European Review for Medical and Pharmacological Sciences 2020; 24: 1807-1814

LINC01116 promotes the proliferation and inhibits the apoptosis of gastric cancer cells

J. CHEN[1], Z.-H. YUAN[2], X.-H. HOU[1], M.-H. SHI[1], R. JIANG[1]

[1]Department of Endoscopic Diagnosis and Treatment Center, Gansu Provincial Hospital, L[illegible]u, Gansu, China
[2]Digestive Department, Gansu Provincial Hospital, Lanzhou, Gansu, China

Abstract. – OBJECTIVE: To detect the relative expression of long intergenic non-protein coding ribonucleic acid (LINC) 01116 in gastric cancer (GC) tissues and cells and analyze the correlations of LINC01116 expression with the clinicopathologic characteristics of patients and investigate the biological functions of LINC01116 *via in vitro* experiments.

PATIENTS AND METHODS: The quantitative Real Time Fluorescence-Polymerase Chain Reaction (qRT-PCR) was applied to detect the relative expression level of LINC01116 in 73 cases of tissues and cells in GC patients. The patients were divided into LINC01116 high expression group and LINC01116 low expression group, an[illegible] correlations of LINC01116 with patient's [illegible]logical characteristics were statistically ana[illegible]d. *In vitro* experiments [cell counting kit-8 (C[illegible]) assay, colony formation assay, and flow cyto[illegible]try] were adopted to investigate the influences [illegible]LINC01116 on the biological fun[illegible] GC cell[illegible]

RESULTS: According to the [illegible]ults [illegible]RT-PCR, the expression of LINC0111[illegible] upreg[illegible]ed in 54 out of 73 cases of tissue[illegible] chan[illegible]d it was upregulated in GC [illegible] the normal gastric m[illegible]al ep[illegible]cells (GES-1). The statistical anal[illegible] manifeste[illegible] the highly expressed LINC0[illegible]s positively [illegible]ated with the tumor-nod[illegible]ta[illegible] (TNM) stag[illegible]p=0.008), lymph node me[illegible]stasis ([illegible]05), and depth of invasion (p=0.[illegible] of the GC p[illegible]. The patients with high exp[illegible]ion of LINC0111[illegible] GC tissues had a sho[illegible]survival[illegible]ime than tho[illegible] with low expression ([illegible].017). [illegible] interference in the expression of L[illegible]116 [illegible]as sho[illegible] in CCK-8 assay and colony fo[illegible]ssay th[illegible] proliferative capacity of [illegible]ells [illegible]acrea[illegible] The results of flow cytom[illegible]dicate[illegible] cell cycle was arrested at the G1/[illegible]phase, a[illegible] apoptosis rate was increased.

CONCLUSIONS: LINC01116 is highly expressed i[illegible] and cells, and highly expressed LINC01116 [illegible]ndicates poor prognosis of the pa[illegible]nts, promotes the proliferation, and inhibits [illegible]poptosis of GC cells.

Key Words:
Gastric cancer (GC), LINC01116, Prognosis, Proliferation, Apoptosis.

Introduction

The incid[illegible] and deve[illegible] gastric cancer (GC[illegible] complex p[illegible] involving multiple [illegible]ors a[illegible]nes[1], whose etiology and pathogenesis have n[illegible]n completely clarified yet [illegible] resection [illegible] only approach that is[illegible]ly to cure GC at pr[illegible]sent, but due to the [illegible]ical sympto[illegible] of the disease in the early [illegible], most of t[illegible]atients have been in the inte[illegible]diate and [illegible]nced stage when diagnosed; con[illegible]atly [illegible] missed the best timing for operati[illegible]des, even though it can be treated [illegible] operation, the patients are highly vulnerable [illegible]se and metastasis after the operation. [illegible]e, it is extremely urgent to seek for new therapeutic methods for tumors.

Long non-coding ribonucleic acids (lncRNAs) are a category of RNA molecules with a transcript length of over 200 nt, which do not encode proteins but regulate the gene expressions at the epigenetic, transcriptional, and post-transcriptional levels in the form of RNAs[2]. LncRNAs were initially regarded as the "noise" of genomic transcription, without biological functions. Currently, it has been proven that lncRNAs can participate in such regulation processes as X chromosome silencing, genomic imprinting, and chromatin modification. Some reports[3,4] have revealed that lncRNAs are also implicated in the biological process of tumor cells, including proliferation, migration, and apoptosis.

Long intergenic non-protein coding RNA (LINC) 01666 is located in chromosome 2q31.1, with a total length of 1058 bp. Firstly, Fang et al[5] found that the expression of LINC01666 is upregulated in the epithelial ovarian cancer, and the highly expressed LINC01116 can promote the proliferation and invasion and inhibit the apoptosis of ovary cells. Subsequently, some scholars discovered that LINC01116 is able to control the expression of ESR1 through competitive ad-

Corresponding Author: Rui Jiang, MM; e-mail: jiangr6636@163.com

sorption on micro RNA (miR)-145 in the case of breast cancer, thus accelerating the incidence and development of the disease[6]. However, there is no report about the expression of LINC01116 and its biological functions in GC, so this research group took the lead in studying the expression of LINC01116 in GC tissues and cells. It was revealed that the expression was upregulated, further statistical analysis indicated that the highly expressed LINC01116 suggested poor prognosis of the GC patients, and *in vitro* experiment results manifested that LINC01116 played a role similar to an oncogene in GC cells. The outcomes of this research will provide biological targets for predicting the prognosis of GC patients and the theoretical bases for reversing the formation of the malignant phenotype of GC.

Patients and Methods

Tissue Specimens

A total of 73 cases of surgically resected GC specimens were collected from the Depart[illegible] of General Surgery of Gansu Provincial H[illegible] from January 2014 to December 2017. The [illegible]-cal specimens were immediately frozen in li[illegible] nitrogen within 30 min after isolation and t[illegible] transferred into a refrigerator [illegible] for long term preservation. The inclus[illegible] were: (1) patients with gastric aden[illegible]carcinoma [illegible]nfirmed by pathology, (2) those w[illegible]ovided [illegible] imens containing nor[illegible]l p[illegible]ma tis[illegible]s (more than 2 cm a[illegible] from t[illegible]mor margin), and (3) those wh[illegible]hose famil[illegible]roved the acquisition of [illegible]cimens an[illegible]gned the informed cons[illegible]t. Exc[illegible] criteria: (1) patients who unde[illegible]t radiothera[illegible]chemotherapy before th[illegible]eration or (2) tho[illegible]omplicated with othe[illegible]alignan[illegible]mors or gastric metastases. Th[illegible]earch[illegible]s approved by the Ethics Committe[illegible]ansu P[illegible]icial Hospital.

Cultu[illegible]

GC ce[illegible]ne MGC803, AGS, BSG823, SG[illegible]21 and normal gastric mucosal epitheli-[illegible]ES-l (Shanghai Cell Bank of Chi-se Academy of Sciences, Shanghai, China) [illegible] seeded into a Roswell Park Memorial In-st[illegible]1640 (RPMI-1640) medium or Dulbecco's Modified Eagle's Medium (DMEM; HyClone, South Logan, UT, USA) containing 10% fetal bovine serum (FBS; HyClone, South Logan, UT, USA), 100 µg/mL penicillin and 100 µg/mL streptomycin, followed by culture in a cell incubator with 5% CO_2 and saturated humidity at 37°C.

Reverse Transcription and Real Time Fluorescence quantitative-Polymerase Cha[illegible] Reaction (qRT-PCR)

The total RNAs in the car[illegible]oma ti[illegible]para-carcinoma tissues, and hu[illegible]GC cells [illegible] tracted using TRIzol (L[illegible]ogen, [illegible]rlsbad, USA) and then reve[illegible]trans[illegible]d into com-plementary deoxyri[illegible]on[illegible](cDNA) a re-verse transcripti[illegible]t (In[illegible]n, Ca[illegible]d, CA, USA). With t[illegible]NA obta[illegible]template, the qRT-PC[illegible]performed [illegible] ABI 7500 qRT-PCR [illegible]trum[illegible] Applied Biosystems, Foster City, CA, USA). [illegible]elative expression level o[illegible]1116 was d[illegible]d through the $2^{-\Delta\Delta Ct}$ m[illegible]d, and the primer and interference sequenc-[illegible]ncluded: GA[illegible]DH forward, 5'-GGTCATC-[illegible]GAGCTGA[illegible]G-3', reverse, 5'-TTGCT-C[illegible]AAGTC[illegible]AGGA-3'. Linc01116 forward: 5'-[illegible]GGT[illegible]GTCCCAAGTG CC, reverse: 5'-GC[illegible]CTTTTTTGGATTTCTCC-3 si-linc01116 #1 5'UAUUCCUUCA GC-[illegible]GGUC3', si-linc01116 #2 5'-GCAGUCU-[illegible]GAACAUA-3', si-linc01116 #3 5'-GU-CUGCAGCUGAGCCAGUAT-3'. The sequences and primers were designed and synthesized by Invitrogen (Carlsbad, CA, USA).

Cell Counting Kit-8 (CCK-8) Assay

Two groups of cells separately transfected with small interfering (si)-linc01116 and si-negative control (NC) were inoculated into a 96-well plate (3,000 cells/well), with 5 duplicated wells for each group. Later, the cells were cultured in the cell incubator. The Cell Counting Kit-8 (CCK-8) assay (Dojindo Molecural Technologies, Kumamoto, Japan) was conducted at 0, 24, 48, 72, and 96 h, as follows: 10 µL of CCK-8 reagent was added into each well, and after incubation in the cell incubator for 2 h, the absorbance at the wavelength of 450 nm (A_{450}) was measured using a microplate reader.

Colony Formation Assay

The colony formation assay is performed as follows: the cells were inoculated into a 6-well plate (1,000 cells/well), with triplicate wells set for each group, and then cultured in the cell incubator for 10-14 d. The medium was replaced, and the

cell state was observed every 2-3 d. Next, the culture was terminated when the cloned cells grew into a suitable size, and the cells were washed with Phosphate-Buffered Saline (PBS) twice and fixed with cold methanol at 4°C for 15 min, followed by washing in PBS twice and staining with crystal violet solution (1 mL/well) for 20 min.

Detection of Apoptosis via Flow Cytometry

The harvested cells were washed with pre-cooled PBS twice. According to the instructions of the Annexin V-fluorescein isothiocyanate (FITC) apoptosis kit (BD, Franklin Lakes, NJ, USA), the cells were resuspended in 1×binding buffer to 1×10^6 cells/mL first. Then, 100 µL of suspension was added into 5 µL of Annexin V-FITC and 5 µL of propidium iodide (PI), and incubated in the dark at room temperature for 15 min. Next, 400 µL of 1× binding buffer was added and mixed, and the mixture was transferred into a flow cytometry tube, followed by detection *via* a flow cytometer.

Cell Cycle Analysis

The transfected cells and control cells in logarithmic growth phase were harvested through standard digestion with trypsin, then washed with PBS and fixed in 75% ethanol at 4°C overnight. The next day, the cells were incubated with RNase at 37°C for 30 min. After the cells were stained with PI for 30 min. The cultures were collected to analyze the cell cycle by the flow cytometer. The data were presented as the percentage of cells in the G0/G1 and G2/M phases of the cell cycle.

Statistical Analysis

The Statistical Product and Service Solutions (SPSS) 19.0 (IBM Corp., Armonk, NY, USA) software was employed for statistical analysis. The measurement data were presented as ($\bar{x}\pm s$). The *t*-test was adopted for comparison of LINC01116 expression level between the tumor group and the normal group, and the One-way analysis of variance or Mann-Whitney test was adopted for comparison among multiple groups. Fisher's exact test was utilized for comparison of the enumeration data, and the survival curves were plotted using the Kaplan-Meier method, while the prognostic factors were subjected to univariate or multivariate Cox model analysis. $p<0.05$ suggested that the difference was statistically significant.

Results

Upregulated LINC01116 Expression in GC Tissues

First, the relative expression of LINC01116 in the tissues of 73 GC patients was detected by means of qRT-PCR. Compared with that in paracarcinoma tissues, the expression of LINC01116 was upregulated in 54 cases of GC tissues (Figure 1A). Next, qRT-PCR was conducted again to measure the relative expression of LINC01116 in GC cells and it was shown that LINC01116 expression was upregulated in GC cells in comparison with that in GES-1 (Figure 1B). With the mean fold change of LINC01116 expression as the cutoff point, patients were divided into LINC01116 high expression group (n=32, fold change >3.9) and LINC01116 low expression group (n=41, fold change <3.9) (Figure 1C). The chi-square test revealed that the expression level of LINC01116 was positively correlated with the tumor-node-metastasis (TNM) stage ($p=0.008$), lymph node metastasis ($p=$ [illegible]) and depth of invasion ($p=0.007$) of the GC tissues, but had no correlations with the patients' age, gender, tumor location, and other variables (Table I).

Analysis on Correlation Between LINC01116 Expression and Patient's Survival

According to the Kaplan-Meier survival analysis, the patients with high expression of LINC01116 in GC tissues had a shorter survival time than those with low expression (Figure 1D). The Cox's proportional hazards regression model was adopted for univariate analysis of the survival data of the 73 patients. The results manifested that the highly expressed LINC01116 ($p<0.05$) and TNM stage ($p<0.01$) exhibited a statistical significance. Later, the multivariate Cox model analysis indicated that the TNM stage and linc01116 expression could serve as the independent prognostic factors for GC (Table II).

Impact of LINC01116 on GC Cell Proliferation

The impacts of LINC01116 on the biological functions of GC cells were investigated *via in vitro* experiments. Firstly, the LINC01116-specific interference sequences were designed and synthesized. 48 h later, the RNAs in the experimental group and control group were collected and reversely transcribed into cDNAs, and the inter-

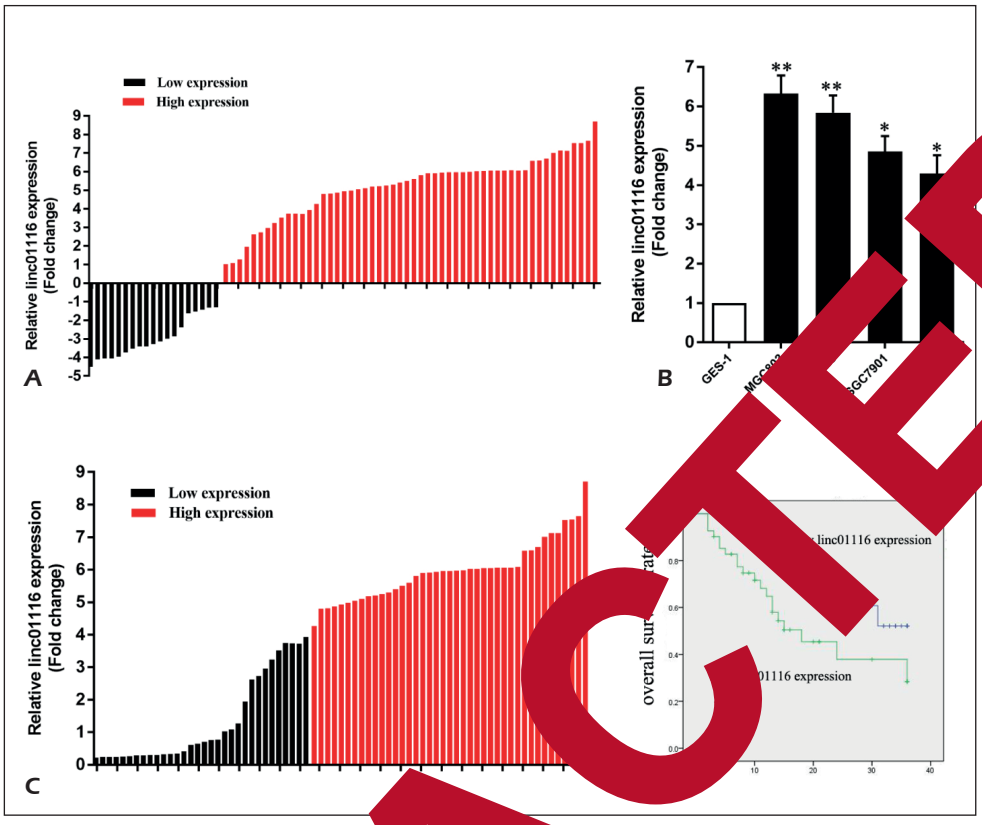

Figure 1. Upregulated LINC01116 expression in G[illegible]gests [illegible]osis. **A**, Relative expression level of LINC01116 in 73 cases of GC tissues detected via qRT-PCR, with g[illegible]alde[illegible]ate dehydrogenase (GAPDH) as an internal reference. **B**, Relative expression level of LINC01116 in G[illegible]ected via qRT-PCR, with GAPDH as the internal reference. **C**, 73 patients are divided into LINC01116 high express[illegible]up and LINC01116 low expression group with the mean fold change of LINC01116 expression in [illegible]e cutoff [illegible]. **D**, Correlation between expression level of LINC01116 and survival time of GC patients inves[illegible]d via [illegible]an-Meier [illegible]val analysis. (**p<0.01, *p<0.05).

ference efficiency wa[illegible]ete[illegible]y qRT[illegible]X (Figures 2A and 2B). Secondly, [illegible]CCK-8 assay was adopted to e[illegible]e the impac[illegible]INC01116 on cell prolife[illegible]n, and it was sho[illegible]that the proliferative c[illegible]acity [illegible]cells declined after the interf[illegible]ce in LINC[illegible] expression (Figures 2C and 2D). The same [illegible]lts as those in CCK[illegible]ssay w[illegible]obtained in the colony formation [illegible]y (Fi[illegible]s 2E and 2F).

Impact of LINC01116 on GC Cell Cycle and Apoptosis

[illegible] si-LINC[illegible]16 and si-NC were transiently tr[illegible]d into GC cells, which were harvested [illegible]8 h, and the distribution of the GC cell cycle was determined through flow cytometry. Compared with that in the control group, the cell cycle was arrested at the G1/G0 phase in the experimental group (Figures 3A and 3B). Then, the cells were treated using the same methods for 48 h, and the apoptosis rate was measured by means of flow cytometry. It was indicated that the apoptosis rate was raised in the si-LINC01116 group (Figures 3C and 3D).

Discussion

It was estimated[7] that there would be about 1,033,700 new cases and about 782,700 deaths of GC in 2018 according to the Global Cancer Statistics, and the incidence and the mortality rates of the disease rank the 5th and 3rd, respectively, among those of all the malignant tumors. China has a high incidence of GC, with approximately 410,000 new cases every year, accounting for nearly 40% around the world[8]. Due to the insidious onset and atypical clinical manifestations of GC in most cases, the majority of the GC patients have been in the intermediate and advanced stage when diagnosed, missing the best timing for radical resection, so the clinical treatment effect is far from satisfactory[9].

Table I. Correlation between linc01116 expression and clinicopathological characteristics of gastric cancer patients (n = 73).

Characteristics	Linc01116 Low No. Case (%)	Linc01116 High No. Case (%)	*p* Chi-squared test p-value
Age (years)			
>60	12	23	0.157
≤60	20	18	
Sex			
Male	15	27	
Female	17	14	
Tumour size (cm)			
>4	18	16	
≤4	14	25	
Differentiation			
Well	2	3	
moderate	13	8	
Poor	11	25	
undiffer	6		
TNM staging			
I+II	19		
III+IV	13		
Lymph lode metastasis			
No	22	10	0.005*
Yes	10	27	
Tumor location			
Gastric antrum	15		
Corpora ventriculi	10		0.756
Preventriculus	7		
Invasion degree			
T1	11		
T2	11	8	0.007*
T3	5	14	
T4	5	13	

*Overall $p<0.05$.

LncRNAs refer to ... molecules that do ... encode ... but have extensive regula... effects on t... expression, which ... licated in ... regulation of multiple vital activities at the epigenetic, transcriptional, and post-transcriptional levels[10]. Studies[11-13] over the past few years have discovered that lncRNAs are abnormally expressed in

Table II. ...variate and multivari... alysis of over-survival in gastric cancer patients (n=73).

Va...es	Univariate analysis			Multivariate analysis		
	...R	95% CI	*p*-value	HR	95% CI	*p*-value
	0.852	0.427-1.700	0.650			
A...	0.672	0.338-1.339	0.259			
T... size (cm)	1.435	0.718-2.869	0.306			
	0.968	0.650-1.444	0.875			
...ivasion degree	0.955	0.706-1.292	0.767			
...ymph lode metastasis	0.988	0.497-1.963	0.972			
...r location	0.828	0.525-1.303	0.414			
T... staging	3.238	1.483-7.070	0.003*	2.946	1.331-6.519	0.008*
Linc01116 expression	2.387	1.138-4.802	0.021*	2.201	0.966-4.299	0.042*

HR, hazard ratio; 95% CI, 95% confidence interval, * Overall $p<0.05$.

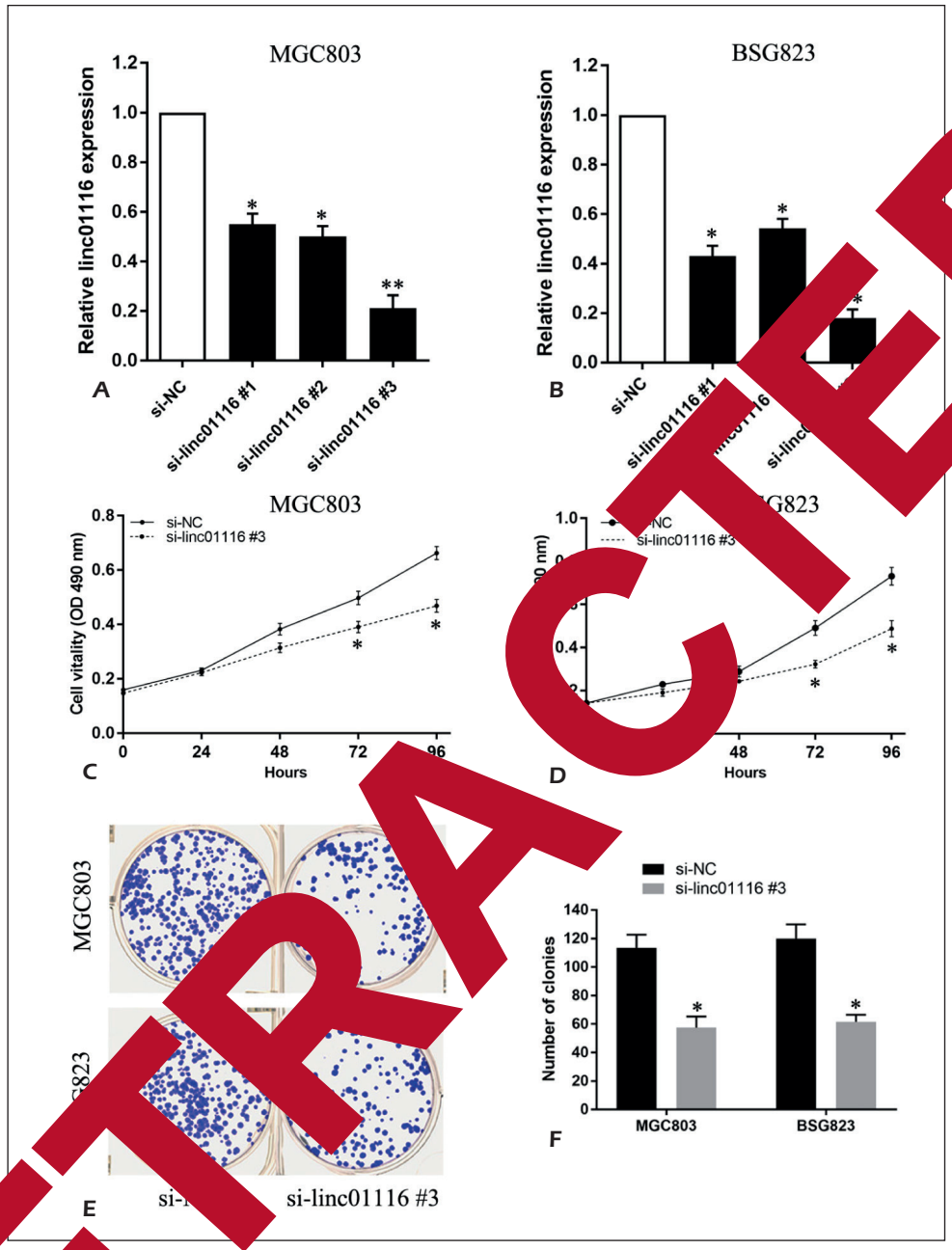

Fig. 4. Impact of LINC01116 on GC cell proliferation. **A-B**, LINC01116 expression in MGC803 and BSG823 cells was detected via RT-PCR. **C**, Impact of LINC01116 on GC cell proliferation detected via CCK-8 assay. It is shown that the proliferative capacity of the cells declines after the interference in LINC01116 expression. **E-F**, The results of colony formation assay indicate that the proliferative capacity of the cells is weakened in si-LINC01116 group compared with that in si-NC group (magnification ×). (**p<0.01, *p<0.05).

tissues and play crucial roles in promoting and maintaining the progression of tumors, becoming the hotspots of research on tumorigenesis. It is generally believed that lncRNAs have 4 modes of actions, namely signal transduction, molecule blocking, guiding role, and central platform, and they can participate in the epigenetic and transcriptional or post-transcriptional regulation of the genes through the interaction among the 4 modes[14,15].

According to literature, the expression of lncRNA Sox2ot is upregulated in the GC tissues, which can be regarded as a biomarker for poor prognosis of GC patients[16]. LncRNA SNHG5 is

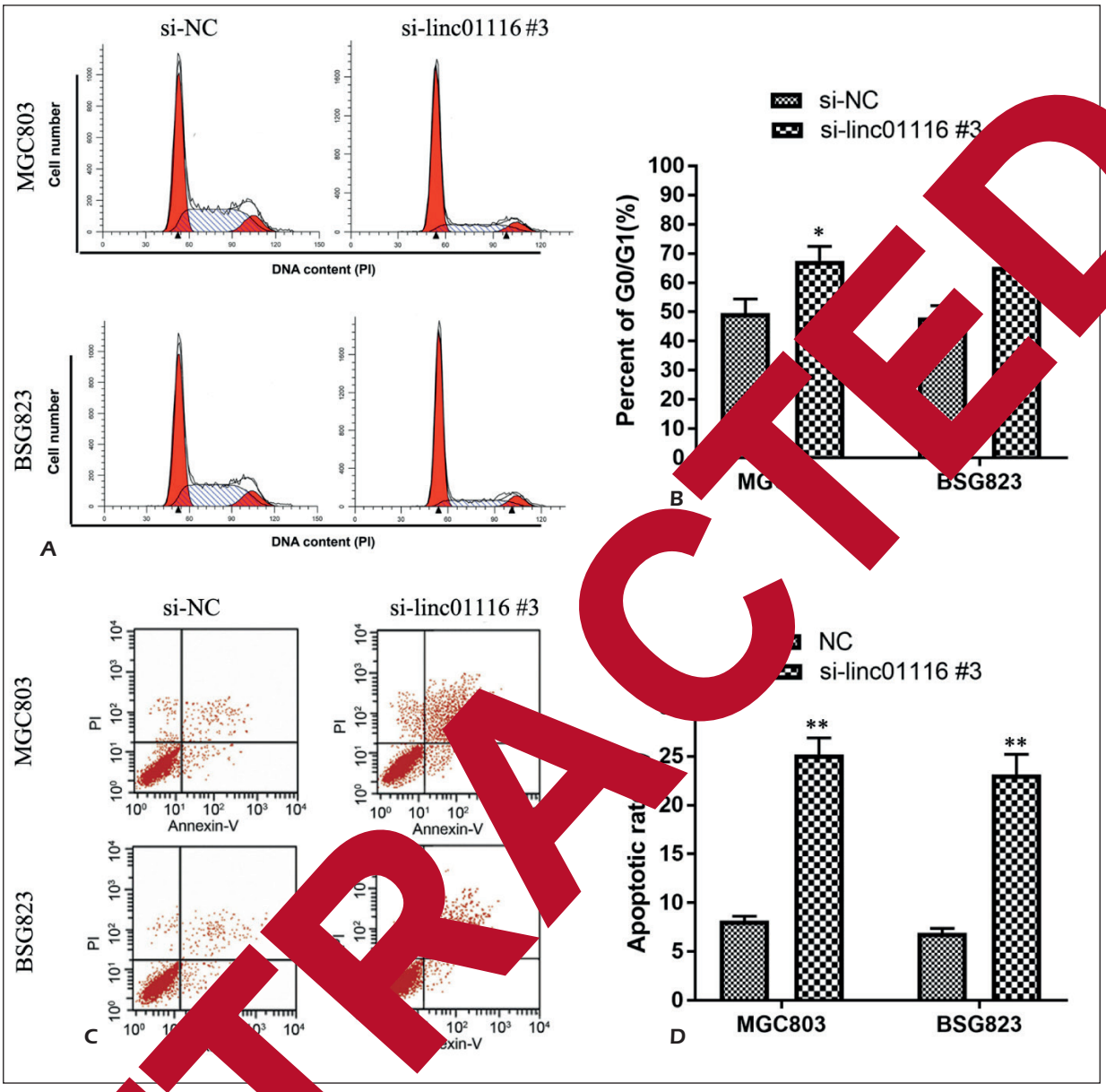

Figure 3. ...acts of LINC011... GC cell cycle and apoptosis. **A-B**, The results of flow cytometry manifest that the cell cycle is ...ed at the G1/G0 phase ... the interference in LINC01116 expression. **C-D**, The results of flow cytometry manifest t... apopt...ate is increased after the interference in LINC01116 expression. (**p<0.01, *p<0.05).

...ble ...ressi...e occurrence and development of ...t of ...ugh targeted regulation on MT... expres... . Yan et al[18] found that lncR...OTAIR can control the PI3K/AKT pathway to ...te the cisplatin resistance of GC by ...sorption on miR-126. It was found for the first ...by this research group that the expression of L...01116 was upregulated in GC tissues and cells and positively associated with the clinical stage and other factors of the patients. Besides, the highly expressed LINC01116 implied poor prognosis of the patients. Furthermore, the results of *in vitro* experiments manifested that the interference in LINC01116 expression could suppress the proliferation and apoptosis of GC cells. It was reported in the literature that LINC01116 can targetedly regulate the expression of IL-6R through miR-520a-3p in osteosarcoma, thus promoting cell proliferation and invasion[19]. In addition, in the case of glioma, LINC01116 is able to accelerate the occurrence and development of tumors *via* targeted regulation on VEGFA[20]. In subsequent

studies of this research, the molecular mechanisms of upregulated LINC01116 expression in promoting the proliferation and inhibiting the apoptosis of the GC cells will be deeply explored, thereby providing a theoretical basis for the targeted treatment of GC in the clinic.

Conclusions

In this study we demonstrated that LINC01116 is highly expressed in GC tissues and cells, and highly expressed LINC01116 indicates poor prognosis of the patients, promotes the proliferation, and inhibits the apoptosis of GC cells.

Conflict of Interests

The authors declared that they have no conflict of interests.

References

1) Yoon H, Kim N. Diagnosis and management of high risk group for gastric cancer. Gut Live... 9: 5-17.
2) Ju C, Liu R, Zhang YW, Zhang Y, Zhou R, Su... Lv XB, Zhang Z. Mesenchymal stem cell-ass... ed lncRNA in osteogenic differentiation. Bio... Pharmacother 2019; 115: 108912.
3) Wang KC, Chang HY. Molec... anisms ... long noncoding RNAs. Mo... 43: 904-914.
4) Clark MB, Mattick JS. ... noncod... NAs in cell biology. Semin Cel... Biol... 376.
5) Fang YN, Huan... Li H, T... Zhang QG, Wang L, Wu J... C01116 prom... e progression of epith... n cancer via ... ating cell apoptosis... Rev... Pharmacol Sci 2018; 22: 5127-5...
6) Hu ... Chen Q, Ding ... cRNA LINC01116 co... es with miR-145 for t... egulation of ESR1 ...ession ... east cancer. Eur Rev Med Pharmacol Sci ...; 22: 1987-1993.
7) ... ...ombet M, ...erjomataram I, Mathers C, Par... Pinero... Lnaor A, Bray F. Estimating ...he gl... anc... idence and mortality in 2018: ...LOBO... ces and methods. Int J Cancer ...19; 144: ...1953.
8) Yang L, Zheng R, Wang N, Yuan Y, Liu S, Li H, Zhang S, Zeng H, Chen W. Incidence and mortality of stomach cancer in China, 2014. Chin J Cancer Res 2018; 30: 291-298.
9) Tu RH, Lin JX, Li P, Xie JW, Wang JB, Lu J... Cao LL, Lin M, Zheng CH, Huang CM... significance of postoperative pn... nia afte... curative resection for patients wi... stric cancer. Cancer Med 2017; 6: 2757-2765.
10) Xie ZY, Wang P, Wu YF, Shen HY. Lo... coding RNA: the functional reg... of me... mal stem cells. World J Ste... ls 2019; 11...
11) Hu X, Sood AK, Dan... Zhan... The ... long noncoding RN... cance... e dark ma... er matters. Curr Opin... t De... 18; 48: ...15.
12) Fang Y, Fullwo... J. ... ctions. ... mechanisms of lo... on-cod... As in ... cer. Genomics Pr... nics Bioinfo... 6; 14: 42-54.
13) Haem... M, ... ier T. Long n... -coding RNAs in canc... and de... ment: where do we go from he... t J Mol Sci... 16: 1395-1405.
14) ... J, Chang HY. ... ue features of long ...on-coding RNA biogenesis and function. Nat Rev Genet 201...; 17: 47-62.
15) Orom UA, De... T, Beringer M, Gumireddy K, Gar...ini A, Bussot... Lai F, Zytnicki M, Notredame C, ...ng Q, G... R, Shiekhattar R. Long noncoding ... ancer-like function in human cells. Ce... ...43: 46-58.
16) Zhang Y, Yang R, Lian J, Xu H. LncRNA Sox2ot overexpression serves as a poor prognostic bio...r in gastric cancer. Am J Transl Res 2016; 8: ...035-5043.
17) Zhao L, Guo H, Zhou B, Feng J, Li Y, Han T, Liu L, Li L, Zhang S, Liu Y, Shi J, Zheng D. Long non-coding RNA SNHG5 suppresses gastric cancer progression by trapping MTA2 in the cytosol. Oncogene 2016; 35: 5770-5780.
18) Yan J, Dang Y, Liu S, Zhang Y, Zhang G. LncRNA HOTAIR promotes cisplatin resistance in gastric cancer by targeting miR-126 to activate the PI3K/AKT/MRP1 genes. Tumour Biol 2016. [Epub ahead of print].
19) Zhang B, Yu L, Han N, Hu Z, Wang S, Ding L, Jiang J. LINC01116 targets miR-520a-3p and affects IL6R to promote the proliferation and migration of osteosarcoma cells through the Jak-stat signaling pathway. Biomed Pharmacother 2018; 107: 270-282.
20) Ye J, Zhu J, Chen H, Qian J, Zhang L, Wan Z, Chen F, Sun S, Li W, Luo C. A novel lncRNA-LINC01116 regulates tumorigenesis of glioma by targeting VEGFA. Int J Cancer 2019. doi: 10.1002/ijc.32483. [Epub ahead of print].