Introduction

Breast cancer (BC) is one of the most frequent cancers, which mostly occur in the females. The incidence rate is increasing, accompanied by the young age of BC patients in recent years (1, 2). Triple-negative breast cancer (TNBC) is a subtype of BC, which is featured by the absence of estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor-2 (HER2) (3). Despite of improvements in the screening, operation, and chemo-radiotherapy methods, the TNBC patient’s prognosis is still not optimistic (4, 5). Hence, it is necessary to explore novel potential therapeutic targets.

Non-coding RNAs (ncRNAs) mainly include long non-coding RNAs (lncRNAs) and microRNAs (miRNAs) (6, 7). In recent years, lncRNAs have been reported to act as important regulators in various biological processes of human cancers via various approaches, such as the regulation of transcription, translation, protein modification, and the formation of RNA-protein or protein-protein complexes (8). A large amount of evidence has suggested that lncRNAs act as tumor promoters or tumor suppressors in the TNBC development (9). In addition, many lncRNAs are identified as potential therapeutic targets for TNBC treatment (10). Even so, there are some lncRNAs underlying TNBC remain to be explored. In the current study, we mainly focused on the role of a novel lncRNA glucuronidase beta pseudogene 11 (GUSBP11) in the TNBC.

MicroRNAs (miRNAs) are crucial regulators in the TNBC development (11). For example, miR-29b-3p contributes to the TNBC progression through the TRAF3 regulating (12); miR-613 represses cell migration and invasion via inhibiting Daam1 in the TNBC (13). Besides, miRNAs can exert functions post-transcriptionally via degrading mRNA or inhibiting the translation via binding to the 3’ untranslated region (3’ UTR) of the targeted genes (14). The controller role of miR-579-3p in the melanoma progression has been revealed in a previous study (15), but we still don’t know whether it can function in the TNBC and its underlying mechanism remain to be unveiled. In this study, we uncovered the involvement of miR-579-3p in the GUSBP11-mediated TNBC progression.

Our research group focused on the role of sphingolipid transporter 2 (SPNS2) in the TNBC progression. We speculated that GUSBP11 inhibited TNBC cell malignancy via miR-579-3p/SPNS2 axis. Therefore, we analyzed the expression pattern of the genes in the TNBC cell lines and examined the related biological functions. Collectively, this study was aimed to investigate the impacts of the GUSBP11/miR-579-3p/SPNS2 axis in the TNBC progression.

Original Article

**GUSBP11 Inhibited The Progression of Triple Negative Breast Cancer via Targeting The miR-579-3p/SPNS2 Axis**

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**Abstract**

**Objective:** Growing evidences have exposed the important roles of long noncoding RNAs (lncRNAs) in the triple negative breast cancer (TNBC) inhibition. The function of glucuronidase beta pseudogene 11 (GUSBP11) in the TNBC occurrence remains obscure. To detect the function of GUSBP11 in TNBC progression and explore its downstream molecular mechanism.

**Materials and Methods:** In this experimental study, using quantitative reverse transcription real-time polymerase chain reaction (RT-qPCR), we measured the GUSBP11 expression in the TNBC cell lines. Gain-of-function assays, including colony formation, flow cytometry, and western blot were used to identify the probable effects of GUSBP11 overexpression on the malignant behaviors of TNBC cell lines. Moreover, mechanism assays, including RNA immunoprecipitation (RIP), RNA pull down and luciferase reporter assays were taken to measure the possible mechanism of GUSBP11 in the TNBC cell lines.

**Results:** GUSBP11 expressed at a low RNA level in the TNBC cell lines. Overexpression of GUSBP11 RNA expression inhibited the proliferation, migration, epithelial-to-mesenchymal transition (EMT) and stemness while elevated the apoptosis of the TNBC cell lines. GUSBP11 positively regulated the expression of sphingolipid transporter 2 (SPNS2) via acting as a competing endogenous RNA (ceRNA) of miR-579-3p, thereby supressing the development of TNBC cell lines.

**Conclusion:** GUSBP11 impedes TNBC progression via modulating the miR-579-3p/SPNS2 axis.

**Keywords:** GUSBP11, miR-579-3p, SPNS2, Triple-Negative Breast Cancer

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Materials and Methods

Cell culture

In this experimental study, human BC cell lines (MDA-MB-231, MDA-MB-436, MDA-MB-453, SKBR3, MCF-7, BT-474, AU565, T-47D, ZR-75-1) were all obtained from the American Type Culture Collection (ATCC, Manassas, VA, USA). Human BC cell lines (CAL-120, SUM190 and SUM1315) were obtained from COBIOER (Nanjing, China). The HEK293T cell line was cultured in the ATCC-formulated Eagle’s Minimum Essential Medium (EMEM, M0200, Sigma-Aldrich, St. Louis, MO, USA). MDA-MB-231, MDA-MB-436, MDA-MB-453 cell lines were cultured in the RPMI-1640 Medium (A4192301, Gibco, Rockville, MD, USA). The BT-474 cell line was grown in the Hybric Medium (ATCC46-X, ATCC, Manassas, VA, USA). AU565, T-47D, ZR-75-1 and SUM190 cell lines were grown in the Dulbecco’s Minimum Essential Medium (A4192101, Gibco, Rockville, MD, USA). The MCF-10A cell line was cultured in the McCoy’s 5a Medium (16600108, Thermo Fisher Scientific, Rockford, IL, USA). The SUM1315 cell line was cultured in the Dulbecco’s Minimum Essential Medium (A4192101, Gibco, Rockville, MD, USA). The BT-474 cell line was grown in the Hybric Medium (ATCC46-X, ATCC, Manassas, VA, USA). AU565, T-47D, ZR-75-1 and SUM190 cell lines were grown in the Dulbecco’s Minimum Essential Medium (A4192101, Gibco, Rockville, MD, USA). The SKBR3 cell line was grown in the McCoy’s 5a Medium (16600108, Thermo Fisher Scientific, Rockford, IL, USA). MCF-7 and CAL-120 cell lines were grown in the Dulbecco’s Minimum Essential Medium (A4192101, Gibco, Rockville, MD, USA). The BT-474 cell line was grown in the Hybric Medium (ATCC46-X, ATCC, Manassas, VA, USA). AU565, T-47D, ZR-75-1 and SUM190 cell lines were grown in the Dulbecco’s Minimum Essential Medium (A4192101, Gibco, Rockville, MD, USA). The SKBR3 cell line was grown in the McCoy’s 5a Medium (16600108, Thermo Fisher Scientific, Rockford, IL, USA). MCF-7 and CAL-120 cell lines were grown in the Dulbecco’s Minimum Essential Medium (A4192101, Gibco, Rockville, MD, USA). The BT-474 cell line was grown in the Hybric Medium (ATCC46-X, ATCC, Manassas, VA, USA). AU565, T-47D, ZR-75-1 and SUM190 cell lines were grown in the Dulbecco’s Minimum Essential Medium (A4192101, Gibco, Rockville, MD, USA).

Cell transfection

For overexpression, the full-length cDNA sequences of GUSBP11 were inserted into the pcDNA3.1 vectors (15042907, Sigma-Aldrich, St. Louis, MO, USA) to construct pcDNA3.1/GUSBP11 plasmids. Likewise, the whole length of YY1, p300 and HDAC2 was separately inserted into pcDNA3.1 vectors to generate their overexpression vectors. Empty pcDNA3.1 vector was used as the negative control (NC) for all overexpression vectors. Besides, miR-579-3p and NC mimics, the specific shRNAs to SPNS2 and nonspecific shRNAs (sh/NC) were purchased from GenePharma (Shanghai, China). Transfections were conducted using Lipofectamine 3000 (Invitrogen) and terminated after 48 hours. For rescue assays, we severally transfected pcDNA3.1, pcDNA3.1/GUSBP11, pcDNA3.1/GUSBP11+miR-579-3p mimics and pcDNA3.1/GUSBP11+sh/SPNS2#1 into MDA-MB-231 and MDA-MB-453 cell lines.

Quantitative reverse transcription real-time polymerase chain reaction

Total RNA was extracted from the cell lines using TRIzol Reagent (15596026, Thermo Fisher Scientific, Rockford, IL, USA). Next, PrimeScript RT master mix (RR036Q, Takara, Japan) was employed for reverse transcription of RNA. Then, SYBR Premix Ex TaqTM II (RR0155, Applied Biosystems, Foster city, CA, USA) was utilized to examine the gene expression based on 2−ΔΔCt method. GAPDH or U6 was used as the internal reference. Samples were assayed in triplicate and results were obtained from three independent experiments.

Colony formation assay

Transfected TNBC cell lines (500 cells per well) were planted into 6-well plates. After 12 days, the culture medium was discarded and the cell lines were fixed with a Methanol solution (67-56-1, Bojing Chemical Co., Ltd, Shanghai, China) for 15 minutes, and stained by 0.5% crystal violet (V5265, Sigma-Aldrich, St. Louis, MO, USA) for 10 minutes at room temperature. The number of colonies was manually counted. Samples were assayed in triplicate and results were obtained from three independent experiments.

5-Ethynyl-2'-deoxyuridine

5-Ethynyl-2'-deoxyuridine (EdU) staining was performed using a BeyoClick™ Cell Proliferation Kit (C0075L, Beyotime, Guangzhou, China). Transfected TNBC cell lines were added with EdU and incubated for 2 hours at room temperature. After washing, cell lines were fixed with 4% paraformaldehyde. The nucleus was stained by DAPI (D9542, Sigma-Aldrich, St. Louis, MO, USA) and images were captured via an inverted microscope (Olympus, Japan). Samples were assayed in triplicate and results were obtained from three independent experiments.

Terminal-deoxynucleotidyl Transferase Mediated Nick End labeling (TUNEL)

TUNEL reagent (12156792910, Roche, Basel, Switzerland) was commercially acquired for TUNEL experiment. Transfected cell lines (1×10⁵) were planted into the 96-well plates, fixed by 4% paraformaldehyde, permeabilized with 0.1% Triton-X100, and then treated with TUNEL kit (Merck KGaA, Darmstadt, Germany) for 1 hour. Finally, cell nucleus was subjected to DAPI (D9542, Sigma-Aldrich, St. Louis, MO, USA) and images were captured using an inverted microscope (Olympus, Japan). Samples were assayed in triplicate and results were obtained from three independent experiments.

Flow cytometry analysis

Transfected cell lines were collected and placed into the 6-well plates. Flow cytometer was used following the instruction (17-344, Sigma-Aldrich, St. Louis, MO, USA), and the Annexin V-FITC/PI double staining kit...
(APOAF, Sigma-Aldrich, St. Louis, MO, USA) was purchased from Invitrogen. After staining for 15 minutes, cell lines were reaped for flow cytometry. Samples were assayed in triplicate and results were obtained from three independent experiments.

Transwell assay

Cell lines (5 × 10⁴) were seeded into the upper chamber of the insert (pore size 8 μm; 3428, Corning, NY, USA) and incubated in the serum-free DMEM medium. The DMEM medium containing 10% FBS was added to the lower chamber. After incubation for 24 hours in the 5% CO₂ at 37°C, the upper membrane cells were wiped, and the migrated cells through the membrane were fixed with 4% paraformaldehyde (E672002, Sangon Biotech, Shanghai, China) and stained with 0.1% crystal violet (V5265, Sigma-Aldrich, St. Louis, MO, USA). The images were observed via an inverted microscope (DMi1, Leica, Wetzlar, Germany). Samples were assayed in triplicate and results were obtained from three independent experiments.

Sphere formation assay

Cell lines were cultured in the serum-free DMEM medium treated with insulin (12643, Sigma-Aldrich, St. Louis, MO, USA), 20 ng/mL human recombinant epidermal growth factor (EGF, GF144, Sigma-Aldrich, St. Louis, MO, USA) and 10 ng/mL basic fibroblast growth factor (bFGF, 2255, Sigma-Aldrich, St. Louis, MO, USA). After 14 days of culture, the sphere formation was observed using a microscope (DMi1, Leica, Wetzlar, Germany). Samples were assayed in triplicate and results were obtained from three independent experiments.

ChIP assay

Following the protocol, an EZ ChIP Chromatin Immunoprecipitation kit (17-295; Millipore, Billerica, MA, USA) was applied to ChIP assay. Chromatin was cross-linked and sonicated to 200-1000-bp fragments, followed by immunoprecipitation with anti-YY1 or anti-IgG antibody (401455-2ML-M, Millipore, Billerica, MA, USA) which was selected as the NC. RT-qPCR was eventually carried out for enrichment detection. Samples were assayed in triplicate and results were obtained from three independent experiments.

RNA immunoprecipitation

RNA immunoprecipitation (RIP) assay was implemented via an RNA-binding protein immunoprecipitation kit (17-704, Sigma-Aldrich, St. Louis, MO, USA). Transfected cell lines were lysed, and then hatched with RIP buffer containing magnetic beads conjugated with anti-Ago2 antibody. After being washed and purified, the immunoprecipitated RNA was analyzed via RT-qPCR. Samples were assayed in triplicate and results were obtained from three independent experiments.

RNA pull down assay

GUSBP11 biotin probe (Ribobio, Guangzhou, China) or wild-type or mutant-type of miR-579-3p were transcribed into the cell lines. Transfected cell lysates were hatched with Dynabeads M-280 Streptavidin (11206D, Thermo Fisher Scientific, Rockford, IL, USA) overnight at 4°C according to the manufacturer’s requirements. Then, the beads were washed and eluted. RNAs were extracted by TRIzol reagent (15596026, Thermo Fisher Scientific, Rockford, IL, USA) and evaluated by RT-qPCR. Samples were assayed in triplicate and results were obtained from three independent experiments.

Luciferase reporter assays

The sequence of GUSBP11 promoter was sub-cloned into pGL3 vector (Promega, Madison, WI, USA). And, overexpression plasmids were co-transfected into the cell lines to evaluate the activity of GUSBP11 transcription.

The GUSBP11 fragment or SPNS2 3'UTR fragment covering the miR-579-3p binding site was inserted into the pmirGLO vector (Promega, Madison, WI, USA). And then, the cell lines were severally co-transfected with luciferase reporter vectors containing GUSBP11-Wt/Mut or SPNS2 3'UTR-WT/Mut and miR-579-3p mimics/NC mimics using Lipofectamine 3000 (L3000075, Invitrogen, Carlsbad, CA, USA). The Firefly and Renilla luciferase activity was measured at 48 hours after transfection with a dual-luciferase reporter assay kit (E1910, Promega, Madison, WI, USA). Samples were assayed in triplicate and results were obtained from three independent experiments.
independent experiments.

Statistical analysis

All experimental data were shown as mean ± standard deviation (SD) of three independent experiments and analyzed by GraphPad Prism 5.0 (San Diego, CA, USA). The significant difference of the groups was assessed using Student’s t test and one-way analysis of variance (ANOVA). Also, P<0.05 indicated statistically significant data.

Results

Overexpression of GUSBPII in the RNA level suppresses the TNBC cell growth

Searching online database (http://gepia2.cancer-pku.cn), IncRNA GUSBPII was determined to be down-regulated in all types of BC tissues in comparison with the normal tissues (Fig.1A-E). To further explore the potential role of GUSBPII in the specific cancer types, we evaluated its RNA level in all subtypes of BC cell lines. In comparison with the human normal mammary cell line (MCF-10A), GUSBPII expression was only obvious down-regulated in the TNBC cell lines, including MDA-MB-436, MDA-MB-453 and MDA-MB-231 (Fig.1F), suggesting that GUSBPII down-regulation might be correlated with the TNBC progression. Next, we designed gain-of-function assays to identify the functional role of GUSBPII overexpression in the TNBC. At first, pcDNA3.1/GUSBPII was transfected into the MDA-MB-231 and MDA-MB-453 cell lines which presented the lowest RNA level of GUSBPII (Fig.1G). It was observed in the colony formation experiments that the number of colonies in the TNBC cell lines was decreased after the overexpression of GUSBPII (Fig.1H). Consistently, the EdU positive stained cells were lessened up to 30% when GUSBPII was up-regulated (Fig.1I). On the contrary, a rise of about 7% in the apoptosis rate was observed in MDA-MB-231 and MDA-MB-453 cell lines due to GUSBPII up-regulation (Fig.1J, K). All these data suggested that GUSBPII was down-regulated in the TNBC cells and its overexpression impeded cell growth.

GUSBPII up-regulation represses invasion, migration and stemness of the TNBC cell lines

We continued to detect the effects of GUSBPII on other biological properties of the TNBC cell lines. Through Transwell assays, we found that the invasive and migratory abilities of TNBC cell lines were repressed by GUSBPII elevation (Fig.2A, B). Consistently, we observed that the overexpression of GUSBPII led to an increase in the protein expression of E-cadherin while a decrease in the protein expression of MMP2, MMP7, N-cadherin and Vimentin, which indicated that GUSBPII up-regulation repressed the epithelial-mesenchymal transition, namely epithelial-to-mesenchymal transition (EMT) process in the TNBC cell lines (Fig.2C). Up-regulation of GUSBPII significantly suppressed sphere formation in the MDA-MB-453 and MDA-MB-231 cell lines, in different aspects including number and size (Fig.2D). Moreover, we also examined the RNA as well as protein levels of stemness markers using RT-qPCR and western blot. It was uncovered that the levels of NANOG, OCT4 and SOX2 were all decreased under GUSBPII overexpression (Fig.2E, F).
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**Fig. 2:** GUSBP11 up-regulation represses cell migration, EMT and stemness in the TNBC cell lines. 

- **A, B.** Transwell assays were performed to analyze the migration and invasion of the TNBC cell lines after GUSBP11 overexpression (scale bar: 50 μm). 
- **C.** Protein levels of EMT markers as well as cell invasion-related factors were tested in the TNBC cell lines after GUSBP11 overexpression. 
- **D.** The sphere formation assay was taken to measure the effect of GUSBP11 elevation on the stemness of the TNBC cell lines (scale bar: 100 μm). 

**E, F.** The RNA level and protein level of stemness markers after GUSBP11 overexpression. Three independent experiments were conducted (n=3). EMT; Epithelial-to-mesenchymal transition, TNBC; Triple negative breast cancer, and **; P<0.01.

**YY1/p300/HDAC2 complex induces transcription inhibition of GUSBP11 and suppresses its expression**

To explore the upstream molecular mechanism of GUSBP11 RNA in the TNBC, we used UCSC, an online database (http://genome.ucsc.edu/), and found that YY1 and p300 are two transcription factors that acted on the GUSBP11 promoter. Through further screening in the JASPAR (http://jaspar.genereg.net/), we obtained three binding sequences of YY1 in the GUSBP11 promoter (Fig. 3A). Therefore, we constructed these three mutated sequences in order and then, verified the specific binding sites through luciferase reporter assay. Data revealed that YY1 might bind to the site 2 of GUSBP11 promoter, where the luciferase activity of the HEK293T cell line showed an enhancement in the Site2-MUT group (Fig. 3B). Through ChIP assay, it was verified that YY1 was enriched in the GUSBP11 promoter in contrast to the control IgG group (Fig. 3C).

It has been reported that the YY1, p300 and HDAC2 can form a complex that regulates the development of colorectal cancer (16). Therefore, we conducted ChIP assay to verify the interaction of YY1/p300/HDAC2 axis and the GUSBP11 promoter in the TNBC cell lines. Intriguingly, we uncovered that the enrichment of GUSBP11 RNA in the immunoprecipitates conjugated to anti-YY1 was higher after overexpression of those three factors (Fig. 3D). Similarly, the result of luciferase reporter assay in the HEK293T cell line showed that the activity of GUSBP11 promoter was decreased a lot after overexpression of YY1, HDAC2 and p300, whereas this decreased tendency was more obvious when they were all overexpressed (Fig. 3E). Finally, the expression level of GUSBP11 was found to be reduced after individually overexpression of YY1, p300 or HDAC2, while this tendency of GUSBP11 expression was more evident after the co-overexpression of them (Fig. 3F).
**GUSBP11 positively regulates SPNS2 expression in the TNBC cell lines**

In this part, we tried to verify the interaction between GUSBP11 and SPNS2. According to GEPIA 2 database, we discovered that SPNS2 expression was markedly declined in the TNBC tissues in contrast to normal tissues (Fig.4A). Meanwhile, a positive correlation between the GUSBP11 expression and the SPNS2 expression was observed (Fig.4B). Applying RT-qPCR, it was revealed that SPNS2 was down-regulated in the TNBC cell lines in comparison with the MCF-10A cell line (Fig.4C). Afterwards, we explored whether GUSBP11 and SPNS2 could regulate each other. We found that SPNS2 expression was up-regulated in the MDA-MB-231 and MDA-MB-453 cell lines transfected with pcDNA3.1/GUSBP11 at both RNA and protein levels (Fig.4D). However, SPNS2 overexpression did not affect the RNA expression of GUSBP11 (Fig.4E, Fig.S1A, See Supplementary Online Information at www.celljournal.org). To further probe the potential mechanism of GUSBP11 on the regulating SPNS2 expression in the TNBC cell lines, we performed subcellular fractionation and FISH assays to determine the subcellular localization of GUSBP11 in the TNBC cell lines. The results indicated that GUSBP11 was majorly distributed in the cytoplasm, implying that GUSBP11 regulated SPNS2 at post-transcriptional level (17, 18, Fig.4F, G). To strengthen our hypothesis, we conducted luciferase reporter assay and determined that GUSBP11 had no effect on the activity of the SPNS2 promoter in RNA level (Fig.4H). As competitive endogenous RNA (ceRNA) mechanism is known as a common post-transcriptional regulatory method, we decided to explore whether GUSBP11 may modulate the SPNS2 expression through acting as a ceRNA to target certain miRNA in the TNBC cell lines. According to the result of RIP assays, both GUSBP11 and SPNS2 were highly enriched in the anti-Ago2 groups (Fig.4I), which supported the ceRNA model. Furthermore, a series of functional assays were taken to verify the effects of SPNS2 overexpression in the TNBC cell lines, and results showed that increased SPNS2 expression led to suppress cell proliferation, along with attenuated migration, invasion and EMT in the TNBC cell lines (Fig.S1B-J, See Supplementary Online Information at www.celljournal.org).

**GUSBP11 positively regulates the SPNS2 expression via interacting with miR-579-3p**

We searched starBase (http://starbase.sysu.edu.cn) website to look for possible miRNAs combined with both GUSBP11 and SPNS2. As illustrated in the Figure 5A, two miRNAs (miR-579-3p and miR-664b-3p) were observed at the intersection. Through RNA pull down assays, it was shown that miR-579-3p was abundantly enriched in the GUSBP11 biotin probe groups, while the other candidate miR-664b-3p showed no obvious change (Fig.5B). Therefore, miR-579-3p was chosen for further analyses. RIP data validated that GUSBP11, miR-579-3p and SPNS2 were effectively abundant in the anti-Ago2 groups, indicating that these three RNAs co-existed in the RISCs (Fig.5C). Besides, we uncovered that the enrichment of GUSBP11 and SPNS2 was enhanced in the wild type of miR-579-3p group, while no obvious change was seen in the control group or the mutant group (Fig.5D). The respective binding sites of GUSBP11 and SPNS2 on the miR-579-3p were predicted via StarBase website (Fig.5E). We overexpressed miR-579-3p expression via the transfection of miR-579-3p mimics in the TNBC cell lines (Fig.5F), and it was then manifested from luciferase reporter assays that miR-579-3p mimics declined the luciferase activity of GUSBP11-WT and SPNS2 3’UTR-WT groups, while barely affected the GUSBP11-Mut and SPNS2 3’UTR-Mut groups (Fig.5G).

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**Fig.4: GUSBP11 acts as a ceRNA to positively regulate SPNS2 expression in the TNBC cell lines.**

A. Box plot from GEPIA 2 database indicated the expression of SPNS2 in the 135 tumor TNBC tissues and 291 normal tissues. B. The correlation between GUSBP11 and SPNS2 expression was presented via GEPIA 2 database. C. The mRNA level of SPNS2 in the TNBC cell lines MDA-MB-231, MDA-MB-436 and MDA-MB-453 in comparison with the MCF-10A cell line. D. SPNS2 expression at both RNA and protein levels in the TNBC cell lines transfected with pcDNA3.1/GUSBP11. E. The GUSBP11 RNA level in the TNBC cell lines with SPNS2 overexpression. F. G. The cellular location of GUSBP11 in the TNBC cell lines was determined by subcellular fractionation and FISH experiments (scale bar: 10 μm). H. The luciferase activity of SPNS2 promoter in the GUSBP11-overexpressed TNBC cell lines. I. The enrichment of GUSBP11 and SPNS2 in the Anti-Ago2 groups in contrast to the control IgG group was measured by RIP assays. Three independent experiments were conducted (n=3). TNBC, Triple negative breast cancer; *p<0.05, and **p<0.01.
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GUSBP11 regulates SPNS2 expression via interacting with the miR-579-3p in the TNBC cell lines. A. Potential miRNAs combined with the GUSBP11 and SPNS2 were predicted through starBase. B. The abundance of miR-579-3p and miR-664b-3p in the GUSBP11 biotin probe groups was measured by RNA pull down assays. C. The enrichment of GUSBP11, miR-579-3p and SPNS2 in the Anti-Ago2 groups was examined via RIP assays. D. The enrichment of GUSBP11 and SPNS2 in the bio-miR-579-3p-WT or bio-miR-579-3p-Mut groups was measured by RNA pull down assays. E. Respective binding sites of GUSBP11 and SPNS2 on the miR-579-3p were predicted via starBase website. F. MiR-579-3p expression in the TNBC cell lines transfected with miR-579-3p mimics. G. The luciferase activity of GUSBP11-WT/Mut or SPNS2 3’UTR-WT/Mut in the TNBC cell lines when miR-579-3p was up-regulated. Three independent experiments were conducted (n=3). TNBC; Triple negative breast cancer and **; P<0.01.

GUSBP11 represses cell migration, EMT and stemness in the TNBC cell lines via interacting with miR-579-3p to increase SPNS2 expression

The impacts of the GUSBP11/miR-579-3p/SPNS2 axis on the cell migration, EMT and stemness were also determined. In Transwell assays, we found that the overexpression of miR-579-3p or the silencing of SPNS2 could counteract the repressive cell migration and invasion in the TNBC caused by GUSBP11 up-regulation (Fig.S2A, B, See Supplementary Online Information at www.celljournal.org). Meanwhile, the repressed EMT caused by GUSBP11 overexpression was offset after the co-transfection of miR-579-3p mimics or sh/SPNS2#1 (Fig.S2C, See Supplementary Online Information at www.celljournal.org). Additionally, miR-579-3p elevation or SPNS2 deletion could restore the reduced number of spheres that was mediated by the GUSBP11 up-regulation (Fig.S2D, See Supplementary Online Information at www.celljournal.org). Meanwhile, the levels of stemness markers reduced by GUSBP11 silencing were recovered after overexpression of miR-579-3p or knockdown of SPNS2 (Fig.S2E, F, See Supplementary Online Information at www.celljournal.org).

Discussion

Recently, emerging evidences have shown that lncRNAs
are implicated in the development of TNBC (19). Thus, a better understanding of lncRNAs might contribute to effective treatment of the TNBC patients. According to recent studies, GUSBP11 has been registered to be closely linked to gastric cancer (20) and neck squamous cell carcinoma (21). Nonetheless, the function of GUSBP11 in the TNBC occurrence remains largely obscure. In our research, we discovered that GUSBP11 was down-regulated in the TNBC cell lines. Overexpression of GUSBP11 obviously inhibited cell growth, migration, EMT and stemness in the TNBC cell lines. All these data demonstrated that GUSBP11 exerted anti-oncogenic functions on the TNBC progression.

Transcriptional regulation is a mechanism that can regulate RNA expression. Previous studies have reported that lncRNAs can be activated by their upstream transcription factors and thus up-regulating lncRNAs in the human cancers (22, 23). Additionally, lncRNAs can be down-regulated by their upstream transcription suppressors (24). Here, we also investigated the upstream mechanism of GUSBP11 in the TNBC cell lines. YY1/p300/HDAC2 complex has been reported to be efficient in the TNBC cell lines. YY1/p300/HDAC2 complex affinity to its promoter region.

Competitive endogenous RNA (ceRNA) mechanism is known as a common post-transcriptional regulatory method and lncRNAs have been extensively reported to affect cancer development via ceRNA model (26, 27). Accumulating evidence have pointed that lncRNAs can compete for miRNA response elements (MREs) with the driver genes to be involved in cancer development by acting as a ceRNA to interact with miRNA (28). Our study also demonstrated that GUSBP11 functioned as a ceRNA to positively regulate SPNS2 expression in the TNBC cell lines. As reported previously, SPNS2 enhances proliferation, migration and invasion colorectal cancer cell line via controlling S1P/S1PR1/3 axis and Akt and ERK pathway (29). SPNS2 plays crucial roles in repressing the migratory ability in the non-small cell lung cancer cell line (30). However, we found that SPNS2 presented a low RNA level in the TNBC cell lines, and it was further validated that overexpression of SPNS2 significantly suppressed the malignant cell behaviors in the TNBC. As known, miRNA is a key part of ceRNA mechanism and numerous miRNAs exert important roles in the TNBC progression (31). MiR-221/222 enhances the Wnt/β-catenin signaling to facilitate TNBC aggressiveness (32). MiR-211-5p inhibits tumor cell growth and metastasis in the TNBC cell lines as well as the TNBC xenograft model via targeting SETBP1 (33). In this study, we found that miR-579-3p was a common miRNA combined with GUSBP11 and SPNS2. It has been documented that miR-579-3p is down-regulated in the squamous cell lung carcinoma cell line, while its overexpression represses this progression (34). Moreover, miR-579-3p is related to melanoma progression and resistance to target treatments (15). In our study, we confirmed that GUSBP11 inhibited the progression of TNBC via targeting the miR-579-3p/SPNS2 axis.

However, due to the limited time and materials, there still existed several limitations in this study which required for further verification. Also, clinical data should be complemented to enrich the significance of our current study. We will make further clinical investigation in our future research.

Conclusion

GUSBP11 restrains cell proliferation and promotes cell apoptosis in the TNBC cell lines via sponging miR-579-3p to elevate SPNS2 expression.

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Authors’ Contribution

G.W.: Participated in study design, data collection and evaluation, drafting and statistical analysis. P.S.: Contributed to all experimental work, data and statistical analysis, and interpretation of data. C.Q.: Drafted the manuscript. All authors have read and approved the manuscript.

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