

Research Article

Prognostic significance of lncRNA DANCR expression in human cancers: a systematic review and meta-analysis

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Several studies demonstrated that lncRNA differentiation antagonizing non-protein coding RNA (lncRNA DANCR) expression might have the potential capacity to predict the cancer prognosis; however, definite conclusion has not been obtained. The aim of this meta-analysis was to evaluate the prognostic value of lncRNA DANCR expression in cancers. PubMed, Web of Science, Scopus, and Embase were comprehensively searched for relevant studies. Studies meeting all inclusion standards were included into this meta-analysis. The analysis of overall survival (OS), disease-free survival (DFS), or clinicopathological features was conducted. Total 11 studies containing 1154 cancer patients were analyzed in this meta-analysis. The results showed, compared with low lncRNA DANCR expression, high lncRNA DANCR expression was significantly associated with shorter OS (hazard ratio [HR] = 1.85; 95% CI = 1.52–2.26; $P < 0.01$) and DFS (HR = 1.82; 95% CI = 1.43–2.32; $P < 0.01$) in cancers. Besides, high lncRNA DANCR expression predicted deeper tumor invasion ($P < 0.01$), earlier lymph node metastasis ($P < 0.01$), earlier distant metastasis ($P < 0.01$), and more advanced clinical stage ($P < 0.01$) compared with low lncRNA DANCR expression in cancer populations. High lncRNA DANCR expression was associated with worse prognosis compared with low lncRNA DANCR expression in cancers. lncRNA DANCR expression could serve as a prognostic factor of human cancers.

Introduction

Cancer has become a crucial public health problem and a leading cause of death worldwide [1,2]. Despite of tremendous improvement of diagnosis and treatments, the prognosis of many cancer patients at terminal stage remains disappointing [2,3]. The lack of efficient biomarkers to serve as treatment targets and predict the prognosis is considered as the main reason for this dilemma. Therefore, a growing number of researchers begin to look for optimal biomarkers of human cancers [4,5].

With the rapid development of high-throughput sequencing technology, increasing lncRNAs are discovered and have become the research hotspots [6]. lncRNA, greater than 200 nts in length, is a major type of ncRNAs without protein-coding capability [7]. Recently, lncRNAs have been proved to be closely associated with tumorigenesis, differentiation, invasion, and metastasis of cancers [8,9]. lncRNA differentiation antagonizing non-protein coding RNA (lncRNA DANCR), a kind of lncRNA, is located on human chromosome 4 [10]. Recently, accumulating studies have supported a substantial role of lncRNA DANCR expression in the cancer prognosis [11–21]. However, conclusion has not been reached for the contradictory results amongst different publications [11–21]. Here, we conducted this systematic review and meta-analysis to determine the prognostic value of lncRNA DANCR expression in cancers.

Received: 15 September 2018
Revised: 20 January 2019
Accepted: 07 February 2019

Version of Record published:
12 August 2021

Materials and methods

The present study was performed in accordance with Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) [22] (Supplementary Table S1)

Literature search and selection

PubMed, Web of Science, Scopus, and Embase were comprehensively searched up to 15 January 2019. The strategy was as following: ('lncRNA differentiation antagonizing non-protein coding RNA' OR 'lncRNA DANCR' OR 'lncRNA DANCR' OR 'DANCR') AND ('cancer' OR 'tumor' OR 'neoplasm' OR 'carcinoma'). There was no restriction on the language. References of retrieved studies were also checked to avoid missing relevant studies. All studies were selected according to inclusion and exclusion criteria.

Inclusion and exclusion criteria

The study was considered to be eligible if it satisfied the following criteria: (1) patients were pathologically diagnosed as cancers; (2) prognostic value of lncRNA DANCR expression in cancers was assessed; (3) overall survival (OS), disease-free survival (DFS), recurrence-free survival (RFS), or clinicopathological feature was reported; (4) patients were divided into two groups based on the expression level of lncRNA DANCR; (5) full text and sufficient data were provided. The following studies were excluded: reviews, comments, letters, case reports, cell experiments, animal experiments, unpublished studies, and duplications.

Data extraction and quality evaluation

Data extraction and quality evaluation were independently operated by two authors. Any disagreement would be solved by discussing with the third author. The following items were extracted: first author, publication year, country, sample size, gender, expression level of lncRNA DANCR, cancer type, outcomes, and analysis model of OS. As for prognostic variables (e.g., OS, DFS, and RFS), HR and corresponding 95% CI were directly extracted from published studies or indirectly calculated from survival curves if only survival curves were available [23]. Moreover, if HR and 95% CI were simultaneously provided in the multivariate analysis and univariate analysis, the former were used. The analysis model of OS was considered as univariate analysis when HR and 95% CI were indirectly calculated from survival curves. Quality of included studies was assessed with Newcastle–Ottawa Scale (NOS). We considered studies with scores no less than six as high-quality studies [24].

Statistical analysis

For prognostic variables, such as OS, DFS, and RFS, HR and 95% CI were pooled to assess the relationship between lncRNA DANCR expression and cancer prognosis. As for dichotomous, such as gender, lymph node metastasis, and clinical stage, odds ratio (OR) and 95% CI were applied to detect the overall effects. Heterogeneity was assessed using Cochran's Q test and Higgins I-squared statistics. $I^2 > 50\%$ and/or $P < 0.10$ suggested obvious heterogeneity amongst studies, as a result, a random-effect model was utilized. Alternatively, a fixed-effect model was used. Sensitivity analysis was done by omission of each single study. Publication bias was evaluated using Begg's test and funnel plots. All analyses were conducted by Reviewer Manager 5.3 (Cochrane Collaboration, Copenhagen, Denmark) and Stata 12.0 (Stata Corporation, College Station, Texas, U.S.A.). All *P* values were two sides and difference was considered significant when *P* value was less than 0.05.

Results

Literature search and selection

A total of 118 articles were initially retrieved from four common databases (Figure 1). A total of 38 articles remained for further evaluation after the removal of duplicates. Then, 23 articles were directly excluded by scanning titles or abstracts. Regarding to the remaining 15 articles, four articles were excluded by evaluating full-texts. Ultimately, 11 studies were included for further analysis [11–21].

Basic information of included studies

The basic information of studies included was listed in Table 1. A total of 11 studies containing 1154 cancer patients were included into this research [11–21]. Especially, Yuan et al. study consisted of two cohorts (cohort 1: Chinese population; cohort 2: Korea population) [21]; therefore, 12 cohorts were analyzed in this research. Seven studies reported the clinical stage of patients (I/II: 235 patients; III/IV: 317 patients) [11,13–16,18,19]. Besides, lncRNA



PRISMA 2009 Flow Diagram

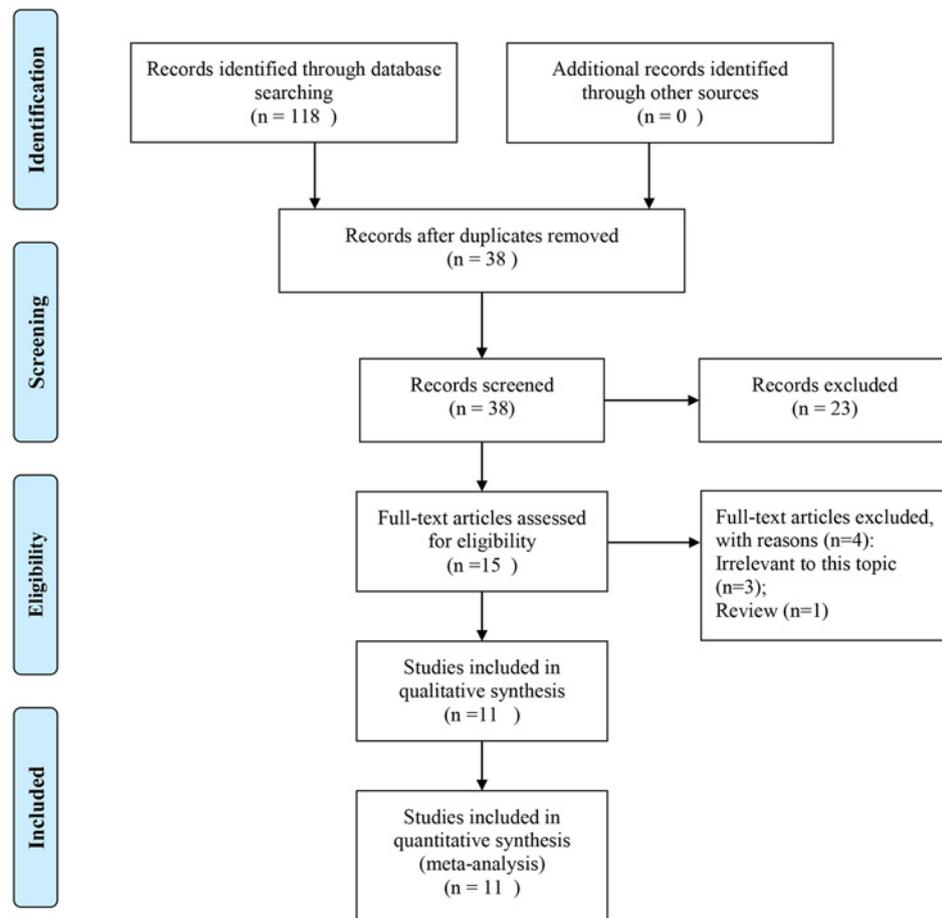


Figure 1. Flow chart of literature search and selection

DANCR expression in cancer tissues was evaluated using quantitative reverse transcription polymerase chain reaction (qRT-PCR) in all studies [11–21]. Three studies used the median value [13,14,21] and one study used the normalized value to divide patients into high or low lncRNA DANCR expression groups [16]; however, the other studies failed to provide the definite cut-off value [11,12,15,17–20]. Additionally, seven types of cancer were investigated, including gastric cancer [11,14,15], osteosarcoma [12,19], non-small cell lung cancer [17], colorectal cancer [13,18], breast cancer [16], and glioma [20] as well as hepatocellular carcinoma [21]. Patients received surgical treatment in eight studies [11–13,15,16,18–20]; nevertheless, treatment of patients in the other studies was not available [14,17,21]. Regarding to outcomes, nine studies reported clinicopathological parameters (CPs) [11–16,18–20], eight studies reported OS [11–13,16,17,19–21], two studies reported DFS [12,13], and one study reported RFS [21]. Moreover, OS was evaluated using multivariate analysis model in three cohorts [12,13,21] and univariate analysis model in six cohorts [11,16,17,19–21]. NOS score was larger than six in all studies, which indicated all studies were with high quality [11–21].

Meta-analysis for the association between lncRNA DANCR expression and prognosis

Eight studies evaluated the correlation between lncRNA DANCR expression and OS, and all of them were included into the analysis [11–13,16,17,19–21]. As shown in Figure 2, a fixed-effect model was used because there was no

Table 1 Basic information of included studies

Study	Country	Sample size (n)	Clinical stage (I+II/III+IV)	Detection methods	Cut-off value	Cancer type	Treatments	Outcomes	Analysis model	NOS
Hao 2017 [11]	China	118	48/70	qRT-PCR	NA	Gastric cancer	Surgery	CP, OS	U	7
Jiang 2017 [12]	China	34	NA	qRT-PCR	NA	Osteosarcoma	Surgery	CP, DFS, OS	M	8
Jiang 2018 [17]	China	128	NA	qRT-PCR	NA	NSCLC	NA	OS	U	6
Liu 2015 [13]	China	104	37/67	qRT-PCR	Median	Colorectal cancer	Surgery	CP, DFS, OS	M	8
Mao 2017 [14]	China	60	33/27	qRT-PCR	Median	Gastric cancer	NA	CP	NA	6
Pan 2018 [15]	China	65	19/46	qRT-PCR	NA	Gastric cancer	Surgery	CP	NA	6
Sha 2017 [16]	China	63	37/26	qRT-PCR	≤0.5 / ≥2.0†	Breast cancer	Surgery	CP, OS	U	7
Wang 2018 [19]	China	95	42/53	qRT-PCR	NA	Osteosarcoma	Surgery	CP, OS	U	7
Yang 2018 [20]	China	82	NA	qRT-PCR	NA	Glioma	Surgery	CP, OS	U	7
Yuan 2016 [21]	China	135	NA	NA	Median	Hepatocellular carcinoma	NA	RFS, OS	M	7
Yuan 2016 [21]	Korea	223	NA	NA	Median	Hepatocellular carcinoma	NA	RFS, OS	U	6
Zeng 2018 [18]	China	47	19/28	qRT-PCR	NA	Colorectal cancer	Surgery	CP	NA	6

†The normalized values ≤0.5 and ≥2.0 were used to determine low-expression and high-expression of DANCR expression, respectively. M, multivariate; NA, not available; NSCLC, non-small cell lung cancer; U, univariate.

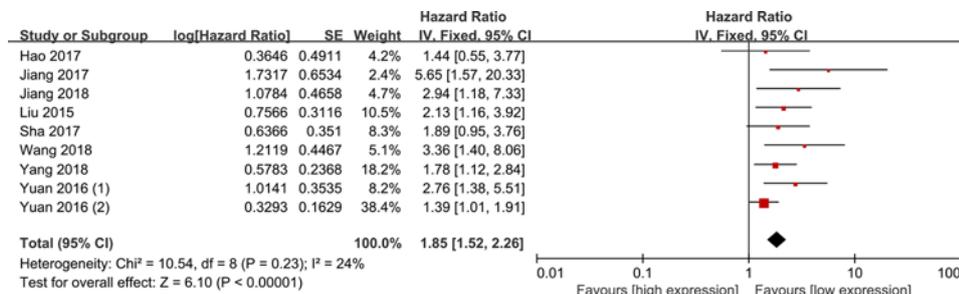


Figure 2. Meta-analysis of the association between lncRNA DANCR expression and OS

obvious heterogeneity amongst included studies ($I^2 = 24\%$, $P=0.23$). High lncRNA DANCR expression was significantly correlated with shorter OS compared with low lncRNA DANCR expression in cancers (HR = 1.85; 95% CI = 1.52–2.26; $P<0.01$).

To further explore the prognostic value of lncRNA DANCR expression in cancers, subgroup analysis was performed (Table 2). Significant relationship between high lncRNA DANCR expression and shorter OS was detected in all subgroup analyses ($P<0.05$).

Two studies reported DFS [12,13] and one study reported RFS [21], and all of them were included into the analysis for DFS (Figure 3). A fixed-effect model was used because of the moderate heterogeneity ($I^2 = 43\%$, $P=0.15$). Compared with patients with low lncRNA DANCR expression, patients with high lncRNA DANCR expression tended to have a shorter DFS (HR = 1.82; 95% CI = 1.43–2.32; $P<0.01$).

Meta-analysis for the association between lncRNA DANCR expression and CPs

Meta-analyses for the association between lncRNA DANCR expression and CPs were conducted (Table 3). There was no obvious relationship between the expression level of lncRNA DANCR and age ($P=0.26$), gender ($P=0.42$), tumor

Table 2 Subgroup analysis for the association between lncRNA DANCR expression and OS

Variables	Cohorts (n)	HR (95% CI)	P value	Heterogeneity		Model
				I ² (%)	P value	
Analysis model						
Multivariate	3	2.63 (1.71–4.05)	<0.01‡	0	0.4	Fixed
Univariate	6	1.69 (1.35–2.11)	<0.01‡	9	0.36	Fixed
Sample size (n)						
>100	5	1.71 (1.34–2.18)	<0.01‡	24	0.27	Fixed
≤100	4	2.16 (1.54–3.03)	<0.01‡	26	0.25	Fixed
Cut-off value						
Median	3	1.66 (1.28–2.15)	<0.01‡	49	0.14	Fixed
Others	6	2.14 (1.59–2.90)	<0.01‡	1	0.41	Fixed
Treatments						
Surgery	6	2.08 (1.56–2.76)	<0.01‡	0	0.47	Fixed
Others	3	2.01 (1.17–3.47)	0.01‡	58	0.09	Random
Cancer type						
Gastrointestinal cancers	4	1.64 (1.28–2.11)	<0.01‡	24	0.27	Fixed
Others	5	2.24 (1.63–3.08)	0.01‡	8	0.36	Fixed

‡ The association was considered significant when $P < 0.05$.

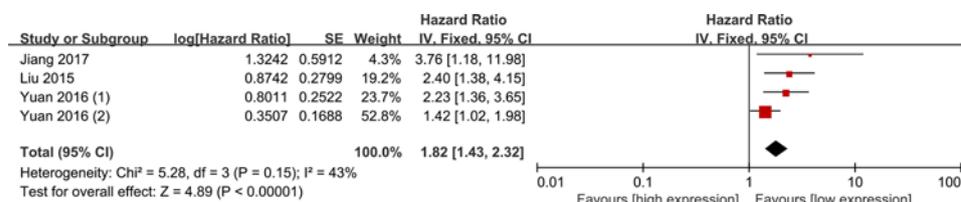


Figure 3. Meta-analysis of the association between lncRNA DANCR expression and DFS

Table 3 Meta-analysis for the association between lncRNA DANCR expression and CPs

Variables	Studies (n)	Patients (n)	OR (95% CI)	P value	Heterogeneity		Model
					I ² (%)	P value	
Age (old versus young)	7	467	1.25 (0.85–1.83)	0.26	0	0.81	Fixed
Gender (male versus female)	7	523	1.16 (0.81–1.67)	0.42	40	0.13	Fixed
Tumor size (large versus small)	7	539	1.31 (0.50–3.46)	0.59	84	<0.01	Random
Tumor differentiation (poor versus well)	5	394	1.99 (0.85–4.70)	0.11	73	<0.01	Random
Invasion depth (T3/T4 versus T1/T2)	3	216	2.68 (1.43–5.04)	<0.01‡	0	0.41	Fixed
Lymph nodes metastasis (yes versus no)	5	339	5.49 (3.29–9.16)	<0.01‡	0	0.67	Fixed
Distant metastasis (yes versus no)	3	207	4.75 (2.17–10.41)	<0.01‡	0	0.72	Fixed
Clinical stage (III/IV versus I/II)	6	435	4.11 (2.68–6.31)	<0.01‡	0	0.94	Fixed

‡ The association was considered significant when $P < 0.05$.

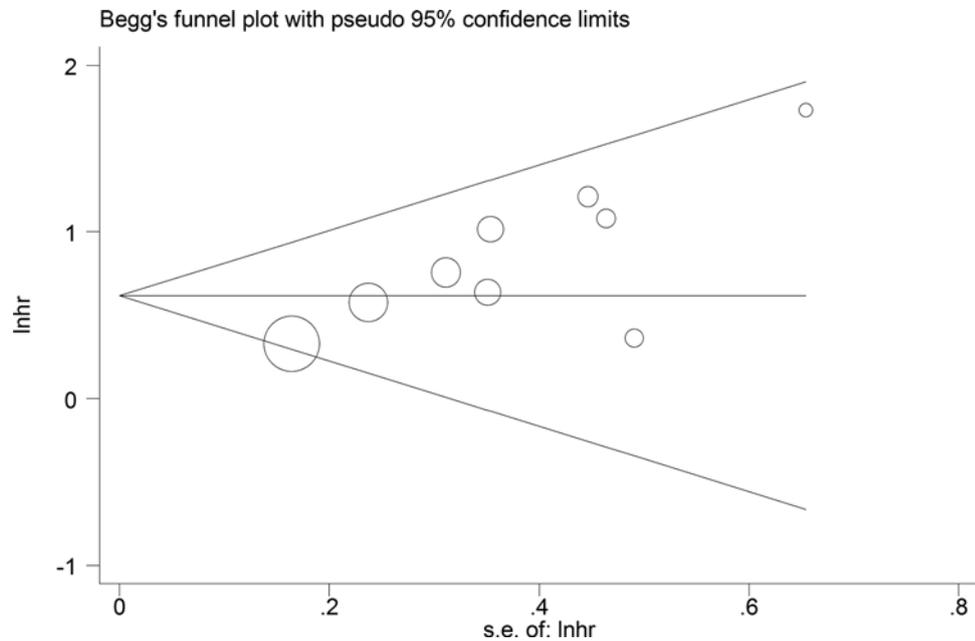


Figure 4. Begg's test for meta-analysis of the association between lncRNA DANCR expression and OS

size ($P=0.59$) or tumor differentiation ($P=0.11$). However, compared with low expression level of lncRNA DANCR, high expression level of lncRNA DANCR was significantly associated with deeper tumor invasion ($P<0.01$), earlier lymph node metastasis ($P<0.01$), earlier distant metastasis ($P<0.01$), and more advanced clinical stage ($P<0.01$).

Publication analysis and sensitivity analysis

Begg's test for the meta-analysis of OS showed that there was no obvious publication bias amongst studies (Figure 4). Funnel plots demonstrated that there was no distinct publication bias with respect to the meta-analyses of DFS and CPs (Figure 5). Sensitivity analysis indicated that the pooled results of OS were not influenced by omitting each single study (Figure 6).

Discussion

lncRNAs have been proved to play a vital role in the tumorigenesis, differentiation, invasion, and metastasis of cancers [25,26]. Many lncRNAs have the potential capacity to predict the cancer progression and prognosis [27,28]. Recently, many studies have found that lncRNA DANCR expression might be involved with the prognosis of cancers; however, dispute remains for conflicting data amongst different studies [11–21].

In our study, we discovered that high lncRNA DANCR expression was significantly associated with shorter OS and DFS in cancers. We also found, compared with patients with low lncRNA DANCR expression, patients with high lncRNA DANCR expression tended to have deeper depth of invasion, earlier lymph node metastasis, earlier distant metastasis, and more advanced clinical stage. Unexpectedly, we failed to observe the relationship of lncRNA DANCR expression with tumor size or differentiation; however, it should be noted that the results were not reliable enough because of the distinct heterogeneity amongst included studies. Overall, high lncRNA DANCR expression was an unfavorable factor in the cancer prognosis. To our knowledge, the present study was the first meta-analysis to explore the prognostic and clinicopathological value of lncRNA DANCR expression in human cancers.

Many researches have tried to elucidate the prognostic role of lncRNA DANCR expression in cancers [11–13]; however, the underlying mechanism remains unclear. Yang et al. found that down-expression of lncRNA DANCR could increase the expression of miR-33a-5p, reduce the EMT and increase the apoptosis of glioma cells [20]. Differently, Li et al. study demonstrated that high lncRNA DANCR expression could positively affect the progression of glioma through activating the Wnt/ β -catenin signaling [29]. Besides, lncRNA DANCR could mediate cisplatin resistance in glioma cells via activating the AXL/PI3K/Akt/NF- κ B signaling pathway [30]. Wang et al. study revealed that lncRNA DNACR facilitated the invasion and metastasis of osteosarcoma by promoting the ROCK1-mediated progression through decoying both miR-1972 and miR-335-5p [19]. Besides, lncRNA DANCR could promote the

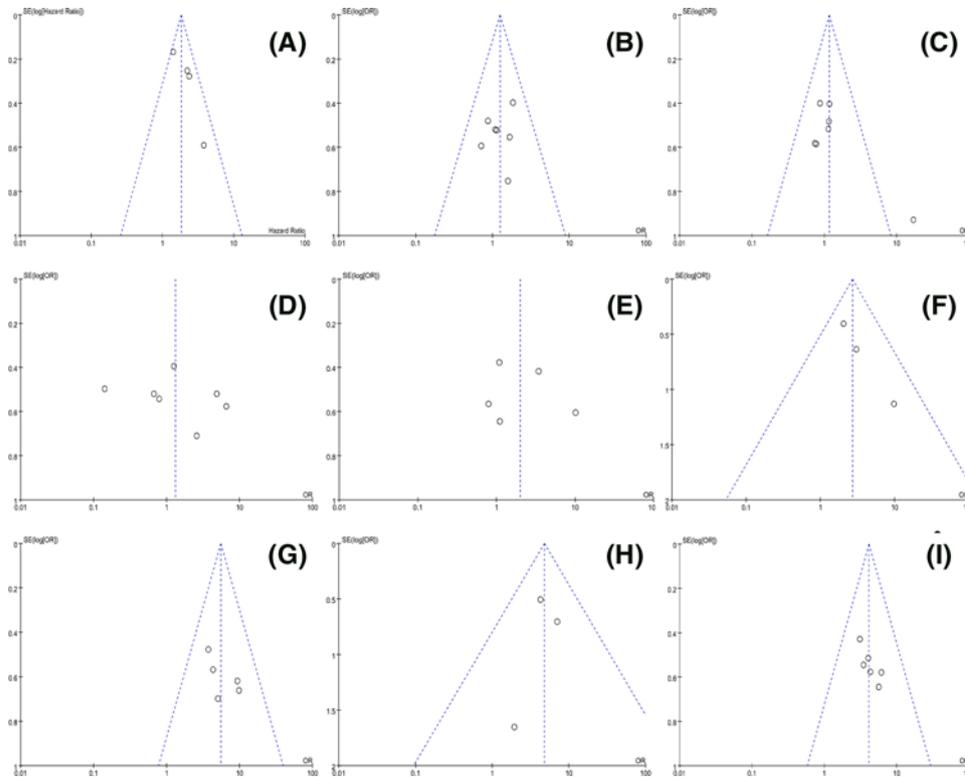


Figure 5. Funnel plots for the meta-analyses of the association between lncRNA DANCER expression and DFS or CPs (a, age; b, gender; c, tumor size; d, tumor differentiation; e, depth of invasion; f, lymph node metastasis; g, distant metastasis; h, clinical stage)

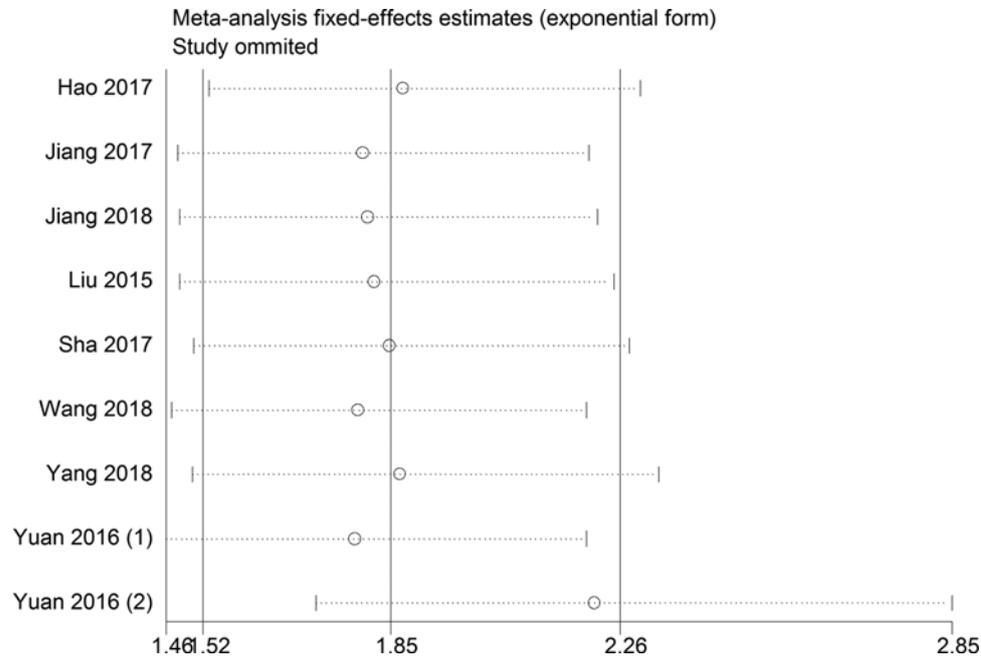


Figure 6. Sensitivity analysis for the meta-analysis of the association between lncRNA DANCER expression and OS

HSP27 expression and its mediation of metastasis via miR-577 sponging in colorectal cancer [31]. Zhen et al. results showed lncRNA DANCR could promote the progression of lung cancer by sequestering the miR-216a [32]. Lu et al. study, also focussing on lung cancer, discovered that lncRNA DANCR expression regulated mTOR expression by directly binding to miR-496 [33]. In gastric cancer, Pan et al. found SALL4 could facilitate the lncRNA DANCR expression and exert its oncogenic activities via activating the β -catenin pathway [15]. As for prostate cancer, Jia et al. study revealed that lncRNA DANCR promoted the tumor invasion and metastasis through the down-expression of TIMP2/3 [34].

Several limitations should be considered when interpreting our results. First, only 11 studies were included into this meta-analysis, which might reduce the stringency of results. Second, most studies included were conducted in China which might result in regional bias. Third, HR and 95% CI were extracted from survival curves in several studies as described by Tierney et al. [23], which might be affected by the subjective factors of operators; however, this method has been widely accepted and used in meta-analyses [35–37]. Fourth, the prognostic value of lncRNA DANCR expression in specific cancer was not determined in the present study because of limited included studies. With a view to these limitations, prospective studies with larger population and longer follow-up time are warranted to clarify this issue.

Conclusion

High lncRNA DANCR expression was associated with shorter OS, shorter DFS, and worse clinicopathological features compared with low lncRNA DANCR expression in human cancers. lncRNA DANCR expression could serve as a promising prognostic factor of human cancers.

Competing interests

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

Funding

The authors declare that there are no sources of funding to be acknowledged.

Author contribution

J.G. and W.L. were responsible for study design. W.L. and Q.P.W. were responsible for literature search. W.L. and Q.P.W. were responsible for data extraction. W.L., Q.P.W., and J.G. were responsible for data analysis. J.G. and W.L. were responsible for drafting the manuscript. All authors approved the final version of the manuscript.

Abbreviations

CP, clinicopathological parameter; DANCR, differentiation antagonizing non-protein coding RNA; DFS, disease-free survival; HR, hazard ratio; NOS, Newcastle–Ottawa Scale; OR, odds ratio; OS, overall survival; qRT-PCR, quantitative reverse transcription PCR; RFS, recurrence-free survival.

References

- Torre, L.A., Bray, F., Siegel, R.L., Ferlay, J., Lortet-Tieulent, J. and Jemal, A. (2015) Global cancer statistics, 2012. *CA Cancer J. Clin.* **65**, 87–108, <https://doi.org/10.3322/caac.21262>
- Siegel, R.L., Miller, K.D. and Jemal, A. (2018) Cancer statistics, 2018. *CA Cancer J. Clin.* **68**, 7–30
- Chen, W., Zheng, R., Baade, P.D., Zhang, S., Zeng, H., Bray, F. et al. (2016) Cancer statistics in China, 2015. *CA Cancer J. Clin.* **66**, 115–132, <https://doi.org/10.3322/caac.21338>
- Zhao, Y., Si, G., Zhu, F., Hui, J., Cai, S., Huang, C. et al. (2017) Prognostic role of platelet to lymphocyte ratio in hepatocellular carcinoma: a systematic review and meta-analysis. *Oncotarget* **8**, 22854–22862, <https://doi.org/10.18632/oncotarget.22557>
- Zhou, Y., Cheng, S., Chen, S. and Zhao, Y. (2018) Prognostic and clinicopathological value of SIRT3 expression in various cancers: a systematic review and meta-analysis. *Onco. Targets Ther.* **11**, 2157–21567, <https://doi.org/10.2147/OTT.S157836>
- Mercer, T.R., Dinger, M.E. and Mattick, J.S. (2009) Long non-coding RNAs: insights into functions. *Nat. Rev. Genet.* **10**, 155–159, <https://doi.org/10.1038/nrg2521>
- Khalil, A.M., Guttman, M., Huarte, M., Garber, M., Raj, A., Rivea Morales, D. et al. (2009) Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. *Proc. Natl Acad. Sci. U.S.A.* **106**, 11667–11672, <https://doi.org/10.1073/pnas.0904715106>
- Ponting, C.P., Oliver, P.L. and Reik, W. (2009) Evolution and functions of long noncoding RNAs. *Cell* **136**, 629–641, <https://doi.org/10.1016/j.cell.2009.02.006>
- Martens-Uzunova, E.S., Bottcher, R., Croce, C.M., Jenster, G., Visakorpi, T. and Calin, G.A. (2014) Long noncoding RNA in prostate, bladder, and kidney cancer. *Eur. Urol.* **65**, 1140–1151, <https://doi.org/10.1016/j.eururo.2013.12.003>

- 10 Kretz, M., Webster, D.E., Flockhart, R.J., Lee, C.S., Zehnder, A., Lopez-Pajares, V. et al. (2012) Suppression of progenitor differentiation requires the long noncoding RNA ANCR. *Genes Dev.* **26**, 338–343, <https://doi.org/10.1101/gad.182121.111>
- 11 Hao, Y.P., Qiu, J.H., Zhang, D.B. and Yu, C.G. (2017) Long non-coding RNA DANCR, a prognostic indicator, promotes cell growth and tumorigenicity in gastric cancer. *Tumour Biol.* **39**, <https://doi.org/10.1177/1010428317699798>
- 12 Jiang, N., Wang, X., Xie, X., Liao, Y., Liu, N., Liu, J. et al. (2017) lncRNA DANCR promotes tumor progression and cancer stemness features in osteosarcoma by upregulating AXL via miR-33a-5p inhibition. *Cancer Lett.* **405**, 46–55, <https://doi.org/10.1016/j.canlet.2017.06.009>
- 13 Liu, Y., Zhang, M., Liang, L., Li, J. and Chen, Y.X. (2015) Over-expression of lncRNA DANCR is associated with advanced tumor progression and poor prognosis in patients with colorectal cancer. *Int. J. Clin. Exp. Pathol.* **8**, 11480–11484
- 14 Mao, Z., Li, H., Du, B., Cui, K., Xing, Y., Zhao, X. et al. (2017) lncRNA DANCR promotes migration and invasion through suppression of lncRNA-LET in gastric cancer cells. *Biosci. Rep.* **37**, <https://doi.org/10.1042/BSR20171070>
- 15 Pan, L., Liang, W., Gu, J., Zang, X., Huang, Z., Shi, H. et al. (2018) Long noncoding RNA DANCR is activated by SALL4 and promotes the proliferation and invasion of gastric cancer cells. *Oncotarget* **9**, 1915–1930, <https://doi.org/10.18632/oncotarget.23019>
- 16 Sha, S., Yuan, D., Liu, Y., Han, B. and Zhong, N. (2017) Targeting long non-coding RNA DANCR inhibits triple negative breast cancer progression. *Biol. Open* **6**, 1310–1316, <https://doi.org/10.1242/bio.023135>
- 17 Wang, S. and Jiang, M. (2018) The long non-coding RNA-DANCR exerts oncogenic functions in non-small cell lung cancer via miR-758-3p. *Biomed. Pharmacother.* **103**, 94–100, <https://doi.org/10.1016/j.biopha.2018.03.053>
- 18 Wang, Y., Lu, Z., Wang, N., Feng, J., Zhang, J., Luan, L. et al. (2018) Long noncoding RNA DANCR promotes colorectal cancer proliferation and metastasis via miR-577 sponging. *Exp. Mol. Med.* **50**, 57, <https://doi.org/10.1038/s12276-018-0082-5>
- 19 Wang, Y., Zeng, X., Wang, N., Zhao, W., Zhang, X., Teng, S. et al. (2018) Long noncoding RNA DANCR, working as a competitive endogenous RNA, promotes ROCK1-mediated proliferation and metastasis via decoying of miR-335-5p and miR-1972 in osteosarcoma. *Mol. Cancer* **17**, 89, <https://doi.org/10.1186/s12943-018-0837-6>
- 20 Yang, J.X., Sun, Y., Gao, L., Meng, Q. and Yang, B.Y. (2018) Long non-coding RNA DANCR facilitates glioma malignancy by sponging miR-33a-5p. *Neoplasma* **65**, 790–798, <https://doi.org/10.4149/neo.2018.170724N498>
- 21 Yuan, S.X., Wang, J., Yang, F., Tao, Q.F., Zhang, J., Wang, L.L. et al. (2016) Long noncoding RNA DANCR increases stemness features of hepatocellular carcinoma by derepression of CTNBN1. *Hepatology* **63**, 499–511, <https://doi.org/10.1002/hep.27893>
- 22 Moher, D., Liberati, A., Tetzlaff, J. and Altman, D.G. (2009) Preferred reporting items for systematic reviews and meta-analyses: the PRISMA statement. *PLoS Med.* **6**, e1000097, <https://doi.org/10.1371/journal.pmed.1000097>
- 23 Tierney, J.F., Stewart, L.A., Ghersi, D., Burdett, S. and Sydes, M.R. (2007) Practical methods for incorporating summary time-to-event data into meta-analysis. *Trials* **8**, 16, <https://doi.org/10.1186/1745-6215-8-16>
- 24 Stang, A. (2010) Critical evaluation of the Newcastle-Ottawa scale for the assessment of the quality of nonrandomized studies in meta-analyses. *Eur. J. Epidemiol.* **25**, 603–605, <https://doi.org/10.1007/s10654-010-9491-z>
- 25 Bach, D.H. and Lee, S.K. (2018) Long noncoding RNAs in cancer cells. *Cancer Lett.* **419**, 152–166, <https://doi.org/10.1016/j.canlet.2018.01.053>
- 26 Jiang, C., Li, X., Zhao, H. and Liu, H. (2016) Long non-coding RNAs: potential new biomarkers for predicting tumor invasion and metastasis. *Mol. Cancer* **15**, 62, <https://doi.org/10.1186/s12943-016-0545-z>
- 27 Lu, R., Chen, J., Kong, L. and Zhu, H. (2018) Prognostic value of lncRNA ROR expression in various cancers: A meta-analysis. *Biosci. Rep.* **38**, BSR20181095, <https://doi.org/10.1042/BSR20181095>
- 28 Xie, H., Ma, B., Gao, Q., Zhan, H., Liu, Y., Chen, Z. et al. (2018) Long non-coding RNA CRNDE in cancer prognosis: review and meta-analysis. *Clin. Chim. Acta* **485**, 262–271, <https://doi.org/10.1016/j.cca.2018.07.003>
- 29 Li, J. and Zhou, L. (2018) Overexpression of lncRNA DANCR positively affects progression of glioma via activating Wnt/beta-catenin signaling. *Biomed. Pharmacother.* **102**, 602–607, <https://doi.org/10.1016/j.biopha.2018.03.116>
- 30 Ma, Y., Zhou, G., Li, M., Hu, D., Zhang, L., Liu, P. et al. (2018) Long noncoding RNA DANCR mediates cisplatin resistance in glioma cells via activating AXL/PI3K/Akt/NF-kappaB signaling pathway. *Neurochem. Int.* **118**, 233–241, <https://doi.org/10.1016/j.neuint.2018.03.011>
- 31 Wang, Y., Lu, Z., Wang, N., Feng, J., Zhang, J., Luan, L. et al. (2018) Long noncoding RNA DANCR promotes colorectal cancer proliferation and metastasis via miR-577 sponging. *Exp. Mol. Med.* **50**, 1–17, <https://doi.org/10.1038/s12276-018-0082-5>
- 32 Zhen, Q., Gao, L.N., Wang, R.F., Chu, W.W., Zhang, Y.X., Zhao, X.J. et al. (2018) lncRNA DANCR promotes lung cancer by sequestering miR-216a. *Cancer Control* **25**, 1073274818769849, <https://doi.org/10.1177/1073274818769849>
- 33 Lu, Q.C., Rui, Z.H., Guo, Z.L., Xie, W., Shan, S. and Ren, T. (2018) lncRNA-DANCR contributes to lung adenocarcinoma progression by sponging miR-496 to modulate mTOR expression. *Exp. Mol. Med.* **50**, 1–17, <https://doi.org/10.1038/s12276-018-0082-5>
- 34 Jia, J., Li, F., Tang, X.S., Xu, S., Gao, Y., Shi, Q. et al. (2016) Long noncoding RNA DANCR promotes invasion of prostate cancer through epigenetically silencing expression of TIMP2/3. *Oncotarget* **7**, 37868–37881, <https://doi.org/10.18632/oncotarget.9350>
- 35 Chen, S., Zhang, L., Yan, G., Cheng, S., Fathy, A.H., Yan, N. et al. (2017) Neutrophil-to-lymphocyte ratio is a potential prognostic biomarker in patients with ovarian cancer: a meta-analysis. **2017**, 7943467
- 36 Wang, J., Zhao, Y., Qi, R., Zhu, X., Huang, C., Cheng, S. et al. (2017) Prognostic role of podocalyxin-like protein expression in various cancers: a systematic review and meta-analysis. *Biomed. Res. Int.* **8**, 52457–52464
- 37 Zhou, Y., Cheng, S., Fathy, A.H., Qian, H. and Zhao, Y. (2018) Prognostic value of platelet-to-lymphocyte ratio in pancreatic cancer: a comprehensive meta-analysis of 17 cohort studies. *Onco. Targets Ther.* **11**, 1899–1908