-8, Cell Counting Kit-8.

proliferate and form colonies. Our findings in *Figure 4A*,*4B* illustrate that knockdown of SYT7 significantly impeded the proliferation activity and colony formation ability of breast cancer cells (*Figure 4A*,*4B*). Furthermore, we utilized flow cytometry to investigate the impact of SYT7 on the cell cycle of MCF-7 and T47D breast cancer cells. After 48 hours of si-SYT7 transfection, our results demonstrated that si-SYT7 affected the G1, G2, and S phases of the cell cycle compared to the control group. However, we observed no effect during the early stage, suggesting that si-SYT7 does not induce cell cycle arrest (*Figure 4C*).

Knockdown of SYT7 promotes the apoptosis of MCF-7 and T47D cells

In order to investigate the impact of SYT7 knockdown on apoptosis in breast cancer cells, researchers utilized Flow cytometry. The obtained data revealed a significant increase in breast cancer cell apoptosis following SYT7 knockdown (*Figure 5A*). To analyze the expression levels of various proteins apoptosis, such as caspase 3, cleaved-caspase 9, Bcl-2, Bcl-xl, cleaved-PARP, and Bax, Western blot analysis was conducted. The results demonstrated a noticeable elevation in the expression of cleaved-caspase 9, caspase 3, cleaved-PARP, and Bax, accompanied by a substantial reduction in the expression of Bcl-2 and Bcl-xl (*Figure 5B*).

Knockdown of SYT7 inhibits PI3K/AKT signaling pathway

According to previous research, the connection between the malignant growth of breast cancer and the PI3K/AKT

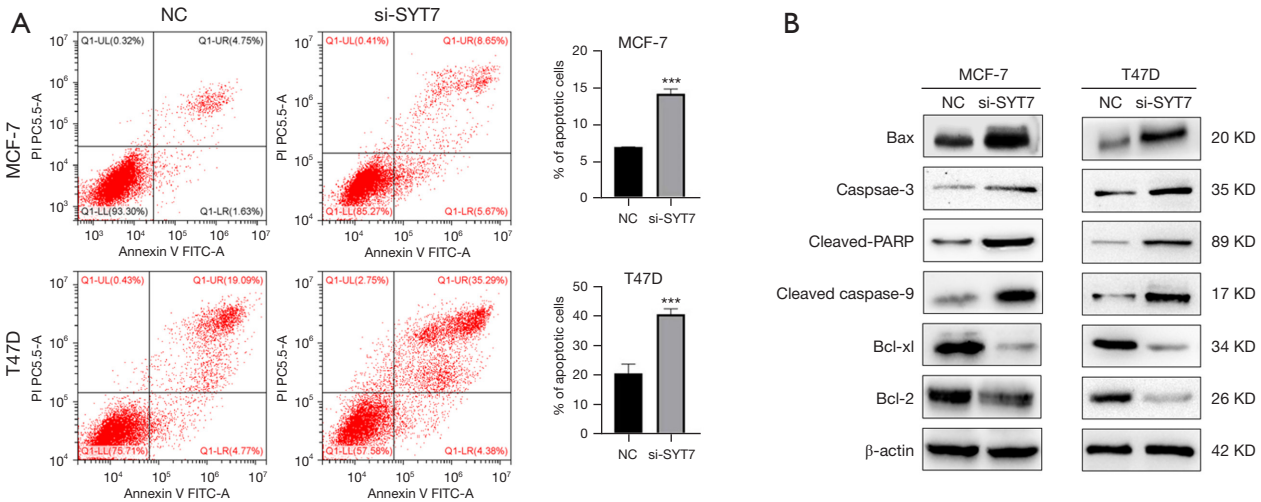

Figure 5 Knockdown of SYT7 promotes the apoptosis of MCF-7 and T47D cells. (A) The percentage of cells undergoing apoptosis was analyzed using flow cytometry in MCF-7 and T47D cells transfected with si-SYT7. (B) Additionally, western blot was employed to detect the expression of proteins associated with apoptosis. ***, P<0.001. NC, negative control; SYT7, synaptotagmin 7; FITC, fluorescein isothiocyanate.

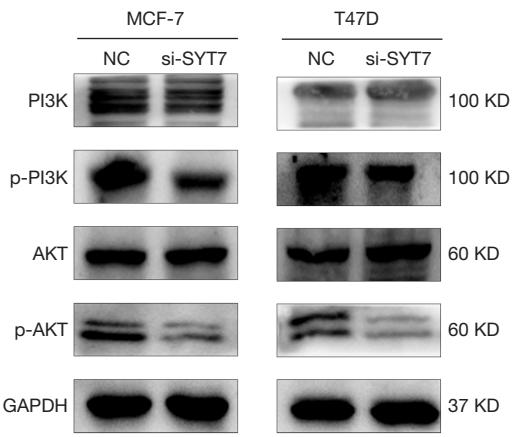

Figure 6 The expression of PI3K, p-PI3K, AKT and p-AKT were detected by western blot in MCF-7 and T47D cells. NC, negative control.

signaling pathway has been well demonstrated. Hence, our study aimed to examine whether SYT7 plays a role in the promotion of breast cancer cell proliferation and suppression of apoptosis via the PI3K/AKT signaling pathway. Following the knockdown of SYT7, there was a notable decrease in the expression levels of p-PI3K and p-AKT, implying that the inhibition of SYT7 can effectively impede the activation of the PI3K/AKT signaling pathway (*Figure 6*).

Discussion

SYT7, a transporter found in cell membranes, has a primary structure comprised of a transmembrane domain at its N-terminus and a Ca^{2+}-binding C2 domain (C2A and C2B) at its C-terminus. The main functions of SYT7 include facilitating the release of neurotransmitters in an asynchronous manner, aiding in the migration of trypanosomatous vertebrae and inflammatory cells, regulating glucagon, and promoting vesicle fusion. Several studies have previously demonstrated that SYT7 is up-regulated in various types of tumors, including gastric cancer (10), lung cancer (15), glioma (12), osteosarcoma (16), and colon cancer (11). Elevated levels of SYT7 expression in these tumors have been linked to an unfavorable prognosis. Our investigation on breast cancer unveiled an elevation in SYT7 expression in both breast cancer tissues and cells. Furthermore, a noteworthy association was observed between SYT7 expression and tumor size, as well as the expression levels of ER and PR in breast cancer patients. Additionally, an increased SYT7 expression, consistent with earlier research findings, signified an unfavorable prognosis for breast cancer patients. These findings propose that SYT7 might act as an oncogene, contributing to the development and advancement of breast cancer, and could potentially serve as a diagnostic indicator.

Previous studies have provided evidence indicating that SYT7 plays a role in promoting cancer in tumors by facilitating tumor cell growth, movement, invasion, and preventing programmed cell death. To validate the biological function of SYT7 in breast cancer, we utilized siRNA to silence SYT7 in MCF-7 and T47D cells. Our objective was to assess the impact of SYT7 on breast cancer development through various experiments, including CCK-8, colony formation assay, transwell assay. The results demonstrated that inhibition of SYT7 significantly suppressed the proliferation and colony formation ability of breast cancer cells, while promoting cell apoptosis. Additionally, we performed western blotting to analyze proteins associated with apoptosis. The data revealed an upregulation of cleaved-caspase 9, caspase 3, cleaved-PARP, and Bax expression levels, with a notable downregulation of Bcl-2 and Bcl-xl in breast cancer cells after knockdown of SYT7. These findings further confirm the role of SYT7 knockdown in inducing apoptosis in breast cancer cells.

Research has indicated that the PI3K/AKT pathway, which is responsible for regulating multiple cellular functions like cell growth, proliferation, protein synthesis, and tumorigenesis, plays a crucial role (17). Breast cancer studies have consistently shown that the PI3K/AKT pathway is very important and common signaling pathway in this type of cancer (18). This pathway serves as a vital intracellular signaling system that facilitates cell growth and survival (19). The overactivation of the PI3K/AKT pathway is associated with the development of ER^+ breast cancer and resistance to endocrine therapy (20-27). Previous studies have shown that inhibiting the PI3K/AKT pathway can trigger apoptosis in breast cancer cells. For example, Yang *et al.* demonstrated that using a specific inhibitor that targets the PI3K/AKT pathway induces caspase-3 and caspase-9 activation, thus promoting cell apoptosis (28). Our study aimed to explore the potential impact of SYT7 on breast cancer promotion. To achieve this, knockdown experiments were conducted on MCF-7 and T47D cells, specifically targeting SYT7. Interestingly, while the expression levels of PI3K and AKT remained unchanged, a noticeable decrease was observed in the levels of p-PI3K and p-AKT following SYT7 knockdown. So, our findings also suggest that SYT7 could inhibit cell signaling pathways, thus showing the effect of inhibiting tumors. Consequently, our findings suggest that SYT7, a potential oncogenic gene, could serve as a valuable target for breast cancer treatment.

Conclusions

In summary, the findings suggest that SYT7 is highly expressed in breast cancer and that its high expression is linked to clinical characteristics and prognosis. Inhibition of SYT7 through knockdown can suppress proliferation and promote apoptosis of breast cancer cells, making it a potential target for breast cancer diagnosis and treatment.

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Footnote

Reporting Checklist: The authors have completed the MDAR reporting checklist. Available at https://tcr.amegroups.com/article/view/10.21037/tcr-24-7/rc

Data Sharing Statement: Available at https://tcr.amegroups.com/article/view/10.21037/tcr-24-7/dss

Peer Review File: Available at https://tcr.amegroups.com/article/view/10.21037/tcr-24-7/prf

Conflicts of Interest: All authors have completed the ICMJE uniform disclosure form (available at https://tcr.amegroups.com/article/view/10.21037/tcr-24-7/coif). The authors have no conflicts of interest to declare.

Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013). The study was approved by the Biomedical Ethics Committee of the First Affiliated Hospital of Chongqing Medical University (No. 2019-208) and informed consent was taken from all the patients.

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