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Research Article

Up-regulation of long non-coding RNA SNHG20 promotes ovarian cancer progression via Wnt/β-catenin signaling

Shanyang He[1,*], Yunhe Zhao[1,*], Xiaoping Wang[2], Yalan Deng[1], Zhiyong Wan[1], Shuzhong Yao[1] and Hongwei Shen[1]

[1]Department of Obstetrics and Gynecology, The First Affiliated Hospital, Sun Yat-sen University, Guangzhou, P.R. China; [2]Department of Organ Transplantation, The First Affiliated Hospital, Sun Yat-sen University, Guangzhou, P.R. China

Correspondence: Shanyang He (hsy5g777@sina.com) and Hongwei Shen (shenhw@mail.sysu.edu.cn)

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Long non-coding RNA small nucleolar RNA host gene 20 (SNHG20) has been demonstrated to play crucial regulatory roles in many types of cancer. However, the biological function of long ncRNA (lncRNA) SNHG20 in ovarian cancer is still unclear. In the present study, we found that lncRNA SNHG20 was significantly increased in ovarian cancer. In addition, lncRNA SNHG20 knockdown suppressed the ovarian cancer progression, whereas overexpression of SNHG20 showed the opposite effects. Moreover, our results also revealed that lncRNA SNHG20 knockdown inhibited Wnt/β-catenin signaling activity by suppressing β-catenin expression and reversing the downstream target gene expression. Taken together, lncRNA SNHG20 plays an pivotal role in ovarian cancer progression by regulating Wnt/β-catenin signaling.

Introduction

Ovarian cancer is the sixth most frequently diagnosed cancer amongst women worldwide, the second most common gynecologic malignancy in females, and the most fatal tumor in female reproductive system [1]. The etiology of ovarian cancers involves both genetic and epigenetic alterations, although the underlying mechanisms are not well understood [2,3]. Despite advances in the detection and treatment of ovarian cancer, it remains the fifth leading cause of cancer deaths in women [4]. Ovarian cancer is typically diagnosed at a late stage, when the tumor has spread beyond the pelvic region into the peritoneal cavity, making complete surgical removal extremely difficult. Thus, it is urgent to identify the functional molecules involving in the progression of ovarian cancer.

Long ncRNAs (lncRNAs) are one type of ncRNAs whose transcripts are longer than 200 nts and have no protein-coding capacity [5]. In recent years, many studies have demonstrated that lncRNAs play crucial roles in human diseases and various cancers [6-8]. In particular, several lncRNAs have elicited the interest of scientists and clinicians because of their specific roles in ovarian cancer [9-11]. They were shown to be associated with various biological activities in ovarian cancer, including cell growth, metastasis, cell senescence, cell apoptosis, and multidrug resistance. All these studies indicate that lncRNAs may play critical roles in the development and progression of ovarian cancer. However, as all we know, the involvement of lncRNAs in ovarian cancer and prognosis is just starting to be investigated. Small nucleolar RNA host gene 20 (SNHG20) localized at 17q25.2 is originally identified in hepatocellular carcinoma (HCC) and suggested to be overexpressed in two HCC cohorts and TGCA dataset [12]. However, its potential prognostic value and biological function in ovarian cancer have not yet been explored.

In the present study, our results revealed that lncRNA SNHG20 was significantly increased in ovarian cancer tissues compared with non-tumorous adjacent tissues. Loss- and gain-of-function assays indicated

*These authors contributed equally to this work.

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that SNHG20 modulated the growth, apoptosis, and colony formation of several ovarian cancer cells. Further investigation suggested that SNHG20 suppression attenuated the activation of Wnt/β-catenin signaling in ovarian cancer cells. The present study might provide a potential target for the diagnosis and treatment of ovarian cancer.

Materials and methods

Clinical samples

From 2014 to 2016, 30 ovarian cancer patients, who received surgical resection at the First Affiliated Hospital of Sun Yat-sen University, were recruited. Informed consent was obtained from every patient before the surgery. Lung cancer tissue was collected immediately after resection and was stored in liquid nitrogen before further use.

Cell culture

Normal human ovarian surface epithelial cell line (HOSE) and ovarian cancer cell lines (SKOV3, OVCA429, OVCA433 and OVCAR3) were purchased from ATCC (American Type Culture Collection). All these cells were maintained in RPMI-1640 medium supplemented with 1% antibiotics (100 units/ml penicillin and 100 μg/ml streptomycin sulphate) and 10% FBS (HyClone, Logan, UT, U.S.A.). All cell lines were cultured at 37°C with a humidified atmosphere of 5% CO_2 in incubator. All cell lines have been tested and authenticated by DNA (short tandem repeat genotyping) profiling before use.

MTT assays

Ovarian cancer cells or normal human ovarian surface epithelial cells were seeded in 96-well plates (10000 cells per well) at 37°C in an incubator containing 5% CO_2. Cells were transfected with 10 nM siRNA mimics or control siRNA (siNC). The sequences of siRNAs (1#si-SNHG20, 5′-GCCUAGGAUCAUCCAGGUUTT-3′; 2#si-SNHG20, 5′-UAUAGCCAUACACAACAGGTT3′, 3#si-SNHG20, 5′-GCCACUCACAAGAGUGUAUTT-3′) and siNC were chemically synthesized. Cell viability was tested by using MTT (Sigma) assay at 0, 24, 48, 72, and 96 h after treatment. Briefly, cells were incubated with MTT at a final concentration of 0.5 mg/ml for 4 h. The supernatant was discarded, and the precipitated formazan was dissolved in DMSO. Absorbance was measured at 490 nm with microplate reader (Molecular Devices, i3). The sequences of siRNAs were listed as follows: 1#si-SNHG20, 5′-GCCUAGGAUCAUCCAGGUUTT-3′; 2#si-SNHG20, 5′-UAUAGCCAUACACAACAGGTT3′, 3#si-SNHG20, 5′-GCCACUCACAAGAGUGUAUTT-3′.

Flow cytometry

Cells were transfected with SNHG20 siRNAs and siNC for 48 h and then flow cytometry analysis were performed for evaluating the rate of apoptotic ovarian cancer cells. Cell apoptosis was analyzed using flow cytometry after staining with propidium iodide (PI) and Annexin V-FITC (BD Bioscience, CA, U.S.A.). Cells were transfected with siNC or si-SNHG20-1 in six-well plates. Cell apoptosis was then analyzed after 48-h transfection. Cell apoptosis assays were conducted in triplicate.

Colony formation assays

The SNHG20 knockdown ovarian cancer cells or SNHG20 overexpressing HOSE cells were plated into six-well plates (5000 cells/well) and incubated in DMEM with 10% FBS at 37°C. Two weeks later, cells were washed with PBS, fixed in methanol for 30 min, and stained with 1% Crystal Violet dye, and the number of colonies counted. Experiments were repeated three times, and values were expressed as mean and S.D.

Western blot

Ovarian cancer cell lysates were prepared with RIPA lysis buffer (Beyotime, China) containing protease inhibitor cocktail (Roche). Protein samples were loaded for SDS/PAGE and transferred on to a nitrocellulose membrane. After a blockage with 5% fat-free milk, the membrane was probed with primary anti-β-catenin (dilution 1:3000, Santa Cruz Biotechnology), anti-cyclin D1 (dilution 1:1000, Santa Cruz Biotechnology), anti-cmyc (dilution 1:3000, Santa Cruz Biotechnology), anti-p-GSK-3b (dilution 1:1000, Santa Cruz Biotechnology), anti-GSK-3b (dilution 1:2000, Santa Cruz Biotechnology) and anti-GAPDH (dilution 1:5000, Santa Cruz Biotechnology) antibody. After washing, the membrane was incubated with horseradish peroxidase conjugated (HRP) secondary antibody (1:10000, Santa Cruz Biotechnology) for 1 h. The signal was visualized using the ECL detection system (Thermo Fisher, U.S.A.) and quantitated by densitometry using Quantity One software (Bio–Rad, Hercules, CA, U.S.A.).

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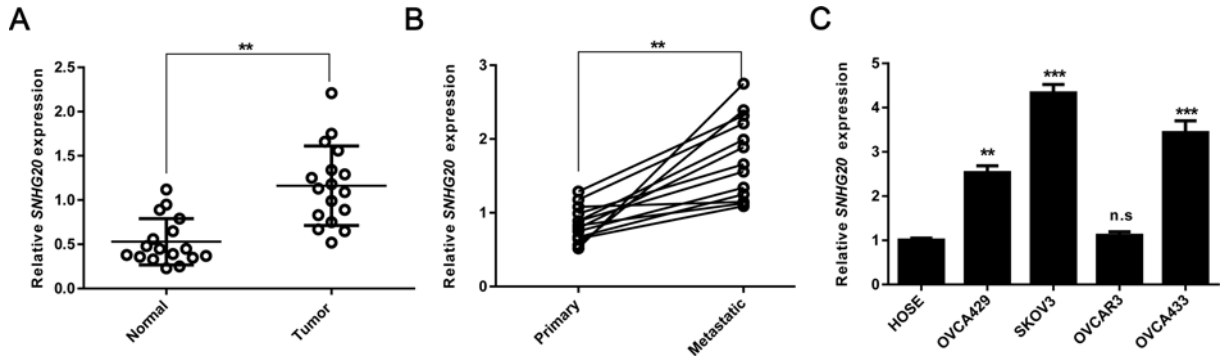

Figure 1. LncRNA SNHG20 expression was increased in ovarian cancer

(**A**) The expression of SNHG20 in 17 ovarian tumor samples and paired adjacent non-tumorous normal tissues was examined by q-PCR. (**B**) The expression in 13 metastatic ovarian tumor samples and paired primary tumor samples was also examined by q-PCR. (**C**) The expression of SNHG20 in HOSE and ovarian cancer cells was determined by q-PCR. qRT-PCR results were normalized by β-actin. Data represent the mean ± S.E.M. from three independent experiments; ***$P<0.001$; **$P<0.01$.

q-PCR analysis

Total RNA was extracted from tissues or cultured cells with TRIzol reagents (Invitrogen, Carlsbad, CA) according to the manufacturer's guide. The total RNA was reverse transcribed into first-strand cDNA using the SuperScript III® (Invitrogen) according to the manufacturer's guide. q-PCR was performed on the SYBR Premix ExTaq kit (TaKaRa) on ABIPRISM 7000 Fluorescent Quantitative PCR System (Applied Biosystems, FosterCity, CA, U.S.A.) according to the instructions. Results were normalized to GAPDH expression levels. The PCR primers were as follows: SNHG20 primers forward: 5′-ATGGCTATAAATAGATACACGC-3′, reverse: 5′-GGTACAAACAGGGAGGGA-3′; E-cadherin primers forward: 5′-TGTAGTTACGTATTTATTTTTAGTGGCGTC-3′, reverse:5′-CGAATACGATCGAATCGAACCG-3′; Cyclin D1 primers forward:5′-GAGACCATCCCCCTGACGGC-3′, reverse: 5′-TCTTCCTCCTCCTCGGCGGC-3′; β-catenin primers forward: 5′-TGCAGTTCG CCTTCACTATG-3′, reverse: 5′-ACTAGTCGTGGAATG GCACC-3′; c-myc primers forward: 5′-GCCCAGTGAGGATATCTGGA-3′, reverse: 5′-ATCGCAGATGAAGCTCTGGT-3′; GAPDH primers forward: 5′-CGCTCTCTGCTCCTCCTGTTC-3′, reverse: 5′-ATCCGTTGACTCCGACCTTCAC-3′. All primers were obtained from Invitrogen, Shanghai, China. All qRT-PCR reactions were performed in triplicate. Relative quantitation of tested gene expression was calculated and normalized by the $2^{-\Delta\Delta C}{}_{t}$ method.

Xenograft tumor model

Six- to eight-week BALB/c (nu/nu) mice were purchased from Shanghai SLAC Laboratory Animal Co. All mice were maintained in a barrier facility at Animal Center of Chongqing Medical University. Stably expressing SNHG20 siRNA or SNHG20 cells were implanted subcutaneously (s.c.) into the right flank of mice. Tumor volume was measured every week. All groups of mice were killed and tumors were weighed at the end point of these experiments.

Statistical analysis

All data were expressed as the means ± S.E.M. Student's *t* test was used for differences, comparisons between two independent groups. Data were analyzed using GraphPad Prism 6.0 (GraphPad Software, La Jolla, CA, U.S.A.). Statistically significant differences were defined as $P<0.05$.

Results

Expression of lncRNA SNHG20 was increased in ovarian cancer

To explore the role of lncRNA SNHG20 in ovarian cancer, its expression in ovarian cancer tissues and corresponding non-tumorous tissues was examined (Figure 1A). The q-PCR analysis showed that SNHG20 expression was significantly increased in ovarian cancer tissues compared with paired adjacent non-tumorous tissues. In addition, the expression of SNHG20 was significantly correlated with tumor metastasis (Figure 1B). These results revealed that lncRNA SNHG20 might play a vital role in ovarian cancer progression. Then, we examined the expression of SNHG20 in a panel of ovarian cancer cells (SKOV3, OVCA429, OVCA433, and OVCAR3) and normal HOSE by q-PCR (Figure

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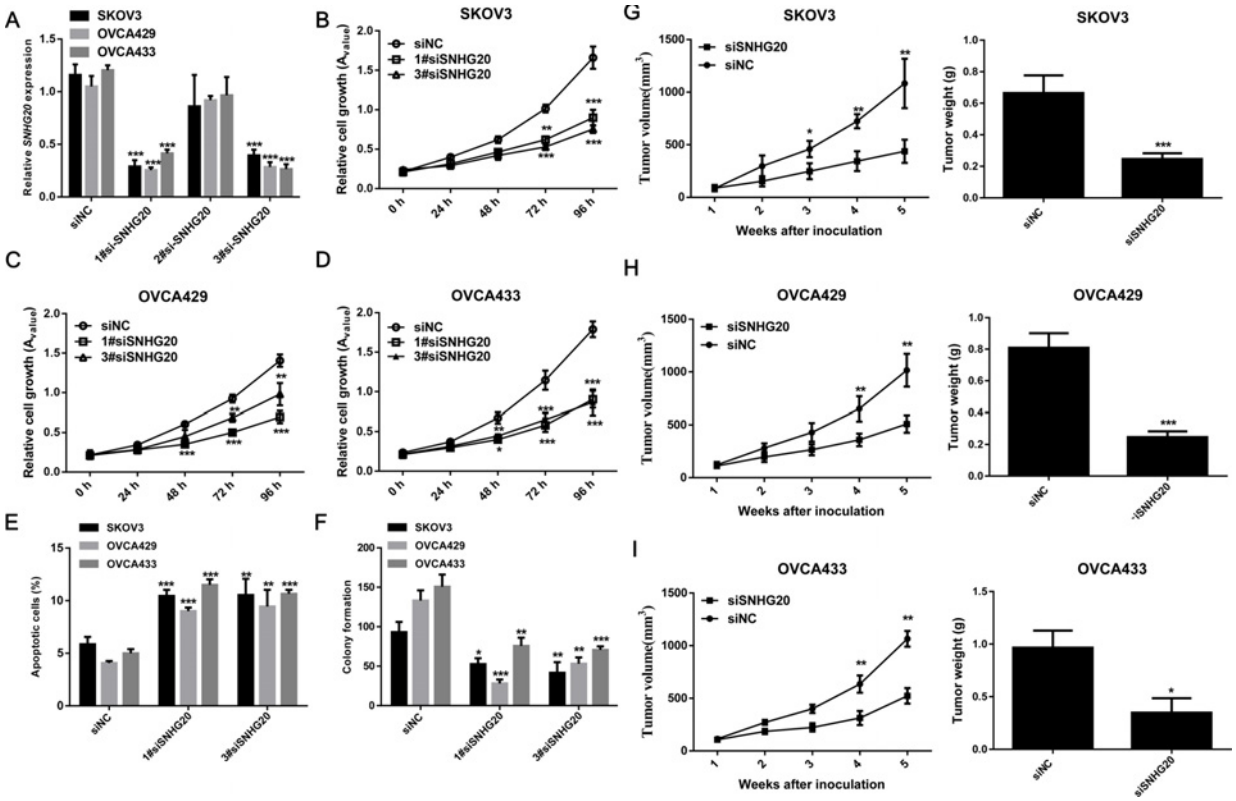

Figure 2. The effect of SNHG20 knockdown on cell growth, apoptosis, and colony formation

(**A**) The mRNA level of SNHG20 in ovarian cancer cells, which were transfected with siSNHG20, was detected, siNC acts as normal control. MTT assays showed SNHG20 knockdown inhibited cell proliferation of SKOV3 (**B**), OVCA429 (**C**), and OVCA433 (**D**) cells. (**E**) Flow cytometry analysis was performed for testing the effect of SNHG20 knockdown on the apoptosis of ovarian cancer cells. (**F**) Colony formation assay measuring colony formation of SNHG20 knockdown ovarian cancer cells. SNHG20 knockdown ovarian cancer cells were inoculated into nude mice and the tumor volume was detected every week. The growth curve of SKOV3 (**G**), OVCA429 (**H**), and OVCA433 (**I**) tumors were determined every week. Colony number was normalized to that obtained with cells transfected with siNC, which was set to 100%. qRT-PCR results were normalized by β-actin. Data represent the mean ± S.E.M. from three independent experiments; ***$P<0.001$, **$P<0.01$, and *$P<0.05$.

1C). To investigate the clinical significance of the SNHG20 expression changes in ovarian cancer, we analyzed the correlations between SNHG20 expression and tumor stages. The q-PCR analysis data showed that there were no significant differences in SNHG20 expression associated with different tumor stages (Supplementary Figure S1). These results suggested that aberrant lncRNA SNHG20 expression may associated with ovarian cancer pathogenesis.

Down-regulation of SNHG20 suppressed ovarian cancer cell growth

To extensively investigate the role of SNHG20 in ovarian cancer progression, its expression was suppressed in ovarian cancer cell lines by RNAi (Figure 2A). MTT assays showed that SNHG20 knockdown apparently abrogated the cell growth of ovarian cancer cells (Figure 2B–D). In addition, flow cytometry analysis indicated that the cell apoptosis was increased in SNHG20 down-regulated ovarian cancer cells (Figure 2E). Moreover, we used a colony formation assay to further examine the role of SNHG20 on growth of ovarian cancer cells. Consistently, SNHG20 knockdown significantly suppressed the colony formation of ovarian cancer cells (Figure 2F). Furthermore, xenograft tumor model showed that SNHG20 knockdown remarkably suppressed the ovarian cancer cell growth *in vivo* (Figure 2G–I). It has been reported that CA125 has profound immunosuppressive effects on antibody-mediated ADCC by primary NK and PBMC derived effector cells. Therefore, we also detected whether CA125 expression was affected by SNHG20 knockdown. The results revealed that SNHG20 knockdown did not affect CA125 level in cell culture supernatants (Supplementary Figure S2). Altogether, these results clarified that SNHG20 may function as an oncogene promoting ovarian cancer progression.

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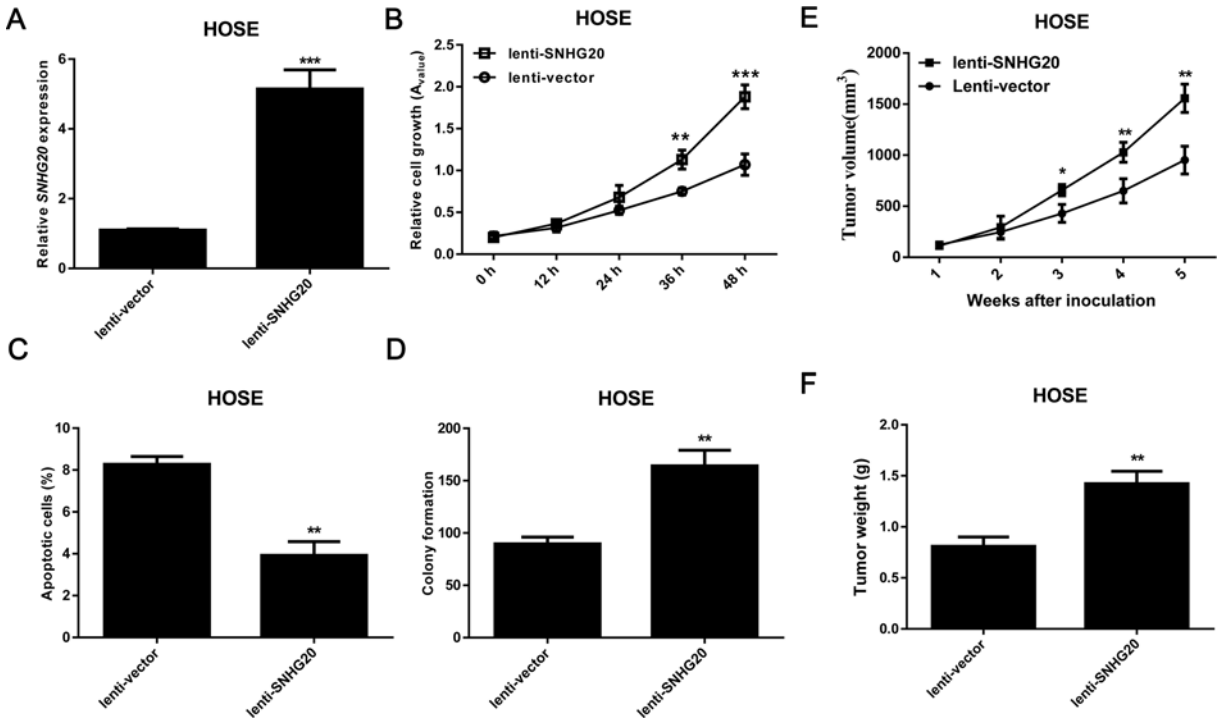

Figure 3. The effect of SNHG20 overexpression on normal ovarian epithelial cell growth, apoptosis, and colony formation

(**A**) HOSE cells were infected with lentivirus carrying SNHG20 and then the mRNA level was examined by q-PCR. MTT assays showed the effects of SNHG20 overexpression on HOSE cell growth (**B**), cell apoptosis (**C**), and colony formation (**D**). Colony number was normalized to that obtained from cells transfected with siNC, which was set to 100%. (**E**) SNHG20 overexpressing HOSE cells were inoculated into nude mice and the tumor volumes were evaluated every week. (**F**) The tumor weight was detected at the end point after we killed all groups of mice. qRT-PCR results were normalized by β-actin. Data represent the mean ± S.E.M. from three independent experiments; ***$P<0.001$, **$P<0.01$, and *$P<0.05$.

Overexpression of SNHG20 promotes ovarian cancer growth

To further evaluate the functional role of SNHG20 in ovarian cancer, lentivirus carrying SNHG20 for overexpression was infected into ovarian cancer cells, while ovarian cells infected with lentivirus carrying empty vector acted as the control (Figure 3A). MTT assays suggested that SNHG20 overexpression promotes normal human ovarian surface epithelial cell growth (Figure 3B). In addition, flow cytometry analysis indicated that SNHG20 overexpression reduced the apoptosis in HOSE cells (Figure 3C). Consistently, colony formation assays also suggested that forced SNHG20 expression promoted the formation of HOSE cancer cell clones (Figure 3D). Furthermore, we also inoculated SNHG20 overexpressing ovarian cancer cell into nude mice. It shows that overexpression of SNHG20 abruptly promoted ovarian cancer cell growth *in vivo* (Figure 3E,F). Taken together, we conclude that SNHG20 overexpression promotes the progression of ovarian cancer.

SNHG20 knockdown inhibits Wnt/β-catenin signaling activation in ovarian cancer cells

As is known, Wnt/β-catenin signaling plays a crucial role in the regulation of cancer cell growth and progression. Therefore, Western blot assays and q-PCR analysis were performed for investigating the effect of SNHG20 on β-catenin expression and a few of the downstream genes of Wnt/β-catenin signaling, such as cyclin D1, c-myc, and E-cadherin in ovarian cancer cells. The results revealed that the expression of E-cadherin in these three ovarian cancers was significantly augmented (Figure 4A,B), whereas the expression of Wnt/β-catenin signaling downstream genes was significantly reduced (Figure 4C–E) in SNHG20 knockdown ovarian cancer cells. Furthermore, the protein level of GSK-3β and p-GSK-3β were also examined by Western blot assay (Figure 4E). It shows that total GSK-3β was not affected by SNHG20 knockdown, whereas the p-GSK-3β protein level was significantly reduced by SNHG20

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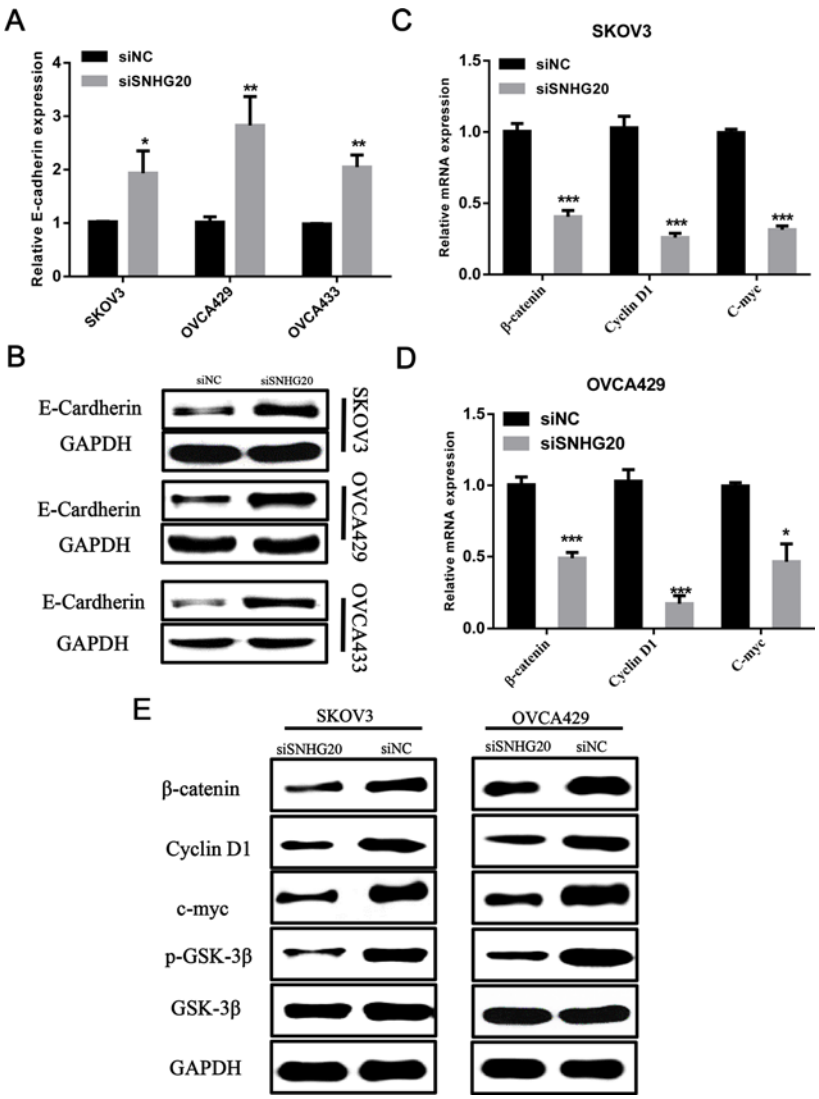

Figure 4. The effect of SNHG20 knockdown on Wnt/β-catenin signaling pathway in ovarian cancer cells

Ovarian cancer cells were transfected with siSNHG20 or siNC, then these cells were subjected to q-PCR (**A**) and Western blot (**B**) for testing the mRNA and protein level of E-cadherin. (**C–E**) The mRNA level and protein level of β-catenin, GSK-3β, p-GSK-3β and several targets of Wnt/β-catenin signaling were examined by q-PCR and western blot in SKOV3 and OVCA429 cells. qRT-PCR results were normalized by β-actin. Data represent the mean ± S.E.M. from three independent experiments; ***$P<0.001$, **$P<0.01$, and *$P<0.05$.

knockdown (Figure 4E). Thus, these data indicated that SNHG20 could attenuate the activation of Wnt/β-catenin signaling.

Discussion

In recent years, accumulating evidence has shown that lncRNAs may play a critical role in cellular biology and human diseases. Several lncRNAs have been identified in gynecological cancer, including HOTAIR, MALAT-1, H19, and HOXA11-AS. It has been reported that lncRNA SNHG20 is significantly increased in HCC and promoted cell invasion by regulating the epithelial-to-mesenchymal transition (EMT) in HCC [13,12]. Other researchers also showed that SNHG20 was increased in CRC tumor tissues compared with non-tumorous adjacent tissues and also predicted poor prognosis in colorectal cancer [14]. However, its role in ovarian cancer has not been investigated now.

In the present study, our results uncovered that SNHG20 was also significantly increased in ovarian cancer tissues compared with paired adjacent normal tissues. This result suggested that SNHG20 might act as a regulatory factor in

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the progression of ovarian cancer. Further investigation showed that SNHG20 expression in metastatic ovarian cancers was higher than that in non-metastatic ovarian cancers. These data suggested that SNHG20 might also regulate the EMT in ovarian cancer cells. To confirm whether SNHG20 worked as an oncogene in ovarian cancer progression, SNHG20 knockdown ovarian cancer cells were subjected to MTT assays. As expected, SNHG20 inhibition significantly suppressed the growth of ovarian cancer cells, whereas overexpression of SNHG20 enhanced normal human ovarian surface epithelial cell growth. Consistently, SNHG20 knockdown induced more apoptotic ovarian cancer cells, whereas SNHG20 overexpressing HOSE cells showed less apoptotic rate. Additionally, SNHG20 knockdown suppressed ovarian cancer cell colony formation. Our data are the same to all relevant studies in other cancer. Therefore, those results illuminated that lncRNA SNHG20 may serve as an oncogene in ovarian cancer progression.

Recent studies demonstrate that lncRNA could regulate ovarian cancer progression via Wnt/β-catenin signaling pathway. For instance, lncRNA CASC2 regulates cell proliferation and metastasis of bladder cancer by activation of the Wnt/β-catenin signaling pathway [15], knockdown of UCA1 increases the tamoxifen sensitivity of breast cancer cells through inhibition of Wnt/β-catenin pathway [16]. Wnt/β-catenin signaling pathway regulates various biological events in ovarian cancer cells, such as gene expression, cell growth, metabolism, apoptosis, metastasis, and drug resistance [17-21]. To shed light on the precise mechanism underlying in SNHG20 promoted ovarian cancer cell growth, the effects of SNHG20 on Wnt/β-catenin signaling pathway were explored. The present study indicated that SNHG20 knockdown suppressed β-catenin expression and reversed the activation level of the Wnt/β-catenin signaling pathway. Furthermore, in terms of protein expression level and mRNA level, SNHG20 knockdown also inhibit several downstream target genes expression of the WNT signaling pathway, such as, cyclin D1, c-myc and E-cadherin. Hence, we considered SNHG20 may be associated with the Wnt/β-catenin signaling in ovarian cancer cells.

In summary, our results suggested that SNHG20 was strikingly up-regulated in ovarian cancer tissues compared with non-tumorous adjacent tissues. SNHG20 knockdown could suppress ovarian cancer cell growth and induce ovarian cancer cell apoptosis. Moreover, SNHG20 knockdown contributed to the inactivation of Wnt/β-catenin signaling ovarian cancer cells. Therefore, SNHG20 might serve as an oncogenetic lncRNA that prompts growth of ovarian cancer cells and activates the Wnt/β-catenin signaling pathway.

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Competing interests

The authors declare that there are no competing interests associated with the manuscript.

Author contribution

SYH, HWS, YHZ conceived and designed the experiments ; SYH, YHZ, XPW and YLD conducted the experiments; XPW and YLD performed the statistical analysis; ZYW and SZY supported the experiments and helped to draft the manuscript.SYH and HWS, wrote the manuscript. All authors read and approved the final manuscript.

Abbreviations

EMT, epithelial-to-mesenchymal transition; HCC, hepatocellular carcinoma; HOSE, human ovarian surface epithelial cell line; lncRNA, long ncRNA; SNHG20, small nucleolar RNA host gene 20.

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