SPANDIDOS PUBLICATIONS

ONCOLOGY LETTERS 15: 2117-2122, 2018

Long non-coding RNA MALAT-1 contributes to maintenance of stem cell-like phenotypes in breast cancer cells

LINGHUAN ZENG, YING CEN and JUNJIE CHEN

Department of Burn and Plastic Surgery, West China Hospital, Sichuan University, Chengdu, Sichuan 610041, P.R. China

Received July 7, 2016; Accepted October 24, 2017

DOI: 10.3892/ol.2017.7557

Abstract. Due to the accumulating evidence that has demonstrated the vital role of cancer stem cells (CSCs) in tumor initiation, progression and metastasis, the mechanisms that maintain the stemness of CSCs have attracted increasing attention. Metastasis-associated lung adenocarcinoma transcript-1 (MALAT-1), a long non-coding RNA, which has been revealed to be associated with the malignant behavior of tumors, performs a critical role in maintaining the stemness in several CSCs. In the present study, it was hypothesized that MALAT-1 promotes stem cell-like phenotypes in breast cancer cells. The present data demonstrated that the expression of MALAT-1 was higher in the CSC subpopulation compared with that in the overall MCF7 cell group and that the knockdown of MALAT-1 decreased the proportion of CSCs. The self-renewal assay also demonstrated that knockdown of MALAT-1 decreased the sphere formation rate *in vitro*. In addition, MALAT-1 is also able to regulate the proliferation, colony formation, migration and invasion of CSCs *in vitro*. The underlying mechanisms may involve the regulation of self-renewal-associated factors, including sex-determining region Y-box 2 (Sox-2). Taken together, the present study demonstrated that MALAT-1 affects the stem cell-like phenotypes in breast cancer cells through regulation of Sox-2.

Introduction

Breast cancer is known as the most frequent malignancy among women worldwide, with an increasing incidence in recent years (1). In the past decades, the expression levels of estrogen receptor, progesterone receptor and human epidermal growth factor receptor 2 have been considered as the most important prognostic markers for the invasiveness of breast tumor (2). The glycosylated transmembrane protein cluster of differentiation CD133, which is associated with shorter disease-free and overall survival times, appears to be a novel promising biomarker for prognosis (3). CD133 was observed to present an association between its expression level and aggressive cellular behavior, including resistance to chemotherapy and radiotherapy in breast tumors, as well as hepatic and colon cancer (4,5). Notably, a wide range of studies has demonstrated that CD133 positively identifies cancer stem cells (6), indicating its association with the stem-like subpopulation in breast tumors.

Cancer stem-like cells (CSCs) derived from breast cancer are considered as the key initiator of breast tumor, and are responsible for maintenance and metastasis. Functionally, CSCs are defined as the subpopulation derived from breast cells, which present the capacity to initiate a tumor in immunocompromised mice, to renew themselves when passaged, and to differentiate into non-self-renewing cells for formation of solid tumors (7). CSCs are also resistant to the effects of radiotherapy, chemotherapy and endocrine therapy in breast tumors, and consequently lead to tumor recurrence (8-10). Thus, the CSC properties of self-renewal, multipotency and chemotherapeutic resistance not only drive tumorigenesis, but also provide resistant advantages for surviving the hostile environment of the circulation, and proliferate in distal tissues (11).

Subsequent to the removal of breast tumors by surgery, an increasing number of patients employ breast reconstruction surgery for improving the quality of lives. However, one of the major concerns regarding breast reconstruction is local recurrence (12-15). Several essential factors are involved in predicting the recurrence, including the subtypes and the malignancy of breast tumors. Thus, more focus on the study of stemness and malignancy of breast tumors was devoted by plastic surgery and breast surgeons.

Metastasis-associated lung adenocarcinoma transcript-1 (MALAT-1) is generally defined as a long non-coding RNA (lncRNA) that consists of ~8,000 nt and is located on chromosome 11q13 (16). It is associated with malignancy in several different types of cancers, including bladder, gallbladder, liver and gastric cancer (16). In breast tumor, MALAT-1 was identified to be significantly downregulated, and thus caused the inhibition of proliferation, colony formation, migration and invasion (14). The underlying mechanisms are possibly involved in inducing cell cycle arrest at G2/M, promoting apoptosis, suppressing epithelial-mesenchymal transition (EMT) and reducing the stem-like properties (15). The accumulating evidence indicates that MALAT-1 acts as an

Correspondence to: Professor Junjie Chen, Department of Burn and Plastic Surgery, West China Hospital, Sichuan University, 17 Guoxue Road, Chengdu, Sichuan 610041, P.R. China
E-mail: chenjunjie_o@163.com

Key words: cancer stem cells, metastasis-associated lung adenocarcinoma transcript-1, sex-determining region Y-box 2, breast cancer cells

oncogenic lncRNA through regulating self-renewal capacity, which leads to malignancy in breast tumors.

In the present study, it was revealed that MALAT-1 is upregulated in the CSC subpopulation in breast tumor cells, and the epigenetic expression of MALAT-1 significantly reduced the proportion of CSCs in MCF7. In addition, it was identified that MALAT-1 regulates the proliferation, colony formation, migration and invasion of CSCs *in vitro*. Therefore, the present study demonstrated that MALAT-1 may serve as a novel biomarker for predicting the malignancy of breast tumor and a potential therapeutic target for breast tumor metastasis.

Materials and methods

Human breast cancer cells. MCF7 cells were previously bought from the American Type Culture Collection (Manassas, VA, USA). Cells were maintained in Dulbecco's modified Eagle's medium (DMEM; Gibco; Thermo Fisher Scientific, Inc., Waltham, MA USA) supplemented with 10% fetal bovine serum (FBS; Gibco; Thermo Fisher Scientific, Inc.) at 37˚C in a 5% CO_2 incubator. The CSCs derived from MCF7 were described previously (17). Single cells were suspended and plated at 1,000 cells/cm^2, and the following treatments were added to the culture media: 100 ng/ml recombinant interleukin-8 (R&D Systems, Inc., Minneapolis, MN, USA), 100 nM SCH563705 (C-X-C chemokine receptor type 1/2 inhibitor; Merck KGaA, Darmstadt, Germany) or 1 μM lapatinib (GlaxoSmithKline Plc., Brentford, UK). The medium was half-refreshed every 3 days. After 21 days, spheres formed and were collected for subsequent culture.

Design and cloning of short hairpin RNA (shRNA) targeting MALAT-1. The lentivirus-encoded shRNA was employed for MALAT-1-knockdown, which was synthesized by Shanghai ShengGong Co., Ltd. (Shanghai, China). The sequences of shRNA targeting to MALAT-1 was 5'-GGGCTTCTCTTA ACATTTA-3' and the scrambled control sequence was 5'-TTC TCCGAACGTGTCACGT-3'. shRNAs were cloned into Plko.1 (GV248; Addgene, Inc., Cambridge, MA, USA) lentiviral vectors and confirmed by sequencing. For each transfection, Lipofectamine® 2000 (Thermo Fisher Scientific, Inc.) was employed to introduce 0.8 μg plasmid into target cells.

RNA isolation and reverse transcription-quantitative PCR (RT-qPCR). Target cells were suspended using TRIzol® reagent (Thermo Fisher Scientific, Inc.) according to the manufacturer's protocol. Total RNA (500 ng) was reverse transcribed into cDNA using the Transcriptional First Strand cDNA Synthesis kit (Omega Bio-Tek, Inc., Norcross, GA, USA) according to the manufacturer's protocol. The relative expression level of MALAT-1 to control GAPDH transcripts was detected by SYBR Green qPCR using the ABI7500 Fast Real-time PCR system (Thermo Fisher Scientific, Inc.). The primer sequences were synthesized as follows: MALAT-1 forward, 5'-AAAGCA AGGTCTCCCCACAAG-3' and reverse, 5'-GGTCTGTGC TAGATCAAAAGGCA-3'; GAPDH forward, 5'-ACCACA GTCCATGCCATCAC-3' and reverse, 5'-TCCACCCTGTTG CTGTA-3'. lncRNA-regulator of reprogramming (ROR) and H19 were employed as internal controls, the primer sequences were as follows: ROR forward, 5'-TCCAAACACATCGCC ACTCT-3' and reverse, 5'-TCCTAGGCCATGAGGAGTCA-3'; H19 forward, 5'-GGAGACTAGGCCAGGTCTC-3' and reverse, 5'-GCCCATGGTGTTCAAGAAGGC-3'. The qPCR amplification was performed in triplicate reactions beginning at 98˚C for 5 min, followed by 35 cycles of 98˚C for 30 sec, and 60˚C for 50 sec. Quantitative normalization of MALAT-1 cDNA was performed in each sample using the expression of the GAPDH as an internal control. The relative level of MALAT-1 transcripts to control GAPDH was determined by the $2^{-\Delta\Delta Cq}$ method (18).

Flow cytometric analysis of CD133+. The singularized cells were incubated with CD133-PE antibodies (Cell Signaling Technology, Inc., Danvers, MA, USA) according to the manufacturer's protocol. Briefly, ~$1x10^6$ cells were centrifuged at 800 x g for 5 min at 4˚C. The supernatant was removed and the pellet was washed three times with ice-cold PBS. CD133 antibody (1 μl) was added, mixed well and incubated for 10 min in the dark at 4˚C. The stained cells were then washed three times with ice-cold PBS and analyzed by flow cytometry.

Self-renewal assay. To assess self-renewal capacity, single target cells were seeded on 6-well plates at 500 cells/well and maintained for 21 days. The secondary spheres were counted and the self-renewal was calculated by dividing the number of secondary spheres formed by the number of primary spheres formed.

Western blot analysis. Total protein was extracted using RIPA buffer (Guangzhou RiboBio Co., Ltd., Guangzhou, China) according to manufacturer's protocol and determined using Pierce™ BCA Protein Assay Kit (cat. no. 23225, Life Technologies, Grand Island, NY, USA) according to the manufacturer's protocol. The primary antibodies against GAPDH (cat. no. ab8245), sex-determining region Y-box 2 (Sox-2; cat. no. ab171380), octamer-binding transcription factor 4 (Oct4; cat. no. ab19857) and stem cell antigen-1 (Sca-1; cat. no. ab51317) (Abcam, Cambridge, UK) were used in the present study. All antibodies were diluted in PBS at 1:2,000 and membranes were incubated for 2 h at room temperature. GAPDH was employed as an internal control. Total protein lysate (50 μg) was separated by 8% SDS-PAGE. The bands were then transferred to polyvinylidene fluoride membranes (EMD Millipore, Billerica, MA, USA) followed by membrane blocking using 5% bovin serum albumin (Sigma Aldrich; Merck KGaA) in PBS for 30 min at room temperature. Secondary goat anti-rat antibody (cat. no. ab7010; 1:5,000; Abcam), goat anti-mouse antibody (cat. no. ab97040; 1:5,000; Abcam) or goat anti-rabbit antibody (cat. no. ab205718; 1:5,000; Abcam) was added for an additional incubation at room temperature for 1 h and immunoblotting was performed and visualized with a chemiluminescence kit (Thermo Fisher Scientific, Inc.), according to manufacturer's protocol.

Transwell assay. A Transwell assay without matrix gel was employed for migration analysis, whereas a Transwell assay with matrix gel was employed for invasion analysis. Chambers were covered with 80 μl Matrigel (BD Biosciences, Franklin Lakes, NJ, USA), or not, diluted with 200 μl DMEM and incubated at 37˚C for 6 h. A total of $2x10^4$ cells were plated in the upper chambers, and 600 μl DMEM supplemented with 10%

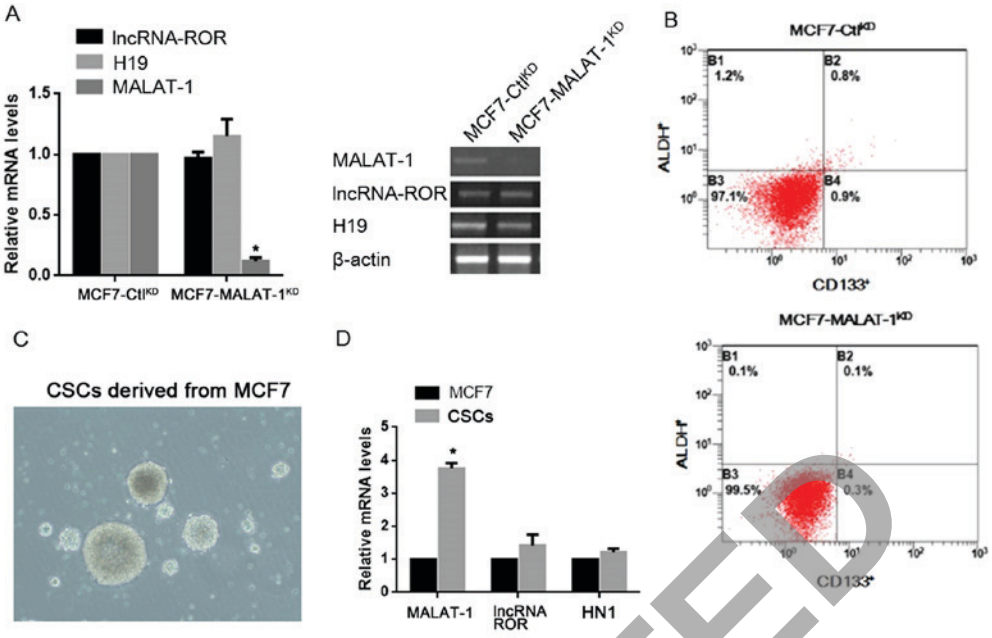

Figure 1. Expression level of MALAT-1 in CSCs and its effects on the proportion of CD133/ALDH positive subpopulation. (A) RT-qPCR and semi-quantitative PCR were performed for detecting lncRNA-ROR, H19 and MALAT-1. (B) CD133 and ALDH staining was performed in MCF7-Ctl^{KD} and MCF7-MALAT-1^{KD} cells by flow cytometry. (C) Culture of CSCs derived from MCF7 (magnification, x40). (D) Detection of MALAT-1, lncRNA-ROR and HN-1 in MCF7 and CSCs by RT-qPCR. *P<0.05. MALAT-1, metastasis-associated lung adenocarcinoma transcript-1; CSC, cancer stem cells; ALDH, aldehyde dehydrogenase; RT-qPCR, reverse transcription-quantitative polymerase chain reaction; lncRNA-ROR, long non-coding RNA-regulator of reprogramming; CD133, cluster of differentiation 133; KD, knockdown.

FBS was added to the lower chamber. Following incubation at 37˚C for 24 h, the cells were fixed with 4% paraformaldehyde for 15 min at room temperature, and stained with 0.5% crystal violet for 30 min at room temperature, and imaged with a fluorescence microscope using a magnification x100.

Cell proliferation assay. Cell Counting Kit-8 (CCK-8; Sigma-Aldrich) was employed for a simple and accurate cell viability assay. In the assay, the WST-8 contained in the reagent was reduced to formazan dye by a dehydrogenase enzyme of the cell mitochondria through electron carrier 1-methoxy phenazinium methylsulfate. Singularized cells at different time points were incubated with 10 μl of CCK-8 solution in separated wells and maintained in 37˚C for 3 h. Cell viability was measured as the absorbance at 450 nm with a microplate reader (Synergy 2 Multi-Mode microplate reader; BioTek Instruments, Inc., Winooski, VT, USA). The mean optical density values from triplicate wells were used as the index of cell viability.

Statistical analysis. All statistical analyses were performed using SPSS software (version 16; SPSS, Inc., Chicago, IL, USA). Data are presented as the mean ± standard deviation from three independent experiments. Paired two tailed Student's t-tests and one-way analysis of variance followed by Tukey's post hoc test were applied for comparisons. P<0.05 was considered to indicate a statistically significant difference.

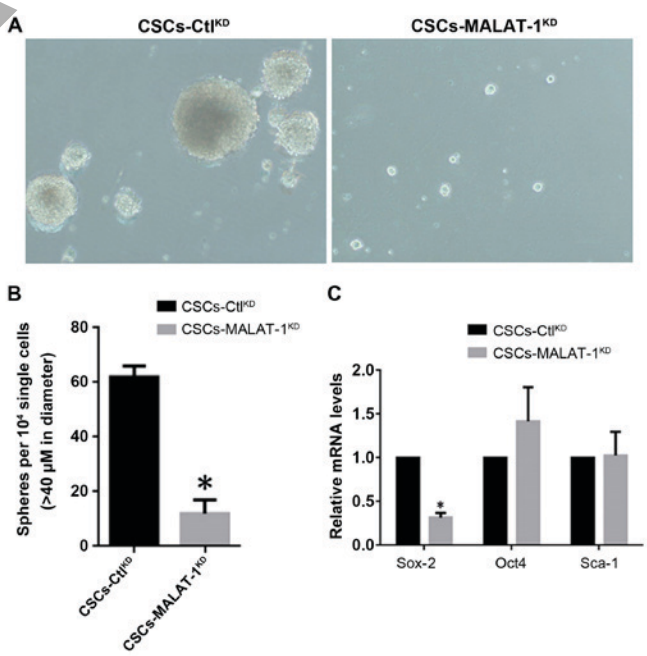

Figure 2. Effects of MALAT-1 on the self-renewal capacity. (A) Culture of CSCs derived from MCF7-Ctl^{KD} and MCF7-MALAT-1^{KD} (magnification, x40). (B) Counts of spheres per 10,000 cells. (C) Detection of Sox-2, Oct4 and Sca-1 mRNA in CSCs-Ctl^{KD} or CSCs-MALAT-1^{KD}. *P<0.05. MALAT-1, metastasis-associated lung adenocarcinoma transcript-1; CSC, cancer stem cells; Sox-2, sex-determining region Y-box 2; Oct4, octamer-binding transcription factor 4; Sca-1, stem cell antigen-1; KD, knockdown.

Results

MALAT-1 is upregulated in CSCs and positively regulated with the proportion of CSCs in breast cancer cells. In order to investigate the roles of MALAT-1 in regulating the stem cell-like phenotypes in breast cancer cells, the expression levels of MALAT-1 were stably knocked down in cultured MCF7 cells (MCF7-MALAT-1^{KD}), as well as that of control cells

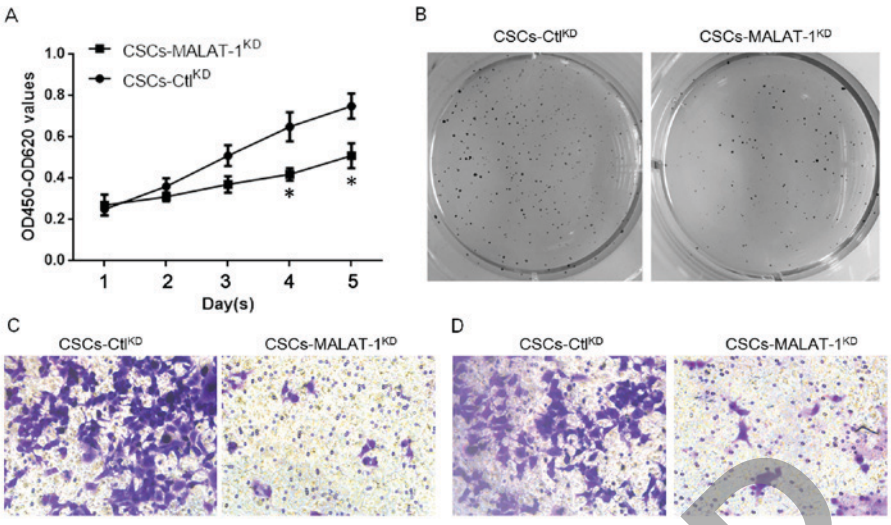

Figure 3. Effects of MALAT-1 on the proliferation, colony formation, migration and invasion in CSCs derived from MCF7. (A) Cell Counting Kit-8 analysis of CSC-Ctl^{KD} or CSC-MALAT-1^{KD}. (B) The colony formation assay was tested in soft agar. (C) Transwell without matrix gel layer was employed for migration assay (magnification, x100). (D) Transwell with matrix gel layer was employed for invasion assay (magnification, x100). *P<0.05. MALAT-1, metastasis-associated lung adenocarcinoma transcript-1; CSC, cancer stem cells; KD, knockdown.

(MCF7-Ctl^{KD}). The knockdown efficacy in the target cells was firstly examined by RT-qPCR, and the results confirmed that MALAT-1 was significantly silenced compared with the negative control MCF7-Ctl^{KD} (Fig. 1A). The alteration of CD133 and ALDH expression, a putative CSC marker in cancer cells, was then assessed, following MALAT-1-knockdown by flow cytometry. The results revealed that the percentage of CD133^{+}/ALDH^{+} subpopulation was markedly reduced compared with control cells (Fig. 1B). Collection of CSCs subpopulation from MCF7 was then performed and involved into RT-qPCR for detecting the expression level of MALAT-1 RNA (Fig. 1C). It was revealed that, the subpopulation of CSCs exhibited significantly higher MALAT-1 expression levels compared with the overall MCF7 population (Fig. 1D). For confirmation of the specific transcriptional alteration of MALAT-1, lncRNA- regulator of reprogramming (ROR) and H19 were employed as controls. As expected, no detectable change was observed using these two lncRNAs in CSCs (Fig. 1D).

MALAT-1 promotes self-renewal capacity in CSCs derived from MCF7. By considering the association of MALAT-1 RNA expression level with the existence of CSCs derived from MCF7, an *in vitro* sphere formation assay was performed to investigate whether MALAT-1 functions in the self-renewal process of CSCs. The CSCs derived from MCF7, which were MALAT-1-knockdown (CSC-MALAT-1^{KD}) or negative control (CSC-Ctl^{KD}), were established by lentivirus infection. It was shown that in CSC-MALAT-1^{KD}, MALAT-1-knockdown markedly reduced the formation of spheres and the diameter of spheres was significantly smaller compared with the CSC-Ctl^{KD} (Fig. 2A and B). The expression levels of CSCs, Sox-2, Oct4 and Sca-1, which are considered as the biomarkers of stem-like cells, were then detected. The results demonstrated that Sox-2 exhibited a significant decrease following knockdown of MALAT-1. However, inconsistently, Oct4 and Sca-1 showed no significant change, indicating that the alteration of Sox-2 was achieved specifically (Fig. 2C).

MALAT-1 regulates proliferation, colony formation, migration and invasion in CSCs derived from MCF7. The effects of MALAT-1 on the physiological processes of CSCs derived from MCF7 were then examined. In order to evaluate its effect on cell proliferation, the CCK-8 assay was employed. The results demonstrated that knockdown of MALAT-1 significantly decreased the proliferation of CSCs following 4 days (Fig. 3A). Consistent with the proliferation, the results of colony formation assay on soft agar of CSCs also indicated that MALAT-1 expression promoted the colony formation of CSCs derived from MCF7 (Fig. 3B). Due to a previous study demonstrating that CSCs interact with angiogenesis (19), the ability of MALAT-1 to regulate the migration and invasion of CSCs was examined. A Transwell assay without matrix gel was employed for migration analysis, whereas a Transwell assay with matrix gel was employed for invasion analysis. The results demonstrated that, as expected, knockdown of MALAT-1 markedly inhibited the migration and invasion ability (Fig. 3C and D).

Discussion

In the past few years, lncRNAs were revealed as important components of the gene regulatory network that may perform critical roles in regulating several physiological processes, including the survival and self-renewal of CSCs (1,20). Several mechanisms of function of lncRNAs in stem cell biology have been uncovered. lncRNA-ROR suppresses the stimulation of p53 under stress and thus inhibits the expression by activated p53 (2,21). Notably, lncRNA-ROR includes several miRNA binding sites, including miR-145, which specifically targets to Oct4, Nanog and Sox-2, and thus positively regulates their mRNA and protein levels (3,22). Further studies have confirmed that neutralization of miR-145 by lncRNA-ROR promotes embryonic stem cell self-renewal (3,22). The same mechanism was also identified, in that lncRNA H19 interacts with p53, disturbs its signaling and also acts as a miRNA sponge to let-7 (4,23).

MALAT-1, which serves as an oncogenic lncRNA, has been shown to be responsible for the malignant behaviors in several types of human tumors (5,24), although the mechanisms of its regulatory roles in CSC-like properties were largely unknown. Among these genes that are aberrantly expressed in CSCs derived from different types of human tumors, Oct4, Nanog, BMI1 proto-oncogene polycomb ring finger, proto-oncogene c-Myc, β-catenin and Sox-2 were significantly decreased in response to knockdown of MALAT-1 (6,25). Taken together, lncRNAs may perform critical roles in regulating the maintenance of CSC-like capacity.

RT-qPCR was performed in order to identify the expression profile of lncRNA-ROR, H19 and MALAT-1 in the breast cancer MCF7 cell line, and its CSC subpopulation identified as CD133-positive. It was revealed that MALAT-1, but not of lncRNA-ROR or H19 was significantly upregulated in CSCs compared with MCF7 cells. Following MALAT-1-knockdown, the subpopulation of CD133-positive significantly decreased. These results indicated that MALAT-1 expression level may positively regulate the expression of CD133 or the portion of CSC subpopulation in MCF7 cells in an uncertain mechanism. Next, the present study provided evidence that MALAT-1 expression is able to promote the self-renewal capacity of cells *in vitro*. Accumulating evidence has demonstrated that CSCs interact with metastasis and recurrence (7,25). It is reported that CD44 expression in breast and pancreatic tumors present enhanced metastatic capacities (8,9,26,27). Thus, the effects of MALAT-1 on the migration and invasion of CSCs were demonstrated by Transwell assay. The results demonstrated that MALAT-1 positively regulates the migration and invasion of CSCs.

The expression level of MALAT-1 appears to be critical in regulating the physiological processes of CSCs, and also of a major population of tumor cells. Compared with adjacent tissues, in lung (10,28), liver (11,29) and prostate (12,30) cancer, MALAT-1 has been revealed to be upregulated, and exhibit a tumor-promoting function. The data in the current study demonstrated that, in the CSC subpopulation, MALAT-1 expression was significantly higher compared with that in the MCF7 cells. However, further studies are required to elucidate whether the expression level of MALAT-1 is the key factor for inducing tumorigenesis via the promotion of CSC formation. Taken together, the results of the present study demonstrated the potential function of long non-coding RNA MALAT-1 in maintaining the stem phenotype of CSC from breast cancer, which indicates it as a potential therapeutic target for treating breast cancer by targeting to CSCs.

References

1. Jemal A, Siegel R, Ward E, Hao Y, Xu J and Thun MJ: Cancer statistics, 2009. CA Cancer J Clin 59: 225-249, 2009.
2. von Minckwitz G, Untch M, Nüesch E, Loibl S, Kaufmann M, Kümmel S, Fasching PA, Eiermann W, Blohmer JU, Costa SD, *et al*: Impact of treatment characteristics on response of different breast cancer phenotypes: Pooled analysis of the German neo-adjuvant chemotherapy trials. Breast Cancer Res Treat 125: 145-156, 2011.
3. Brugnoli F, Grassilli S, Piazzi M, Palomba M, Nika E, Bavelloni A, Capitani S and Bertagnolo V: In triple negative breast tumor cells, PLC-β2 promotes the conversion of CD133 high to CD133 low phenotype and reduces the CD133-related invasiveness. Mol Cancer 12: 165, 2013.
4. Smith LM, Nesterova A, Ryan MC, Duniho S, Jonas M, Anderson M, Zabinski RF, Sutherland MK, Gerber HP, Van Orden KL, *et al*: CD133/prominin-1 is a potential therapeutic target for antibody-drug conjugates in hepatocellular and gastric cancers. Br J Cancer 99: 100-109, 2008.
5. Pohl A, El-Khoueiry A, Yang D, Zhang W, Lurje G, Ning Y, Winder T, Hu-Lieskoven S, Iqbal S, Danenberg KD, *et al*: Pharmacogenetic profiling of CD133 is associated with response rate (RR) and progression-free survival (PFS) in patients with metastatic colorectal cancer (mCRC), treated with bevacizumab-based chemotherapy. Pharmacogenomics J 13: 173-180, 2013.
6. Mizrak D, Brittan M and Alison M: CD133: Molecule of the moment. J Pathol 214: 3-9, 2008.
7. McDermott SP and Wicha MS: Targeting breast cancer stem cells. Mol Oncol 4: 404-419, 2010.
8. Phillips TM, McBride WH and Pajonk F: The response of CD24(-/low)/CD44+ breast cancer-initiating cells to radiation. J Natl Cancer Inst 98: 1777-1785, 2006.
9. Li X, Lewis MT, Huang J, Gutierrez C, Osborne CK, Wu MF, Hilsenbeck SG, Pavlick A, Zhang X, Chamness GC, *et al*: Intrinsic resistance of tumorigenic breast cancer cells to chemotherapy. J Natl Cancer Inst 100: 672-679, 2008.
10. Creighton CJ, Massarweh S, Huang S, Tsimelzon A, Hilsenbeck SG, Osborne CK, Shou J, Malorni L and Schiff R: Development of resistance to targeted therapies transforms the clinically associated molecular profile subtype of breast tumor xenografts. Cancer Res 68: 7493-7501, 2008.
11. Dontu G, Abdallah WM, Foley JM, Jackson KW, Clarke MF, Kawamura MJ and Wicha MS: In vitro propagation and transcriptional profiling of human mammary stem/progenitor cells. Genes Dev 17: 1253-1270, 2003.
12. Lim W, Ko BS, Kim HJ, Lee JW, Eom JS, Son BH, Lee TJ and Ahn SH: Oncological safety of skin sparing mastectomy followed by immediate reconstruction for locally advanced breast cancer. J Surg Oncol 102: 39-42, 2010.
13. Medina-Franco H, Vasconez LO, Fix RJ, Heslin MJ, Beenken SW, Bland KI and Urist MM: Factors associated with local recurrence after skin-sparing mastectomy and immediate breast reconstruction for invasive breast cancer. Ann Surg 235: 814-819, 2002.
14. Ren D, Li H, Li R, Sun J, Guo P, Han H, Yang Y and Li J: Novel insight into MALAT-1 in cancer: Therapeutic targets and clinical applications. Oncol Lett 11: 1621-1630, 2016.
15. Zhao Z, Chen C, Liu Y and Wu C: 17β-estradiol treatment inhibits breast cell proliferation, migration and invasion by decreasing MALAT-1 RNA level. Biochem Biophys Res Commun 445: 388-393, 2014.
16. Bonasio R and Shiekhattar R: Regulation of transcription by long noncoding RNAs. Annu Rev Genet 48: 433-455, 2014.
17. Harrison H, Farnie G, Howell SJ, Rock RE, Stylianou S, Brennan KR, Bundred NJ and Clarke RB: Regulation of breast cancer stem cell activity by signaling through the Notch4 receptor. Cancer Res 70: 709-718, 2010.
18. Livak KJ and Schmittgen TD: Analysis of relative gene expression data using real-time quantitative PCR and the 2(-Delta Delta C(T)) method. Methods 25: 402-408, 2001.
19. Zhao Y, Bao Q, Renner A, Camaj P, Eichhorn M, Ischenko I, Angele M, Kleespies A, Jauch KW and Bruns C: Cancer stem cells and angiogenesis. Int J Dev Biol 55: 477-482, 2011.
20. Ng JH and Ng HH: LincRNAs join the pluripotency alliance. Nat Genet 42: 1035-1036, 2010.
21. Zhang A, Zhou N, Huang J, Liu Q, Fukuda K, Ma D, Lu Z, Bai C, Watabe K and Mo YY: The human long non-coding RNA-RoR is a p53 repressor in response to DNA damage. Cell Res 23: 340-350, 2013.
22. Wang Y, Xu Z, Jiang J, Xu C, Kang J, Xiao L, Wu M, Xiong J, Guo X and Liu H: Endogenous miRNA sponge lincRNA-RoR regulates Oct4, Nanog and Sox2 in human embryonic stem cell self-renewal. Dev Cell 25: 69-80, 2013.
23. Kallen AN, Zhou XB, Xu J, Qiao C, Ma J, Yan L, Lu L, Liu C, Yi JS, Zhang H, *et al*: The imprinted H19 lncRNA antagonizes let-7 microRNAs. Mol Cell 52: 101-112, 2013.
24. Gutschner T, Hämmerle M and Diederichs S: MALAT1-a paradigm for long noncoding RNA function in cancer. J Mol Med (Berl) 91: 791-801, 2013.
25. Jiao F, Hu H, Han T, Yuan C, Wang L, Jin Z, Guo Z and Wang L: Long noncoding RNA MALAT-1 enhances stem cell-like phenotypes in pancreatic cancer cells. Int J Mol Sci 16: 6677-6693, 2015.

26. Al-Hajj M, Wicha MS, Benito-Hernandez A, Morrison SJ and Clarke MF: Prospective identification of tumorigenic breast cancer cells. Proc Natl Acad Sci USA 100: 3983-3988, 2003.
27. Hermann PC, Huber SL, Herrler T, Aicher A, Ellwart JW, Guba M, Bruns CJ and Heeschen C: Distinct populations of cancer stem cells determine tumor growth and metastatic activity in human pancreatic cancer. Cell Stem Cell 1: 313-323, 2007.
28. Schmidt LH, Spieker T, Koschmieder S, Schäffers S, Humberg J, Jungen D, Bulk E, Hascher A, Wittmer D, Marra A, *et al*: The long noncoding MALAT-1 RNA indicates a poor prognosis in non-small cell lung cancer and induces migration and tumor growth. J Thorac Oncol 6: 1984-1992, 2011.
29. Lai MC, Yang Z, Zhou L, Zhu QQ, Xie HY, Zhang F, Wu LM, Chen LM and Zheng SS: Long non-coding RNA MALAT-1 overexpression predicts tumor recurrence of hepatocellular carcinoma after liver transplantation. Med Oncol 29: 1810-1816, 2012.
30. Ren S, Wang F, Shen J, Sun Y, Xu W, Lu J, Wei M, Xu C, Wu C, Zhang Z, *et al*: Long non-coding RNA metastasis associated in lung adenocarcinoma transcript 1 derived miniRNA as a novel plasma-based biomarker for diagnosing prostate cancer. Eur J Cancer 49: 2949-2959, 2013.