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ORIGINAL RESEARCH

RETRACTED ARTICLE: lncRNA differentiation antagonizing nonprotein coding RNA overexpression accelerates progression and indicates poor prognosis in pancreatic ductal adenocarcinoma

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Background: lncRNA differentiation antagonizing nonprotein coding RNA (lncRNA DANCR) has been suggested to play an oncogenic role in multiple cancers. However, to the best of our knowledge, the clinical significance and role of DANCR in pancreatic ductal adenocarcinoma (PDAC) has not been illuminated till now. The present study aims to identify the functional role of DANCR in PDAC.

Methods: The expression of DANCR was detected in PDAC cells and tissues. The correlation of DANCR expression and PDAC clinicopathological features was analysed. Kaplan-Meier method was used to depict the overall survival (OS) rate and shorter progression-free survival (PFS) of PDAC patients and Log-rank test was performed to analyse the difference. Univariate and multivariate Cox regression model were utilized to analyse the risk factors for prognosis. Transwell assay and Matrigel assay were conducted to detect the effect of DANCR on the migration and invasion of PDAC cells, respectively. Colony formation assay and Cell Counting Kit-8 (CCK-8) assay were performed to evaluate the function of DANCR on proliferation. The mechanisms of DANCR exerting its function were also explored.

Results: DANCR was revealed to promote PDAC progression, with relatively higher expression levels in PDAC cell lines and tissues. Correlation analysis of the clinicopathological features and DANCR expression found that high DANCR expression was statistically correlated with vascular invasion (P=0.013), advanced T stage (P=0.005), lymph node metastasis (P<0.001) and advanced TNM stage (P<0.001). Notably, survival analysis discovered that high DANCR expression predicted lower OS rate and shorter PFS period. In addition, high DANCR expression was identified as an independent risk factor for poor OS (HR=1.199, 95% CI=1.113–1.290, P<0.001) and PFS (HR=1.199, 95% CI=1.114–1.290, P<0.001) of PDAC. Moreover, in vitro assays detected that the migration and invasion of Panc1 cells with DANCR deficiency were significantly suppressed in the Transwell assay and the Matrigel assay. However, the motility of BxPC3 cells with DANCR overexpression was obviously increased. In addition, the loss of DANCR suppressed the proliferation of Panc1 cells in the CCK-8 assay and the colony formation assay, while ectopic expression of DANCR in BxPC3 cells promoted the proliferation. Besides, microRNA-33a-5p/AXL signaling pathway may be involved in mediating the function of DANCR.

Conclusion: Overexpression of lncRNA DANCR in PDAC is associated with cancer progression and predicts poor OS and PFS. DANCR could promote the proliferation and metastasis of PDAC cells. DANCR may serve as a potential prognostic marker and therapeutic target in PDAC.

Keywords: lncRNA DANCR, pancreatic cancer, prognosis, proliferation, metastasis

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Introduction

Pancreatic ductal adenocarcinoma (PDAC) is one of the most lethal malignancies. The 5-year survival rate increased only from 3% to 8% over the past 40 years.[1] The reasons for such dismal survival include lack of early detection, presentation at late stages and inadequate current therapies.[2] Most PDAC patients lack specific symptoms at early stage, and only about 20% of PDAC patients have the opportunity to receive curative resection. Carbohydrate antigen (CA) 19-9 is the most commonly used tumor marker for the diagnosis of PDAC in clinical practice; the median sensitivity and specificity of CA19-9 for the diagnosis are only 75.5% and 77.6%, respectively, with a low positive predictive value of 0.5%–0.9%, which does not qualify it as a useful screening parameter.[3–5] No conventional biomarkers have proven to be a specific and reliable tool for the early detection of PDAC.[5] Considering the complexity of cancer biology, combination of different markers as diagnostic or prognostic indices appears promising. Therefore, more explorations are needed to validate novel diagnostic and prognostic markers.

lncRNAs are defined as endogenous cellular RNAs of more than 200 nucleotides in length and lack an open reading frame of significant length (<100 amino acids).[6–8] lncRNAs are found in almost every branch of life and involved in numerous importa biological phenomena, such as imprinting genomic loci, shaping chromosome conformation and allosterically regu enzymatic activity.[8,9] Specific patterns of lncRNA ex ression c ordinate cell state, differentiation, development and ease interestingly, the aberrant expression of cRNAs iscovered to be involved in cancer initiation a p ression thro h transcriptional and posttranscriptional regulati [13,14] In addition, mounting evidence showed at lncRNAs ar xpressed in a tissue-specific manner, w ch make hem an ideal biomarker for cancer diagnosis and thera ti target.[15] l RNAs have shown potential as biom in the d nosis d prognosis of bladder cancer, prost cancer astric ca r, pancreatic cancer, breast cancer and m y ot pes.[16]

lncRNA dif ntiation antagonizing nonprotein coding RNA (DANCR) was st identified as an 855 bp lncRNA downregulated during differentiation by Kretz et al.[17] Subsequently, Yuan et al[18] reported that DANCR could increase the stemness features and predict prognosis in hepatocellular carcinoma. After that, the oncogenic role of DANCR in gastric cancer,[19] colorectal cancer,[20] prostate cancer[21] and lung adenocarcinoma[22] has been reported. However, the clinical significance and role of DANCR in PDAC has not been illuminated yet.

Our study aimed to measure the expression level of DANCR in PDAC cell lines and tissues, and the significance of DANCR in the clinical progression of PDAC was verified. Moreover, the prognostic value of DANCR was analyzed. In addition, the functional role of DANCR in proliferation and metastasis of PDAC was defined by in vitro assays.

Materials and methods

Cell lines and cell culture

The human pancreatic cancer cell lines Panc1, Panc28, AsPC1, MiaPaCa2 and BxPC3 and the human pancreatic ductal epithelial cell line HPDE were purchased from the American Type Culture Collection (ATCC, Manassas, V SA). Cells were cultured in Roswell Park Memori nstitute-1 0 medium (AsPC1, BxPC3 and HPDE) or D EM (Hyclon Thermo Fisher Scientific, Waltham A, USA Panc1, anc28 and MiaPaCa2) supplemented ith 10% BS (H e), 100 U/mL penicillin and 100 mg/mL ept ycin. All cells were cultured in a humidified i bator wi 5% CO at 37°C.

All the si NA and DAN ectopic overexpression plasmid used in the urrent study were synthesized by Gene ma (Shangha China). Transfection was conduc d using the Lipofectamine™ 2000 transfection reagent (Th mo Fisher S entific) according to the protocol recommend by the anufacturer. The transfected cells were ilized for further investigations 48 hours later.

Clinical specimens

The 206 PDAC tissues and paired tumor adjacent tissues were collected from surgical resections at the general surgery department of Dazhou Central Hospital. The tumor-adjacent tissues, defined as normal tissues in routine pathological results, were obtained 2 cm away from the PDAC tissues. These tissues were divided into two groups, the low DANCR expression group (n=120) and the high DANCR expression group (n=86), with the mean DANCR expression level serving as the cutoff value. The clinicopathological characteristics of the PDAC patients are summarized in Table 1. All the patients involved in the current study received radical surgical resection without preoperative chemotherapy or radiotherapy. The collected specimens were snap frozen in liquid nitrogen and stored at −80°C until being used. Tissue specimen collections were made with full informed consent of all patients following institutional ethical guidelines that were reviewed and approved by the ethics committee of Dazhou Central Hospital.

RNA isolation, RNA extraction and quantitative real time (qRT)-PCR

Total RNA was extracted from tissues or cultured cells using TRIzol reagent (Thermo Fisher Scientific). One microgram of

Table 1 Relationship between lncRNA DANCR expression and clinicopathological characteristics of PDAC

Parameters	No of patients (n=206)	DANCR (high/low)	*P*-value
Age			0.067
<60 years	90	44/46	
≥60 years	116	42/74	
Gender			0.133
Male	132	50/82	
Female	74	36/38	
CEA			0.675
<4.5 μg/mL	154	63/91	
≥4.5 μg/mL	52	23/29	
CA19-9			0.965
<37 U/mL	89	37/52	
≥37 U/mL	117	49/68	
Tumor location			0.686
Head and neck	135	55/80	
Body and tail	71	31/40	
Grade			0.571
Well + moderate	141	57/84	
Poor + undifferentiated	65	29/36	
Size			0.195
<4 cm	121	46/75	
≥4 cm	85	40/45	
Neural invasion			0.586
No	86	34/52	
Yes	120	52/68	
Vascular invasion			0.[illegible]3
No	112	38/74	
Yes	94	48/46	
Lymphatic invasion			0.511
No	69	[illegible]38	
Yes	137	55/[illegible]	
T stage			0.005
T1 + T2	138	49/89	
T3 + T4	66	37/29	
Lymph node metastasis			<0.001
No	121	36/[illegible]	
Yes	85	50/35	
Distant metastasis			0.435
No	200	85/115	
Yes		3/2	
TNM st[illegible]			<0.001
Early sta[illegible] (≤[illegible])	113	35/78	
Advanced st[illegible]s (>IIA)	92	51/41	

Abbreviations: DA[illegible]R, differentiation antagonizing nonprotein coding RNA; PDAC, pancreatic ductal adenocarcinoma; CEA, carcinoembryonic antigen.

total RNA was reversely transcribed in a final volume of 20 μL under standard conditions using PrimeScript RT Reagent Kit (TaKaRa, Dalian, China). After the reverse transcription, 1 μL of the complementary DNA was used for subsequent reactions. The qRT-PCR reactions were performed using an ABI7500 System (Thermo Fisher Scientific) and SYBR Green PCR Master Mix (TaKaRa). GAPDH was used as endogenous control. The primers used in this study are as follows: DANCR: forward 5′-GCCACTATGTAGCGGGTTTC-3′, reverse 5′-ACCTGCGCTAAGAACTGAGG-3′; GAPDH: forward 5′-TGCACCACCAACTGCTTAGC-3′, reverse 5′-GGCATGCACTGTGGTCATGAG-3′. All assays were performed in triplicate. Statistical analyses of the results were performed using the $2^{-\Delta\Delta Ct}$ relative quantification method.

Transwell assay and Matrigel assay

The transfected cells and corresponding control cells (1×10^5) were suspended with fresh medium (200 μL) and added into the upper side of Transwell chambers (8 μm pore size; BD Biosciences, San Jose, CA, USA), uncoated (in Transwell assay) or coated (in Matrigel assay) with 50 μL Matrigel (BD Biosciences). The bottom chamber was filled with medium containing 20% FBS, working as chemo-attractant. After 24-hour incubation, non-migrated cells in the upper chamber were removed and then the migrated cells in the downside of the chamber were fixed with 4% paraformaldehyde for 30 minutes and stained with Giemsa (1:10 dilution) for 30 minutes at room temperature. The cell numbers were counted in five random fields of each chamber under the microscope.

Colony formation assay

Triplicate cultures of transfected PDAC cells and corresponding control cells (500 cells/well) were seeded in six-well plates and maintained at 37°C in a 5% CO_2 atmosphere, and the fresh medium was added every 2 days. Two weeks later, formed colonies were fixed with methanol and stained with 0.1% crystal violet (Sigma-Aldrich Co., St Louis, MO, USA). Colonies with more than 50 cells were counted. Each experiment was repeated in triplicate.

Cell Counting Kit-8 (CCK-8) assay

The CCK-8 (Dojindo, Kumamoto, Japan) assay was conducted according to the manufacturer's protocol. Briefly, transfected PDAC cells and corresponding control cells (2×10^4 cells per well) were plated in 24-well plates in triplicate. CCK-8 reagent was added at the indicated time points (0, 24, 48, 72 and 96 hours), and the cells were cultured for a further 4 hours at 37°C. Absorbance at 450 nm was measured using a microplate reader.

Statistical analyses

All statistical analyses were performed using SPSS 16.0 (SPSS Inc., Chicago, IL, USA). Continuous data were analyzed using an independent *t*-test between two groups. Categorical data were analyzed using the chi-squared test or Fisher's exact test as appropriate. Overall survival (OS)

rate and progression-free survival (PFS) rate were calculated using the Kaplan–Meier method and the log-rank test for comparisons. Multivariate survival analyses were performed on all factors that were significant in univariate analyses using the Cox regression model. A *P*-value of <0.05 was considered to represent statistical significance.

Results

DANCR overexpression implicates cancer progression in PDAC

Comparison of DANCR expression in PDAC cell lines with human pancreatic ductal epithelial cell line, HPDE, was carried

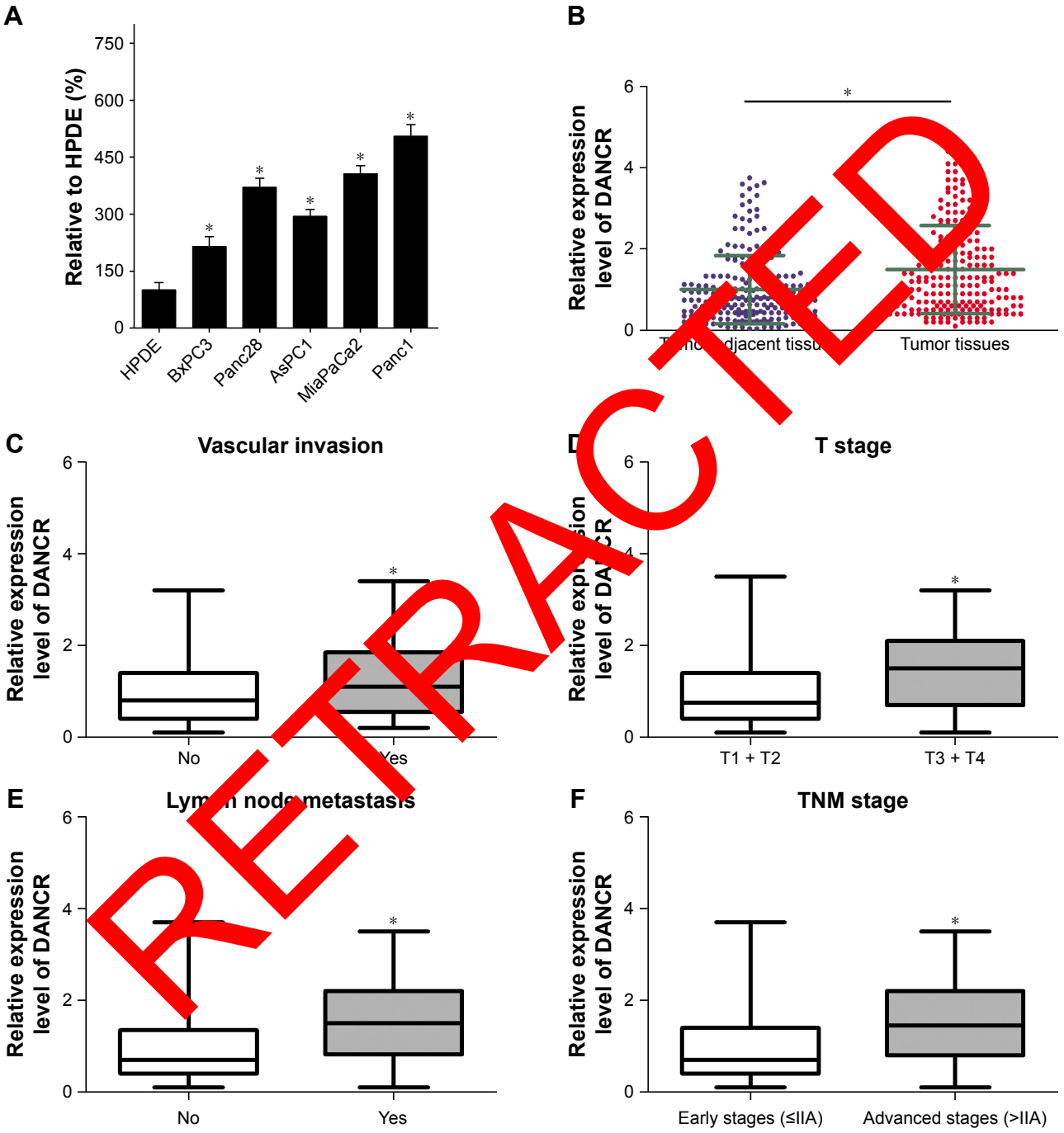

Figure 1 DANCR overexpression implicates cancer progression in PDAC.

Notes: (**A**) Expression of DANCR in five PDAC cell lines (BxPC3, Panc28, AsPC1, MiaPaCa2 and Panc1) and human pancreatic ductal epithelial cell line, HPDE, was measured by qRT-PCR assay. (**B**) The expression level of DANCR in PDAC tissues relative to paired tumor-adjacent tissues was detected by qRT-PCR assay and calculated. (**C**) The expression level of DANCR in PDAC tissues with vascular invasion evaluated by qRT-PCR assay was compared with PDAC tissues without vascular invasion. (**D**) The expression level of DANCR in PDAC tissues with T-stage T1 and T2 detected by qRT-PCR assay was compared with PDAC tissues with T-stage T3 and T4. (**E**) The expression level of DANCR in PDAC tissues with lymph node metastasis detected by qRT-PCR assay was compared with PDAC tissues without lymph node metastasis. (**F**) The expression level of DANCR in PDAC tissues with TNM early stages detected by qRT-PCR assay was compared with PDAC tissues with TNM advanced stages. *$P<0.05$.

Abbreviations: DANCR, differentiation antagonizing nonprotein coding RNA; PDAC, pancreatic ductal adenocarcinoma; qRT-PCR, quantitative real time polymerase chain reaction.

out by the qRT-PCR assay, which revealed that DANCR was overexpressed in five PDAC cell lines compared with HPDE cells ($P<0.05$; Figure 1A). For further determination of the expression pattern of DANCR in PDAC, DANCR expression was evaluated in 206 PDAC tissues and paired tumor-adjacent tissues. Interestingly, PDAC tissues displayed a notably higher DANCR expression level than paired tumor-adjacent tissues ($P<0.05$; Figure 1B). The PDAC tissues were dichotomized with the mean expression level of DANCR serving as the cutoff value, including the high DANCR expression group (n=86) and the low DANCR expression group (n=120). The relationship between DANCR expression and clinicopathological features of PDAC was statistically analyzed, which found that high DANCR expression correlated with vascular invasion ($P=0.013$), advanced T stage ($P=0.005$), lymph node metastasis ($P<0.001$) and advanced TNM stage ($P<0.001$; Table 1). In addition, patients with vascular invasion (Figure 1C), advanced T stage (Figure 1D), lymph node metastasis (Figure 1E) and advanced TNM stage (Figure 1F) exhibited much higher DANCR expression level. Overall, high DANCR expression indicates advanced tumor stage, and DANCR may promote the clinical progression of PDAC.

DANCR overexpression indicates poor prognosis in PDAC

To evaluate the prognostic significance of DANCR in PDAC, the OS rate and PFS rate of PDAC patients with high DANCR expression and low DANCR expression were depicted with the Kaplan–Meier analysis and compared with the log-rank test. As shown in Figure 2A and B, patients with low DANCR expression had a significantly higher OS rate and PFS rate. Univariate analysis found that high DANCR expression (HR =1.224, 95% CI =1.120–1.302, $P<0.001$) was one of the six risk factors related to poor OS of PDAC (Table 2). Besides, multivariate analysis further identified high DANCR expression as an independent risk factor of poor OS of PDAC (HR =1.199, 95% CI =1.113–1.290, $P<0.001$; Table 2). Similarly, univariate analysis found that high DANCR expression (HR =1.219, 95% CI =1.146–1.296, $P<0.001$) was one of the six risk factors related to poor PFS of PDAC (Table 3). In addition, multivariate analysis further identified high DANCR expression as an independent risk factor of poor PFS of PDAC (HR =1.199, 95% CI =1.114–1.290, $P<0.001$; Table 3). Taken together, high DANCR expression predicts poor OS and PFS, and high DANCR expression is an independent risk factor of poor OS and PFS.

DANCR accelerates metastasis and proliferation of PDAC cells

The above-mentioned observations suggested that DANCR expression level may be associated with with clinical progression and poor prognosis of PDAC. The following assays would try to detect the functional role of DANCR in metastasis and proliferation of PDAC. The expression of DANCR was silenced and upregulated in Panc1 cells and BxPC3 cells, respectively (Figure 3A and B). The Transwell assay and the Matrigel assay found that the loss of DANCR obviously inhibited the migration and invasion of Panc1 cells, respectively (Figure 3C). Therefore, the migration and invasion abilities were evidently accelerated after DANCR

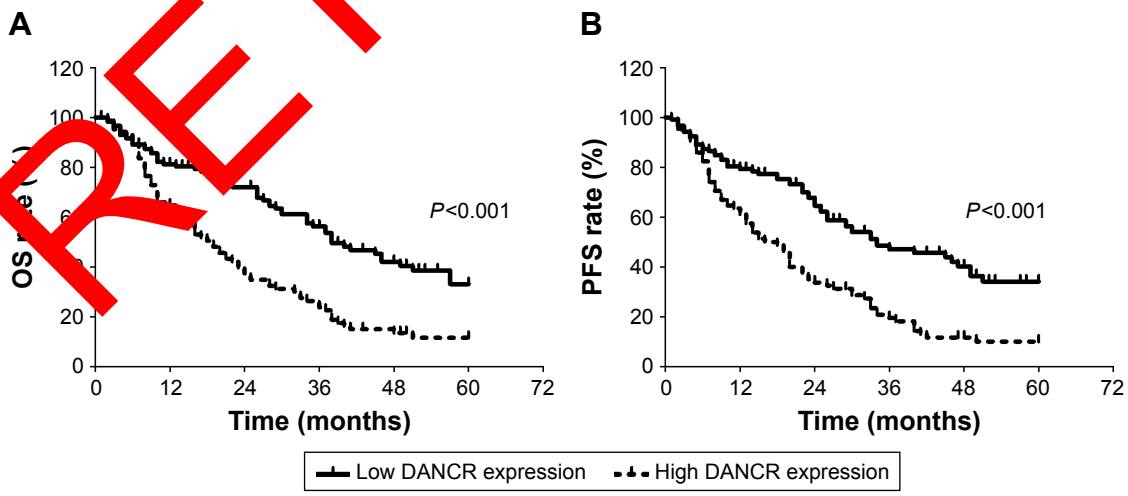

Figure 2 DANCR overexpression indicates poor prognosis in PDAC.
Notes: (**A**) The OS rate of PDAC patients with low DANCR expression and high DANCR expression was depicted with the Kaplan–Meier analysis and compared with the log-rank test. (**B**) The PFS rate of PDAC patients with low DANCR expression and high DANCR expression was depicted with the Kaplan–Meier analysis and compared with the log-rank test.
Abbreviations: DANCR, differentiation antagonizing nonprotein coding RNA; OS, overall survival; PDAC, pancreatic ductal adenocarcinoma; PFS, progression-free survival.

Table 2 Univariate and multivariate analysis of clinicopathologic features for OS of PDAC patients

Parameters	Univariate analysis			Multivariate analysis		
	HR	95% CI	*P*-value	HR	95% CI	*P*-value
Age: ≥60 years vs <60 years	0.837	0.54–1.181	0.311			
Gender: male vs female	1.446	0.992–2.109	0.055			
CEA: ≥4.5 μg/mL vs <4.5 μg/mL	0.940	0.631–1.400	0.760			
CA19–9: <37 U/mL vs ≥37 U/mL	1.030	0.729–1.455	0.867			
Tumor location: head and neck vs body and tail	1.101	0.765–1.585	0.604			
Grade: well + moderate vs poor	1.027	0.717–1.469	0.886			
Size: <4 cm vs ≥4 cm	0.952	0.670–1.351	0.783			
Neural invasion: yes vs no	1.179	0.834–1.667	0.350			
Vascular invasion: no vs yes	1.528	1.084–2.154	0.015	1.463	1.033–2.072	0.032
Lymphatic invasion: no vs yes	0.763	0.535–1.089	0.137			
T stage: T1 + T2 vs T3 + T4	1.863	1.310–2.648	0.001	0.964	.511–1.818	0.909
Lymph node metastasis: no vs yes	1.795	1.275–2.529	0.001	1.344	0.550–3.285	0.516
Distant metastasis: no vs yes	11.172	4.320–28.890	<0.001	6.1	99–16.213	<0.001
TNM stage: early stages (≤IIa) vs advanced stages (>IIa)	1.621	1.151–2.283	0.006	43	0.3 1.885	0.677
DANCR: high vs low	1.224	1.150–1.302	<0.001	1.199	1.113– 0	<0.001

Abbreviations: DANCR, differentiation antagonizing nonprotein coding RNA; OS, overall survival; PDAC, pancrea duc de carcinoma.

overexpression in BxPC3 cells (Figure 3D). Furthermore, the colony formation assay and the CCK-8 assay found that DANCR deficiency notably decreased the colony numbers and OD value of Panc1 cells (Figure 4A and B). Accordingly, DANCR ectopic expression remarkably increased the colony numbers and OD value of BxPC3 cells (Figure 4C and D). These results confirmed that DANCR could accelerate t metastasis and proliferation of PDAC cells.

DANCR may function through up egul ing AXL via microRNA-33a-5p inh bitio

DANCR has been reported to comp tively act with miR-634 and miR-33a-5p, thus reg downstrea rotein expression in glioma and osteosarcoma, r pectively.[23,24] The expression of iR 34 and miR- -5p was also investigated in PDAC cells by qRT CR. The results showed that miR-33-a-5p w noticeably dow gulated in BxPC3 with DANCR ove xpression (Figure 5A), accompanied with increased exp ssion of AX (Figure 5B), the downstream protein of miR- -5p. Ac ordingly, when DANCR was silenced in nc1 cells, the expression of miR-33a-5p was upregulated (F G), while the expression of AXL was significantly suppressed (Figure 5D). However, the expression of miR-34 and its downstream protein, RAB1A, was not changed when DANCR was knocked down or overexpressed (Figure 5A–D). These evidences indicate that DANCR may also function through upregulating AXL via microRNA-33-a-5p inhibition in PDAC cells.

Table 3 Univariate and m ivariate alysis of clinicopathologic features for PFS of PDAC patients

Parameters	Univariate analysis			Multivariate analysis		
	HR	95% CI	*P*-value	HR	95% CI	*P*-value
Age: ≥60 years <60 ye	0.863	0.612–1.218	0.402			
Gender: male female	1.444	0.991–2.105	0.056			
CEA: ≥4.5 μg/m .5 μg/mL	0.950	0.638–1.415	0.801			
CA19–9: <37 U/mL ≥37 U/mL	0.981	0.695–1.385	0.913			
Tumor location: head a eck vs body and tail	1.161	0.810–1.664	0.416			
Grade: well + moderate vs poor	1.056	0.739–1.508	0.765			
Size: <4 cm vs ≥4 cm	0.992	0.699–1.406	0.963			
Neural invasion: yes vs no	1.165	0.824–1.646	0.388			
Vascular invasion: no vs yes	1.416	1.004–1.996	0.047	1.343	0.948–1.903	0.097
Lymphatic invasion: no vs yes	0.795	0.556–1.136	0.208			
T stage: T1 + T2 vs T3 + T4	1.775	1.245–2.530	0.002	0.892	0.488–1.631	0.711
N stage: N1 vs N0	1.769	1.256–2.493	0.001	1.405	0.595–3.315	0.438
M stage: M1 vs M0	10.762	4.170–27.780	<0.001	6.081	2.292–16.131	<0.001
TNM stage: early stages (≤IIa) vs advanced stages (>IIa)	1.593	1.131–2.244	0.008	0.831	0.379–1.821	0.643
DANCR: high vs low	1.219	1.146–1.296	<0.001	1.199	1.114–1.290	<0.001

Abbreviations: DANCR, differentiation antagonizing nonprotein coding RNA; PDAC, pancreatic ductal adenocarcinoma; PFS, progression-free survival.

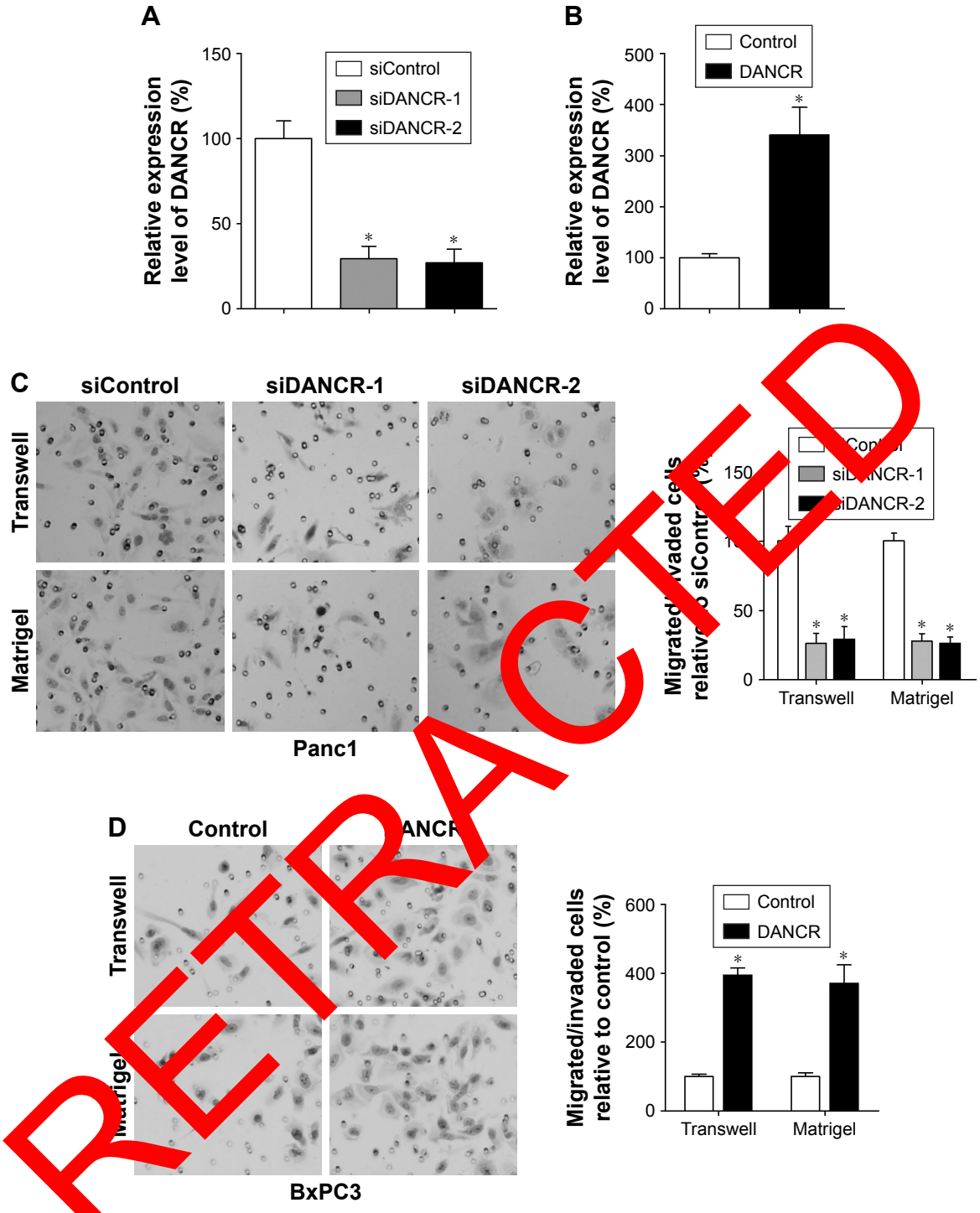

Figure 3 DANCR accelerates metastasis of PDAC cells.
Notes: (**A**) The relative expression level of DANCR in Panc1 cells after DANCR interference was determined by qRT-PCR assay. (**B**) The relative expression level of DANCR in BxPC3 cells after DANCR overexpression was confirmed by qRT-PCR assay. (**C**) The migration and invasion abilities of Panc1 cells with DANCR silencing were analyzed with Transwell assay and Matrigel assay, respectively (right panel). Typical images are shown in the left panel. (**D**) The migration and invasion abilities of BxPC3 cells with DANCR overexpression were revealed with Transwell assay and Matrigel assay, respectively (right panel). Typical images are shown in the left panel. *$P<0.05$.
Abbreviations: DANCR, differentiation antagonizing nonprotein coding RNA; PDAC, pancreatic ductal adenocarcinoma; qRT-PCR, quantitative real time polymerase chain reaction.

Conclusion

Increasing data suggest that lncRNAs play pivotal roles in the progression of PDAC, which indicated that lncRNAs were involved in tumor growth, survival, epithelial–mesenchymal transition (EMT), tumor microenvironment, cancer stem cells (CSCs) and chemoresistance in PDAC.[25] lncRNAs can mediate the expression of miRNA-targeted genes through functioning as miRNA sponge.[26,27] EMT is

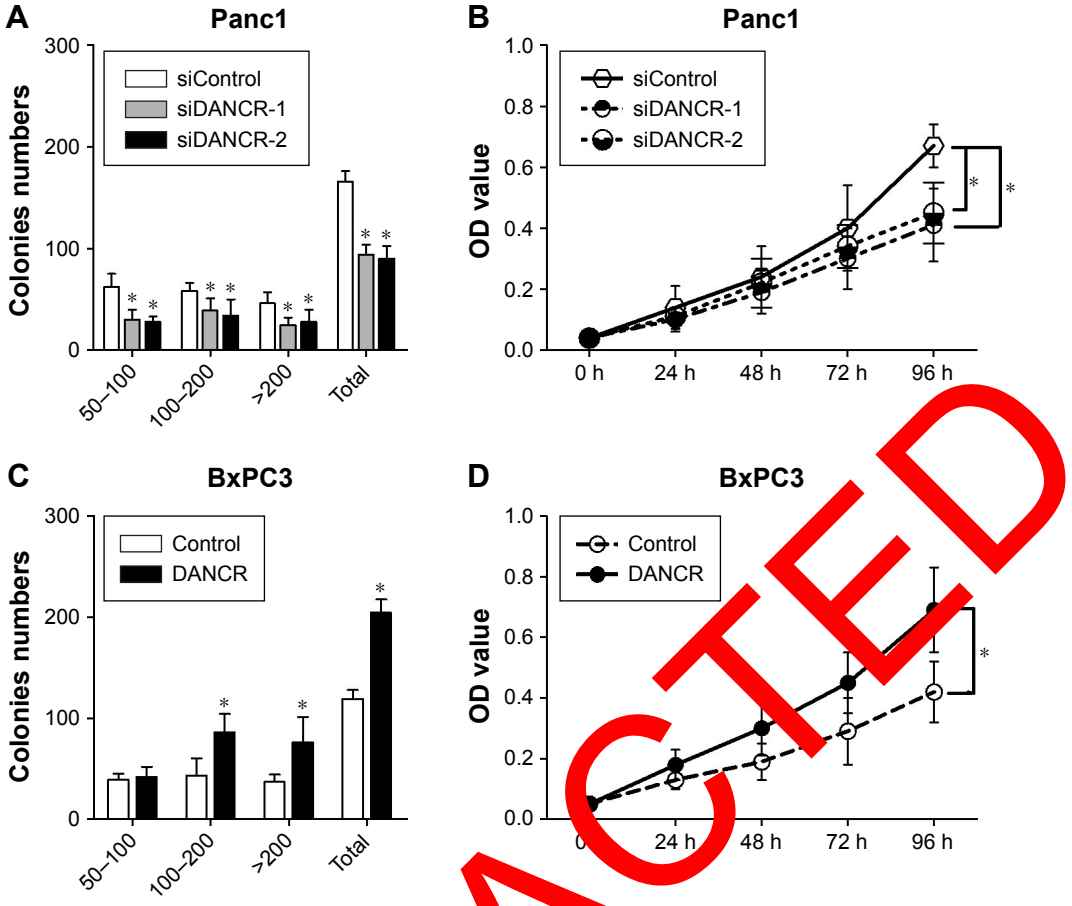

Figure 4 DANCR increases proliferation of PDAC cells.
Notes: (**A**) Colony formation assay was performed to verify the proliferation ability of Panc1 cells after DANCR silencing. The 50–100/100–200/>200 brackets represent cell numbers in each colony. (**B**) The proliferation ability of Panc1 cells with DANCR deficiency was evaluated by CCK-8 assay. (**C**) Colony formation assay was performed to verify the proliferation ability of BxPC3 cells after DANCR overexpression. The 50–100/100–200/>200 brackets represent cell numbers in each colony. (**D**) The proliferation ability of BxPC3 cells with DANCR overexpression was evaluated by CCK-8 assay. *$P<0.05$.
Abbreviations: CCK-8, Cell Counting Kit-8; DANCR, differentiation antagonizing nonprotein coding RNA; h, hour(s); PDAC, pancreatic ductal adenocarcinoma.

an initial step in cancer metastasis.[28] Accumulating studies found that lncRNAs participate in the EMT of PDAC.[29–32] For example, lncRNA regulator of reprogramming was reported to promote the aggressive biological behaviors of PDAC by acting as a regulator of ZEB2, which is a primary transcriptional factor in the EMT progress, and thus increase the invasion and metastasis of PDAC.[29] CSCs are also an important way by which lncRNAs exert their functions in modulating the development of PDAC.[33,34] Chemoradioresistance is an essential reason leading to the relapse of cancer patients. Multiple studies have focused on the potential role of lncRNAs in chemoradioresistance.[35–39] Combination of lncRNAs and conventional chemotherapeutic reagents is considered as a promising way for improving the sensitivity of adjuvant therapy.[39] There are also studies that revealed that lncRNAs could modulate the epigenetic modifications and autophagy in PDAC.[40–42] Obviously, lncRNAs can function in a wide range of cancer biology; however, clinical trials investigating lncRNAs in the treatment of PDAC are rare, and further studies are needed for utilizing lncRNAs in clinical practice.

Since being discovered in 2012,[17] DANCR has attracted much attention for its critical role in cancer biology. DANCR is now regarded as an oncogene for promoting cancer growth and metastasis in hepatocellular carcinoma,[43] glioma,[24] gastric cancer,[44] osteosarcoma,[23] lung adenocarcinoma,[22] prostate cancer[21] and colorectal cancer.[45] DANCR was also implicated to be a diagnostic and prognostic marker.[19,20,43] Mechanistically, DANCR could directly interact with miR-634 and this interaction resulted in the inhibition of RAB1A expression, thus accelerating the progression of glioma.[24] By competitively binding to miR-33a-5p, DANCR could upregulate the expression of the receptor tyrosine kinase AXL and increase the function of CSCs in osteosarcoma.[23] The mechanisms of DANCR mediating cancer progression are relatively rare, which deserves further investigations.

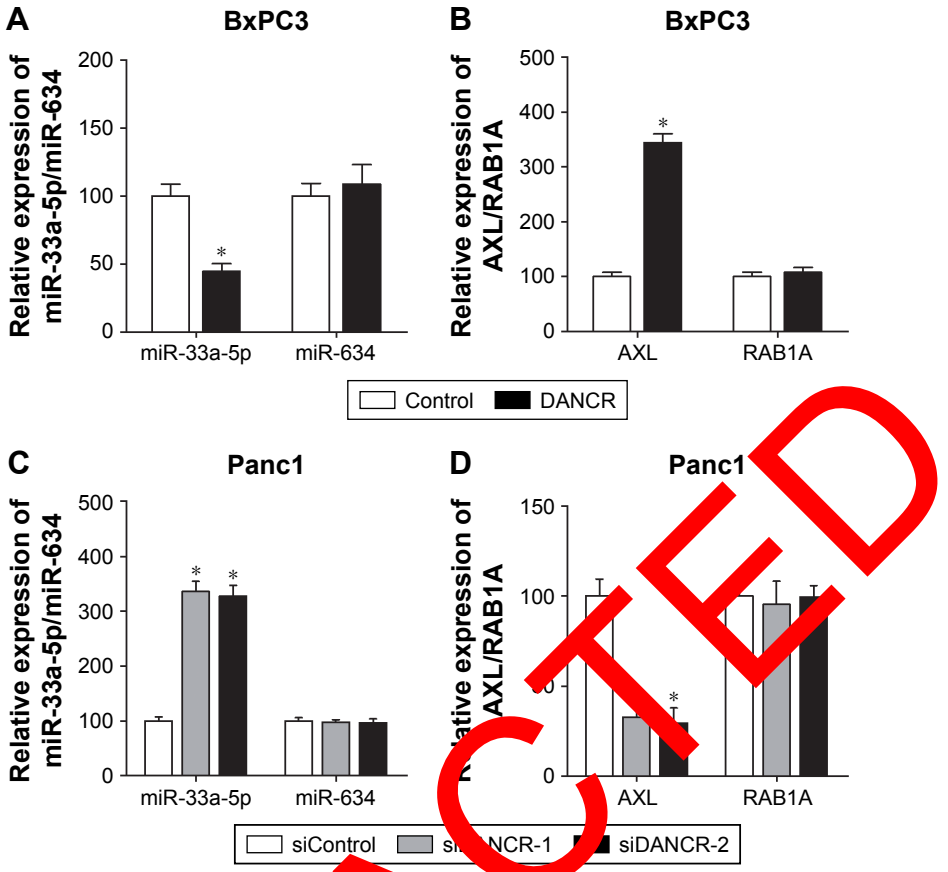

Figure 5 DANCR functions through upregulating AXL via microRNA-33a-5p inhibition.
Notes: (**A**) Expression of miR-33a-5p and miR-634 was measured by qRT-PCR in BxPC3 cells with DANCR overexpression. (**B**) Expression of AXL and RAB1A was detected by qRT-PCR in BxPC3 cells with DANCR overexpression. (**C**) Expression of miR-33a-5p and miR-634 was measured by qRT-PCR in Panc1 cells with DANCR deficiency. (**D**) Expression of AXL and RAB1A was detected by qRT-PCR in Panc1 cells with DANCR deficiency. *$P<0.05$.
Abbreviations: DANCR, differentiation antagonizing non-protein coding RNA; qRT-PCR, quantitative real time polymerase chain reaction.

This study discovered that DANCR was overexpressed in PDAC tissues compared with tumor-adjacent tissues. Further detection found that high DANCR expression was correlated with vascular invasion (P=0.013), advanced T stage (P=0.005), lymph node metastasis ($P<0.001$) and advanced TNM stage ($P<0.001$), all of which are critical factors evaluating cancer progression and prognosis. Moreover, high DANCR expression correlated with poor OS and PFS. Multivariate analysis identified high DANCR expression as an independent survival risk factor for OS and PFS. In addition, DANCR was confirmed to facilitate growth and metastasis of PDAC cells. These results indicated that DANCR is a promising prognostic marker and therapeutic target in PDAC. In addition, DANCR may function through upregulating AXL via microRNA-33a-5p inhibition.

In conclusion, our study confirmed the overexpression of DANCR in PDAC cells and tissues. The clinical significance and prognostic value of DANCR were also detected. In vitro assays demonstrated the oncogenic role of DANCR. These observations demonstrated that DANCR plays a crucial role in the progression of PDAC, and DANCR might potentially serve as a prognostic marker and therapeutic target for PDAC patients.

Disclosure

The author reports no conflicts of interest in this work.

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