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lncRNA FEZF1-AS1 Is Associated With Prognosis in Lung Adenocarcinoma and Promotes Cell Proliferation, Migration, and Invasion

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Long noncoding RNAs (lncRNAs) have been reported to play important roles in tumorigenesis. In the present study, we demonstrated that lncRNA forebrain embryonic zinc finger protein 1 (FEZF1) antisense RNA1 (FEZF1-AS1) is markedly upregulated in human lung adenocarcinoma (LAD) tissues and cell lines and is associated with poor prognosis. Loss of function revealed that deletion of FEZF1-AS1 expression significantly inhibited the LAD cell proliferation, invasion, and migration. Further studies revealed that downregulation of FEZF1-AS1 reduced mRNA and protein expression of its sense-cognate gene FEZF1 in LAD cells, and vice versa. Correlation analysis indicated that there was a positive correlation between FEZF1-AS1 and FEZF1 expression in LAD tissues. Additionally, rescue assay confirmed that the function of FEZF1-AS1 in LAD was mediated by FEZF1. Our findings suggested that dysregulation of FEZF1-AS1 contributed to the progression of LAD, which might be a potential target for LAD therapy.

Key words: Lung adenocarcinoma (LAD); FEZF1-AS1; FEZF1; Poor prognosis; Proliferation; Migration; Invasion

INTRODUCTION

Lung adenocarcinoma (LAD), the most common histological type of non-small cell lung cancer (NSCLC), has been documented as the leading cause of cancer-related deaths[1]. Thorough investigations into oncogenes and tumor suppressor genes have been reported in LAD[2–8], but the precise molecular mechanisms underlying LAD pathogenesis still remain to be fully elucidated. Long noncoding RNAs (lncRNAs), a class of RNA longer than 200 nucleotides with little or no protein coding capacity, have been shown to play crucial roles in multiple biological processes such as development, differentiation, and carcinogenesis through regulating gene expression[9–16]. Dysregulated lncRNA expression has been reported in various types of cancers. For example, Chang et al. reported that upregulation of SNHG6 regulates ZEB1 expression by competitively binding miR-101-3p and interacting with UPF1 in hepatocellular carcinoma[17]. Lu et al. demonstrated that posttranscriptional silencing of the lncRNA MALAT1 by miR-217 inhibits the epithelial–mesenchymal transition via enhancer of zeste homolog 2 (EZH2) in the malignant transformation of HBE cells induced by cigarette smoke extract[18]. Yu et al. revealed that knockdown of lncRNA XIST increases blood–tumor barrier permeability and inhibits glioma angiogenesis by targeting miR-137[19]. FEZ family zinc finger 1 antisense RNA 1 (FEZF1-AS1), located on the opposite strand of the FEZF1 gene, has been recently identified as an lncRNA, and it has been reported to be dysregulated in gastric cancer and colorectal cancer[20,21]. However, its function in LAD remains unknown.

In our present study, we measured the level of FEZF1-AS1 in LAD tissues and cell lines, and we confirmed that high levels of lncRNA FEZF1-AS1 were associated with aggressive phenotypes of LAD cells and with poor prognosis of LAD patients. Furthermore, loss-of-function experiments revealed that silencing FEZF1-AS1 decreased cell proliferation and migration. Further experiments revealed that FEZF1-AS1 silencing decreased its sense-cognate gene FEZF1 mRNA and protein expression in LAD cells, and rescue assay validated that FEZF1 knockdown was involved in the function of FEZF1-AS1. Collectively, our findings indicated that FEZF1-AS1 acts as an oncogene in LAD carcinogenesis and might be a potential therapy target for LAD.

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MATERIALS AND METHODS

Clinical Tissues

LAD clinical tissues and corresponding normal tissues used in this study were prospectively collected from patients of the Sichuan Cancer Hospital and Institute, Sichuan Cancer Center, School of Medicine, University of Electronic Science and Technology of China (Chengdu, P.R. China) from August 2014 to August 2016. The diagnosis of adenocarcinoma was confirmed by histopathology. All the samples were snap frozen in liquid nitrogen immediately after resection. This study was approved by the Institutional Ethics Review Board of the Sichuan Cancer Hospital and Institute, Sichuan Cancer Center, School of Medicine, University of Electronic Science and Technology of China, and all patients provided written informed consent for this study.

Cell Culture and Transfection

Five human LAD cell lines (SPCA-1, NCI-H1299, A549, NCI-H441, and LTEP-a2) and a normal lung epithelial cell line (BEAS-2B) were all purchased from the Cell Bank of the Chinese Academy of Sciences and were cultured with complete medium containing 10% fetal bovine serum (Gibco, Grand Island, NY, USA) and 90% RPMI-1640 (Gibco) at 37°C, 5% CO_2. For knockdown of FEZF1-AS1, small interfering RNAs (siRNAs) that targeted FEZF1-AS1 and the control siRNA were separately transfected into LAD cells. Knockdown of FEZF1-AS1 also used the same method. Transfections were conducted using Lipofectamine 2000 reagents (Thermo Fisher Scientific, Waltham, MA, USA).

RNA Extraction and Real-Time PCR

Total RNA was isolated by TRIzol reagent (Invitrogen, Carlsbad, CA, USA) following the manufacturer's instructions. After RNA extraction, RNA samples were reversely transcribed by High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems, Foster City, CA, USA). The FastStart Universal SYBR Green Master (Roche, CA, USA) was applied for the quantitative RT-PCR. The target gene expression level was calculated with the 2^{-} Ct method, which was normalized to GAPDH mRNA. All assays were performed in triplicate. The expression levels were relative to the fold change of the corresponding controls, which were defined as 1.0.

Cell Viability Assay

2-(2-Methoxy-4-nitrophenyl)-3-(4-nitrophenyl)-5-(2,4-disulfothenyl)-2*H*-tetrazolium salt (CCK-8; Dojindo, Rockville, MD, USA) assay was conducted to evaluate the rate of cell proliferation, according to the manufacturer's instructions. Briefly, log phase cells were trypsinized into a single-cell suspension and plated into 96-well plates at a density of 2 10^3 per well. The CCK-8 solution was added to each well. After 1 h, the absorbance of each well was recorded at 450 nm and read on a microplate reader victor (Enspire 2300 Maltilabel Reader; PerkinElmer, Singapore).

Colony Formation Assay

Cells (500 cells/well) transfected with the indicated vector were plated in six-well plates and incubated at 37°C. Two weeks later, the cells were fixed and stained with 0.1% crystal violet. The number of visible colonies was counted manually.

Transwell Assay

Cell migration/invasion was measured by Transwell chamber (8-um pore size; Corning, Cambridge, MA, USA) without or with Matrigel. Forty-eight hours after transfection, cells in serum-free media were placed into the upper chamber. Media containing 10% FBS was added into the lower chamber. Following 48 h of incubation, cells remaining in the upper membrane were wiped off, while cells that migrated or invaded were fixed in methanol, stained with 0.1% crystal violet, and counted under a microscope. Three independent experiments were carried out. Cells adhering to the bottom surface of the membrane were counted in five randomly selected areas under the microscope field. Each experiment was repeated three times.

Western Blot Analysis and Antibodies

Total protein lysates were separated in 10% sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and were electrophoretically transferred to polyvinylidene difluoride membranes (Roche). Protein loading was confirmed using mouse anti-GAPDH monoclonal antibody. The membranes were blotted with 10% nonfat milk in TBST for 2 h at room temperature, washed, and then probed with the rabbit anti-FEZF1 (1:2,000 dilution) and GAPDH (1:3,000 dilution), overnight at 4°C, followed by treatment with secondary antibody conjugated to horseradish peroxidase for 2 h at room temperature. The proteins were detected using an enhanced chemiluminescence system and exposed to X-ray film. All antibodies were purchased from Abcam (Cambridge, MA, USA).

Luciferase Reporter Assay

We obtained wild-type (WT) and mutant (Mut) FEZF1 3 -UTR reporters from RiboBio (Guangzhou, P.R. China). Tumor cells that were transfected with si-FEZF1-AS1 or control were cultured in 24-well plates. All transfections were finished using Lipofectamine 2000 reagents (Thermo Fisher Scientific). Dual-luciferase

assays were measured using the Dual-Luciferase Reporter Assay (Promega, Madison, WI, USA). The values were normalized to *Renilla* luciferase relative to the control in accordance with the manufacturer's protocol.

Statistical Analysis

Data are shown as the means ± standard error of at least three independent experiments. The SPSS 17.0 software (SPSS Inc., Chicago, IL, USA) was used for statistical analysis. Two-group comparisons were performed with a Student's *t*-test. Multiple-group comparisons were analyzed with one-way ANOVA. The Pearson chi-square test was used to evaluate the relationship between FEZF1-AS1 expression and clinical features. Statistically significant positive correlation between FEZF1-AS1 and FEZF1 expression levels in LAD tissues was analyzed by Spearman's correlation analysis. The Kaplan–Meier method was used to compare the overall survival curves between high FEZF1-AS1 and low FEZF1-AS1 expression groups via the log-rank test. A value of $p < 0.05$ was considered statistically significant.

RESULTS

FEZF1-AS1 Was Overexpressed in LAD Tissues and Was Correlated With Clinical Data

To explore the biological function of FEZF1-AS1 in LAD, we first measured the expression level of FEZF1-AS1 in LAD tissues and corresponding normal tissues. As shown in Figure 1A, the level of FEZF1-AS1 was significantly increased in LAD tissues, compared with the corresponding normal tissues. Using the mean value of FEZF1-AS1 expression as the cutoff value, samples were divided into two groups (FEZF1-AS1 high expression group and FEZF1-AS1 low expression group). Then the relationship between FEZF1-AS1 and clinical data was analyzed by Pearson chi-square test. The result of this analysis showed that the expression level of FEZF1-AS1 was correlated with histological degree ($p = 0.023$) and lymph node metastasis ($p = 0.005$), but was not observably correlated with age, gender, smoking, and TNM stage ($p > 0.05$). Furthermore, the Kaplan–Meier method analysis (log rank test) was performed to analyze the correlation between FEZF1-AS1 expression and overall survival of patients and revealed that a high level of FEZF1-AS1 predicts poor prognosis ($p < 0.001$) (Fig. 1B). These findings indicated that FEZF1-AS1 might contribute to the tumorigenesis of LAD.

Silencing of FEZF1-AS1 Exerted a Growth Inhibition Effect on LAD Cells

To determine the biological effect of FEZF1-AS1 in LAD, we first measured the expression level of FEZF1-AS1 in a panel of LAD cell lines (SPCA-1, NCI-H1299, A549, NCI-H441, and LTEP-a2) and a normal lung epithelial cell line (BEAS-2B). As depicted in Figure 2A, the expression level of FEZF1-AS1 was obviously increased in five LAD cell lines, and we chose A549 and SPC-A1 for the following experiments. Then we inhibited the endogenous expression of FEZF1-AS1 in A549 and SPC-A1 cells by siRNA to further investigate the biological effects of FEZF1-AS1 on LAD cells. Satisfactory transfection efficiency was obtained after 48 h (Fig. 2B). The growth curves determined by CCK-8 assays revealed that the proliferation ability of cells with knockdown of endogenous FEZF1-AS1 was dramatically reduced in A549 and SPC-A1 cells (Fig. 2C). Consistent with the CCK-8 results, colony formation assays also showed that silenced FEZF1-AS1 expression significantly suppressed the colony formation in A549 and SPC-A1 cells. These findings indicated that FEZF1-AS1 enhances LAD cell growth.

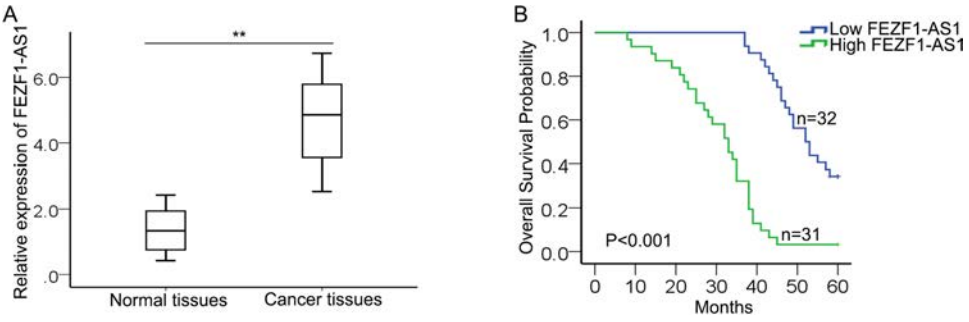

Figure 1. Forebrain embryonic zinc finger protein 1 antisense RNA 1 (FEZF1-AS1) was overexpressed in lung adenocarcinoma (LAD) tissues and was correlated with clinical data. (A) The level of FEZF1-AS1 in LAD tissues and corresponding normal tissues ($n = 63$) was measured by real-time (RT)-qPCR. (B) The level of FEZF1-AS1 and overall survival of patients were analyzed by Kaplan–Meier method analysis (log-rank test). Error bars represent the mean ± SD of at least three independent experiments. $^{**}p < 0.01$ versus control group.

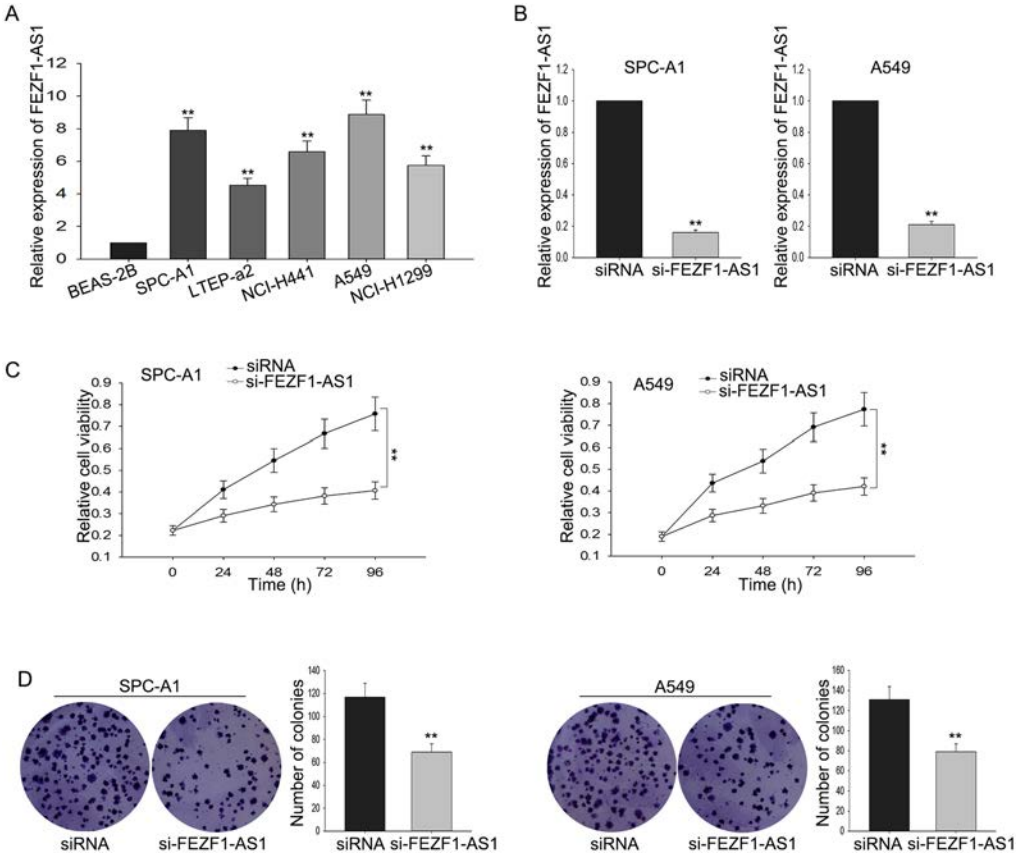

Figure 2. Silenced FEZF1-AS1 exerted growth inhibition effect on LAD cell lines. (A) The level of FEZF1-AS1 in a panel of LAD cell lines (SPCA-1, LTEP-a2, NCI-H441, A549, and NCI-H1299) and a normal lung epithelial cell line (BEAS-2B) was measured by RT-qPCR. (B) A549 and SPC-A1 cells were transfected with si-FEZF1-AS1, and satisfactory transfection efficiency was confirmed by RT-qPCR. (C) Cell counting kit-8 (CCK-8) and (D) colony formation assays were performed to measure the effect of FEZF1-AS1 knockdown on LAD cell proliferation ability. Error bars represent the mean ± SD of at least three independent experiments. $^{**}p < 0.01$ versus control group.

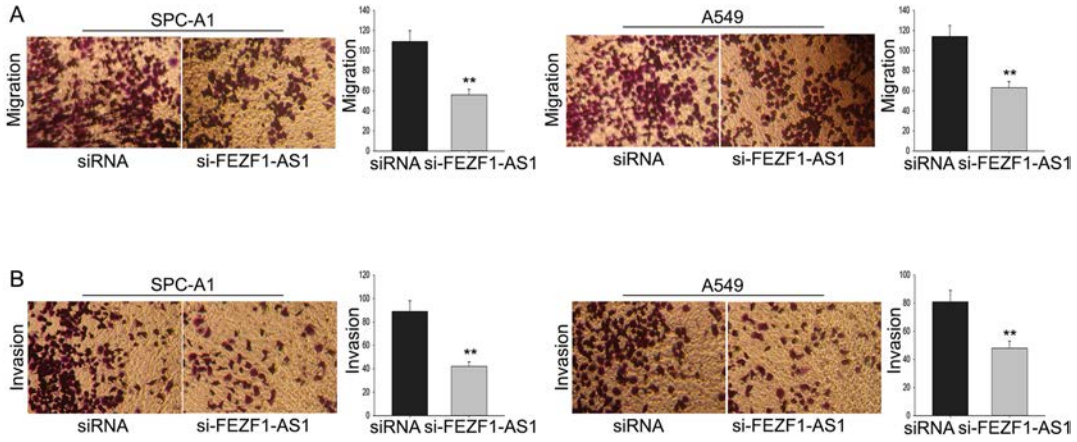

Figure 3. Knockdown of FEZF1-AS1 suppressed LAD cell migration and invasion. (A, B) Transwell assay was performed to determine the migration and invasion capacities of LAD cells when FEZF1-AS1 was silenced. Error bars represent the mean ± SD number of cells from at least three independent experiments. $^{**}p < 0.01$ versus control group.

Knockdown of FEZF1-AS1 Suppressed LAD Cell Migration and Invasion

We then evaluated the effect of FEZF1-AS1 knockdown on LAD cell migration/invasion. Our results showed that the FEZF1-AS1 knockdown inhibited the cell migration and invasion capacities in A549 and SPC-A1 cells (Fig. 3A and B). These results suggested that FEZF1-AS1 could facilitate LAD cell migration and invasion.

FEZF1-AS1 Negatively Modulates FEZF1 Expression

FEZF1-AS1 has been identified as a conserved ~2.6-kb RNA transcribed from the plus strand of chromosome 7, on the opposite strand of the gene coding FEZF1 protein (7q31.32), and thus it could regulate the expression of FEZF1 in colorectal carcinoma[21]. To determine whether FEZF1-AS1 exerted its function in LAD through regulating FEZF1, we examined the expression level of FEZF1 in response to FEZF1-AS1 silencing and the expression level of FEZF1-AS1 in response to FEZF1 silencing. As shown in Figure 4A and B, knockdown of endogenous FEZF1-AS1 in A549 and SPC-A1 cells reduced the expression of FEZF1 at both the mRNA and protein levels. Similarly, we also discovered that knockdown of FEZF1 also decreased the mRNA and protein levels of FEZF1-AS1. siRNA specifically targeted to FEZF1 was transfected into two LAD cell lines. The transfection efficiency was obtained after 48 h (Fig. 4C). We also

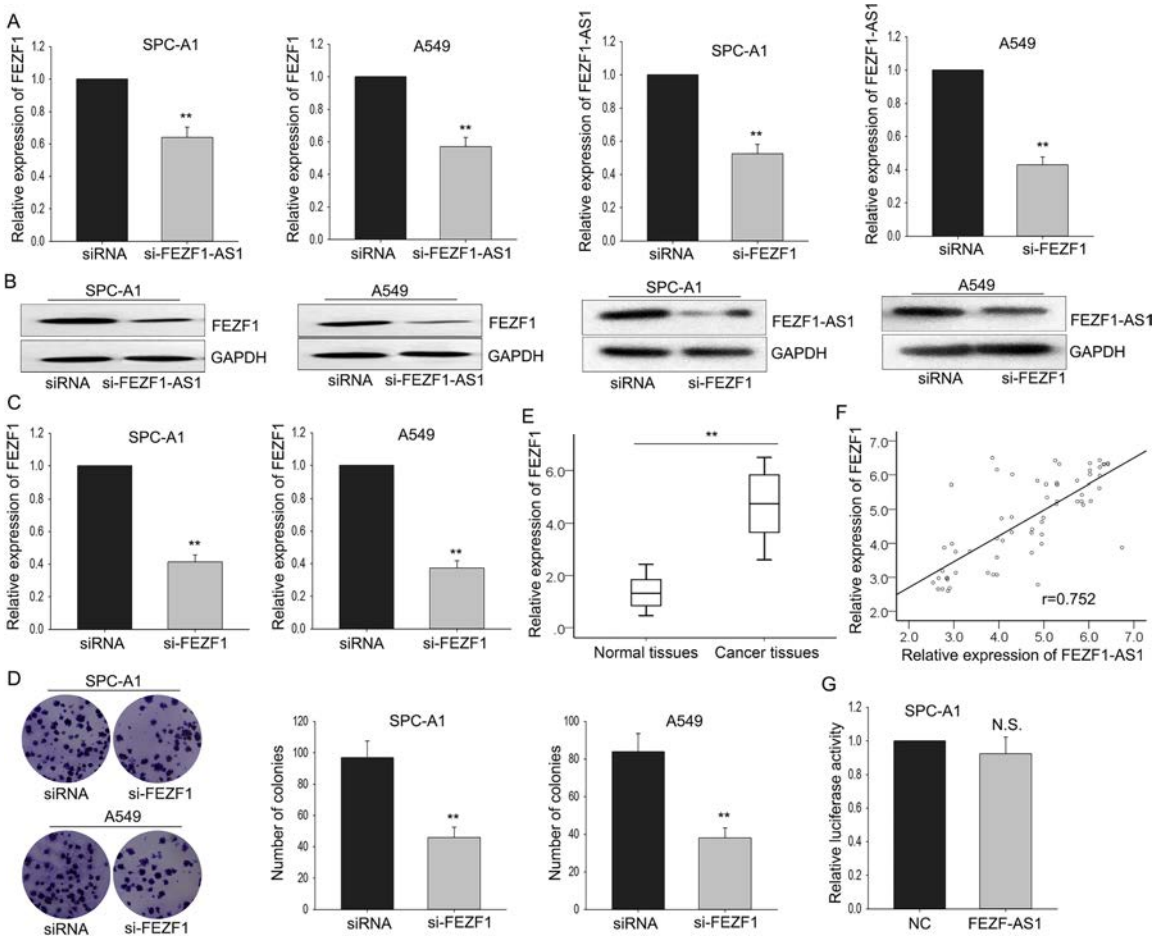

Figure 4. FEZF1-AS1 negatively modulates FEZF1 expression. (A, B) RT-qPCR and Western blot were performed to measure the level of FEZF1 in LAD cells transfected with si-FEZF1-AS1. We also discovered that knockdown of FEZF1 also could negatively affect the mRNA and protein levels of FEZF1-AS1. (C) The siRNA specifically targeted to FEZF1 was transfected into two LAD cells. The transfection efficiency was obtained after 48 h. (D) We also performed colony formation assay to examine the effect of FEZF1 knockdown on cell proliferation, and we found that the colony formation rate was significantly decreased. (E) The level of FEZF1 in LAD tissues and corresponding normal tissues was detected by RT-qPCR. (F) The correlation between FEZF1-AS1 and FEZF1 was analyzed by Spearman's correlation analysis. (G) Dual-luciferase reporter assay showed that the luciferase activity of FEZF1 was not changed by si-FEZF1-AS1 interference. Error bars represent the mean ± SD of at least three independent experiments. $^{**}p < 0.01$ versus control group.

performed colony formation assay to examine the effect of FEZF1 knockdown on cell proliferation, and we found that the colony formation rate was significantly decreased (Fig. 4D). Furthermore, we measured the expression levels of FEZF1 in the same cohort of 63 paired tissue samples by RT-PCR, and the results indicated that FEZF1 expression levels in the tumor tissues of LAD patients were significantly higher than those in corresponding normal tissues (Fig. 4E). Additionally, the correlation between FEZF1-AS1 and FEZF1 in LAD tissues was analyzed, and results showed that the level of FEZF1 was positively correlated with the level of FEZF1-AS1 (Fig. 4F). In order to demonstrate the interaction between FEZF1-AS1 and FEZF1, Dual-luciferase reporter assay was conducted in two LAD cell lines. The results showed that the luciferase activity of FEZF1 was not changed by si-FEZF1-AS1 interference (Fig. 4G). These results suggested that the expression of FEZF1 might be involved in the function exerted by FEZF1-AS1 in LAD cells.

DISCUSSION

It has now become widely known that dysregulation of lncRNAs has been shown in various types of cancers, including LAD. For example, Chen et al. reported that CCAT1 acts as an oncogene and promotes chemoresistance in docetaxel-resistant LAD cells[3]. Chen et al. revealed that low expression lncRNA RPLP0P2 is associated with poor prognosis and decreased cell proliferation and adhesion ability in LAD[4]. MEG3, HOTAIR, LINC01207, and LINC01133 were also reported to be involved in the progression of LAD[5,7,8,22]. However, the biological functions and the molecular mechanisms underlying lncRNAs in LAD still remain largely obscure. lncRNA FEZF1-AS1, located on the opposite strand of gene FEZF1, is a recently identified lncRNA in CRC[21]. In our present study, we reveal that the expression level of FEZF1-AS1 was significantly increased in LAD tissues, LAD cell line, and the high level of FEZF1-AS1 expression was associated with lymph metastasis and histological degree. Results from the Kaplan–Meier analysis revealed that the high level of FEZF1-AS1 expression was correlated with poor prognostic of LAD patients. These findings suggested that FEZF1-AS1 might be involved in the progression of LAD and could serve as a predictor for poor prognosis of LAD patients. To highlight the effect of FEZF1-AS1 in LAD cells, loss-of-function assays were performed, and the results revealed that silencing FEZF1-AS1 expression significantly inhibited LAD cell proliferation, migration, and invasion. Taken together, these findings indicated that FEZF1-AS1 might act as an oncogene and play a promotional role in LAD development and progression. Accumulating documents have demonstrated that lncRNAs exert biological function partly dependent on their genomic location[23,24]. It is well known that some lncRNAs are oriented in the antisense direction with respect to a protein coding loci on the opposite strand and can usually act as a regulator of the gene[25,26]. In our study, FEZF1-AS1 is localized in the antisense DNA strand of the FEZF1 gene and has been reported to regulate FEZF1, contributing to the progression of colorectal carcinoma[21]. Mechanistic experiments revealed that silenced FEZF1-AS1 reduced FEZF1 expression both in the mRNA and protein levels in LAD cells, and the level of FEZF1 in LAD tissues was positively correlated with the level of FEZF1-AS1. These findings indicated that FEZF1 could be regulated by FEZF1-AS1 in LAD cells.

In summary, our study demonstrated that the level of FEZF1-AS1 was upregulated in LAD tissues and revealed that FEZF1-AS1 acted as an oncogene in LAD cells at least partially through regulating FEZF1. These results indicate that FEZF1-AS1 might be a potential therapy target for LAD.

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REFERENCES

1. Siegel RL, Miller KD, Jemal A. Cancer Statistics, 2016. CA Cancer J Clin. 2016;66(1):7–30.
2. Li J, Li S, Chen Z, Wang J, Chen Y, Xu Z, Jin M, Yu W. miR-326 reverses chemoresistance in human lung adenocarcinoma cells by targeting specificity protein 1. Tumour Biol. 2016;37(10):13287–94.
3. Chen J, Zhang K, Song H, Wang R, Chu X, Chen L. Long noncoding RNA CCAT1 acts as an oncogene and promotes chemoresistance in docetaxel-resistant lung adenocarcinoma cells. Oncotarget 2016;7(38):62474–89.
4. Chen J, Hu L, Chen J, Wu F, Hu D, Xu G, Zhu P, Wang Y. Low expression lncRNA RPLP0P2 is associated with poor prognosis and decreased cell proliferation and adhesion ability in lung adenocarcinoma. Oncol Rep. 2016;36(3): 1665–71.
5. Zhang J, Zhu N, Chen X. A novel long noncoding RNA LINC01133 is upregulated in lung squamous cell cancer and predicts survival. Tumour Biol. 2015;36(10):7465–71.
6. Liu Y, Zhou D, Li G, Ming X, Tu Y, Tian J, Lu H, Yu B. Long non coding RNA-UCA1 contributes to cardiomyocyte apoptosis by suppression of p27 expression. Cell Physiol Biochem. 2015;35(5):1986–98.
7. Liu J, Wan L, Lu K, Sun M, Pan X, Zhang P, Lu B, Liu G, Wang Z. The long noncoding RNA MEG3 contributes to cisplatin resistance of human lung adenocarcinoma. PLoS One 2015;10(5):e0114586.
8. Liu Z, Sun M, Lu K, Liu J, Zhang M, Wu W, De W, Wang Z, Wang R. The long noncoding RNA HOTAIR contributes to cisplatin resistance of human lung adenocarcinoma cells via downregulation of p21(WAF1/CIP1) expression. PLoS One 2013;8(10):e77293.
9. Liu FT, Xue QZ, Zhu ZM, Qiu C, Hao TF, Zhu PQ, Luo HL. Long noncoding RNA PVT1, a novel promising biomarker to predict lymph node metastasis and prognosis: A meta-analysis. Panminerva Med. 2016;58(2):160–6.

10. Liu C, Lin J. Long noncoding RNA ZEB1-AS1 acts as an oncogene in osteosarcoma by epigenetically activating ZEB1. Am J Transl Res. 2016;8(10):4095–105.
11. Lin PC, Huang HD, Chang CC, Chang YS, Yen JC, Lee CC, Chang WH, Liu TC, Chang JG. Long noncoding RNA TUG1 is downregulated in non-small cell lung cancer and can regulate CELF1 on binding to PRC2. BMC Cancer 2016;16:583.
12. Li T, Xu C, Cai B, Zhang M, Gao F, Gan J. Expression and clinicopathological significance of the lncRNA HOXA11-AS in colorectal cancer. Oncol Lett. 2016;12(5):4155–60.
13. Li T, Xie J, Shen C, Cheng D, Shi Y, Wu Z, Deng X, Chen H, Shen B, Peng C, Li H, Zhan Q, Zhu Z. Upregulation of long noncoding RNA ZEB1-AS1 promotes tumor metastasis and predicts poor prognosis in hepatocellular carcinoma. Oncogene 2016;35(12):1575–84.
14. Li P, Xue WJ, Feng Y, Mao QS. Long non-coding RNA CASC2 suppresses the proliferation of gastric cancer cells by regulating the MAPK signaling pathway. Am J Transl Res. 2016;8(8):3522–9.
15. Li C, Zhao Z, Zhou Z, Liu R. Linc-ROR confers gemcitabine resistance to pancreatic cancer cells via inducing autophagy and modulating the miR-124/PTBP1/PKM2 axis. Cancer Chemother Pharmacol. 2016;78(6):1199–207.
16. Kim HJ, Eoh KJ, Kim LK, Nam EJ, Yoon SO, Kim KH, Lee JK, Kim SW, Kim YT. The long noncoding RNA HOXA11 antisense induces tumor progression and stemness maintenance in cervical cancer. Oncotarget 2016;7(50): 83001–16.
17. Chang L, Yuan Y, Li C, Guo T, Qi H, Xiao Y, Dong X, Liu Z, Liu Q. Upregulation of SNHG6 regulates ZEB1 expression by competitively binding miR-101-3p and interacting with UPF1 in hepatocellular carcinoma. Cancer Lett. 2016;383(2):183–94.
18. Lu L, Luo F, Liu Y, Liu X, Shi L, Lu X, Liu Q. Posttranscriptional silencing of the lncRNA MALAT1 by miR-217 inhibits the epithelial-mesenchymal transition via enhancer of zeste homolog 2 in the malignant transformation of HBE cells induced by cigarette smoke extract. Toxicol Appl Pharmacol. 2015;289(2):276–85.
19. Yu H, Xue Y, Wang P, Liu X, Ma J, Zheng J, Li Z, Li Z, Cai H, Liu Y. Knockdown of long non-coding RNA XIST increases blood-tumor barrier permeability and inhibits glioma angiogenesis by targeting miR-137. Oncogenesis 2017;6(3):e303.
20. Liu YW, Xia R, Lu K, Xie M, Yang F, Sun M, De W, Wang C, Ji G. LincRNAFEZF1-AS1 represses p21 expression to promote gastric cancer proliferation through LSD1-mediated H3K4me2 demethylation. Mol Cancer 2017; 16(1):39.
21. Chen N, Guo D, Xu Q, Yang M, Wang D, Peng M, Ding Y, Wang S, Zhou J. Long non-coding RNA FEZF1-AS1 facilitates cell proliferation and migration in colorectal carcinoma. Oncotarget 2016;7(10):11271–83.
22. Wang G, Chen H, Liu J. The long noncoding RNA LINC01207 promotes proliferation of lung adenocarcinoma. Am J Cancer Res. 2015;5(10):3162–73.
23. Orom UA, Derrien T, Beringer M, Gumireddy K, Gardini A, Bussotti G, Lai F, Zytnicki M, Notredame C, Huang Q, Guigo R, Shiekhattar R. Long noncoding RNAs with enhancer-like function in human cells. Cell 2010;143(1):46–58.
24. Tian D, Sun S, Lee JT. The long noncoding RNA, Jpx, is a molecular switch for X chromosome inactivation. Cell 2010;143(3):390–403.
25. Nolasco S, Bellido J, Goncalves J, Tavares A, Zabala JC, Soares H. The expression of tubulin cofactor A (TBCA) is regulated by a noncoding antisense Tbca RNA during testis maturation. PLoS One 2012;7(8):e42536.
26. Katayama S, Tomaru Y, Kasukawa T, Waki K, Nakanishi M, Nakamura M, Nishida H, Yap CC, Suzuki M, Kawai J, Suzuki H, Carninci P, Hayashizaki Y, Wells C, Frith M, Ravasi T, Pang KC, Hallinan J, Mattick J, Hume DA, Lipovich L, Batalov S, Engstrom PG, Mizuno Y, Faghihi MA, Sandelin A, Chalk AM, Mottagui-Tabar S, Liang Z, Lenhard B, Wahlestedt C. Antisense transcription in the mammalian transcriptome. Science 2005;309(5740): 1564–6.