Prognostic and clinicopathologic significance of lncRNA SNHG17 in multiple human cancers: a meta and bioinformatic analysis

Ningxin Sun
Weifang Medical University
Yanmei Song
Weifang Medical University
Danyang Li
Weifang Medical University
Weihui Jia
Weifang Medical University
Ke Yang
Weifang Medical University
Jiemin Wang
Weifang Medical University
Hongli Li
Weifang Medical University
Chonggao Yin (yinchg@wfmc.edu.cn)
Weifang Medical University

Research Article

Keywords: LncRNA SNHG17, Cancer, Meta-analysis, Prognostic biomarker, Clinical parameters

Posted Date: April 19th, 2022

DOI: https://doi.org/10.21203/rs.3.rs-1540009/v1

Abstract

Background:

In recent years, some studies have found that long non-coding RNA Small nucleolar RNA host gene 17 (lncRNA SNHG17) is abnormally expressed in a variety of cancers. However, the prognostic and clinical value of lncRNA SNHG17 expression in cancer is still unclear. This meta-analysis aims to comprehensively elaborate the prognostic value of SNHG17 in cancer.

Methods:

PubMed, Web of Science, Embase and Cochrane Library were absolutely searched. Hazards ratios (HRs) or odd ratios (ORs) with 95% confidence intervals (CIs) were pooled to estimate the prognostic value of SNHG17 in cancers, including overall survival (OS), progression-free survival (PFS), disease-free survival (DFS), recurrence-free survival (RFS), age, gender, tumor size, differentiation, metastasis, clinical stage, and lymph node metastasis (LNM). In addition, we further searched for the expression and prognosis of SNHG17 in various cancer through TCGA dataset.

Results:

13 studies containing 1492 cancer patients was finally Selected into this study. The results showed that patients with high SNHG17 expression tended to have shorter OS (HR = 1.78, 95%CI = 1.50-2.10, P < 0.01), DFS (HR = 1.36, 95%CI = 1.06-1.74, P < 0.05), RFS (R = 2.49,95%CI = 1.13-5.49, P < 0.01), and PFS (R = 2.02, 95%CI = 1.24–3.28, P < 0.05). Additionally, increased lncRNA SNHG17 expression was significantly related to worse differentiation (HR = 1.41, 95%CI = 0.82-2.45, P < 0.01), advanced clinical stage (HR = 3.25, 95%CI = 1.77-5.97, P < 0.01), earlier metastasis (HR = 2.33, 95%CI = 1.30-4.19, P < 0.01) and earlier lymph node metastasis (HR = 2.94, 95%CI = 2.15-4.02, P < 0.01). No publication bias was found in all studies and the results were robust. The TCGA dataset further validated that SNHG17 is highly expressed in a variety of cancers and is strongly correlated with OS and DFS.

Conclusion:

The high expression of lncRNA SNHG17 may predict poor prognosis and advanced clinical stage, which means that SNHG17 may be a possible prognostic biomarker of cancer.

Introduction

Cancer leads to a huge disease burden, which is not only one of the leading causes of death in the world, but also an important factor hindering the extension of human life expectancy. 19.1 million new cancer patients and 9.9 million cancer-related deaths reported worldwide in 2020, increasing to 28.4 million and 17.6 million in 2040[1, 2]. Despite improvements in surgical techniques and significant advances in chemotherapy and radiotherapy options over the past few decades, overall cancer survival and prognosis have not improved significantly[3]. The main reason for this result is the lack of effective early screening indicators, which makes it impossible to identify and intervene high-risk patients early. When clinical symptoms appear, it has reached to the middle and late stage. [4]. Therefore, the development of early cancer screening and diagnosis and treatment has become extremely important.

Long non-coding RNAs (lncRNAs) contain a heterogeneous family of RNA molecules over 200 nucleotides in length with no or limited protein-coding potential, lncRNAs are involved in regulating biological processes by regulating gene expression, including chromatin remodeling, transcription, and is involved in the regulation of cellular processes[5–7]. A plethora of reports has reported that many lncRNAs, acting as proto-oncogenes or anti-oncogenes, plays a key role in the pathophysiology of a significant number of human cancers, including cell proliferation, migration, invasion, and metabolism [8]. Recently, numerous results of studies suggest that lncRNAs can act as an independent prognostic factor in certain cancers, Furthermore, A few studies have revealed some lncRNAs correlated with prognosis and clinicopathological features can be used as accurate predictors of cancer prognosis, such as ZEB1-AS1[9], OPI5-AS1[10], SNHG6[11].

Small nucleolar RNA host gene 17 (SNHG17), a 1186 nucleotide lncRNA, is a member of the SNHG family, located on human chromosome 20q11.23. Ma et al. initially reported that SNHG17 overexpression promotes the proliferation and metastasis of colorectal cancer cells by silencing p57[12].SNHG17 has gradually been found to be overextended in lung cancer[13], gastric cancer[14], hepatocellular carcinoma[15, 16], osteosarcoma[17] and other cancer species, and its expression levels have been reported to be associated with a poor prognosis and the clinicopathological characteristics[18]. However, given the discreteness of the current findings and the limited sample size, it is not enough to prove the prognostic value of SNHG17. Therefore, we conducted this meta-analysis to evaluate the value of SNHG17 as a promising prognostic biomarker in multiple human cancers.

Materials And Methods

Publication search strategy

This study adhered to the Preferred Reporting Items stated in the systematic review and meta-analysis (PRISMA). As of March 1, 2022, qualified literature on the prognostic value of SNHG17 expression in human cancer was retrieved in multiple English databases (including PubMed, Web of Science, EMBASE and Cochrane Library). The following keywords are used to search in different databases: (“long noncoding RNA” OR “lncRNA”), (“SNHG17” OR “Small nucleolar RNA host gene 17”), (“cancer” OR “carcinoma” OR “tumor”), AND (“Prognostic Factors” OR “prognosis” OR “Factors, Prognostic”). In addition, a manual search was conducted on the reference list of the registered literature to screen the relevant articles.

Inclusion and exclusion criteria

Inclusion criteria: (1) articles evaluating the prognostic role of SNHG17 in human cancer; (2) The clinicopathological features were reported; (3) Patients were grouped according to the expression level of SNHG17; (4) The data can be extracted directly or measured indirectly through the Kaplan-Meier survival curve;

Exclusion criteria: (1) nonhuman cancer research; (2) reviews, letters or case reports; (3) Data cannot be extracted; (4) Duplicate publications.

Data extraction and quality assessment

The included literature was evaluated by two independent researchers and the necessary data were extracted independently. The valid information extracted is as follows: first author's last name, publication year, country, tumor type, sample size, follow-up months, inspection method, survival analysis, clinical parameters, such as tumor size, clinical stage, age, gender, metastasis, differentiation, and LNM (Lymph node metastasis). Data were

directly extracted from the eligible studies. If the effect quantity cannot be obtained directly from the study, it is extracted indirectly by using Engauge Digitizer (version 4.1) from the survival curve given in the study[19]. The Newcastle Ottawa Scale (NOS) was performed to assess the quality of the included literature, and all studies were of high quality and scored >6.

TCGA cancer genome atlas

The differential expression pattern of SNHG17 between tumor and normal samples in a variety of cancers in TCGA data set was further verified by Gene Expression Profiling Interactive Analysis (http://gepia.cancer-pku.cn/). Furthermore, we also plotted Kaplan Meier (K-M) curves to reflect the relationship between SNHG17 expression and OS or DFS in cancer patients.

Data synthesis and statistical analysis

All analyses were performed by Review Manager 5.3 software and Stata 14.0 software (Stata Corp LLC). Prognostic variables and clinical parameters were analyzed by HRs or ORs and 95% CIs. The heterogeneity between studies was evaluated by I^2, and the fixed effect model was used to study the data with small heterogeneity ($I^2 \leq 50\%$ and $P > 0.05$). On the contrary, the random effect model was applied. Funnel plots and Begg's test was assessed the publication bias in the study. Sensitivity analysis was performed to examine the robustness of results. P-value < 0.05 was considered as significantly statistical.

Results

Selection and description of included studies

The preliminary literature search of relevant lncRNA SNHG17 and cancer clinical parameters in PubMed (n= 17), Web of science (n= 33), Embase (n= 14) and Cochrane Library identified 64 publications (Figure 1). Among them, 32 duplicate literatures and 15 articles unrelated to cancer were removed. After reading the full text, 4 articles were removed, including 1 article unrelated to clinical research and 3 articles unable to extract data. A total of 13 articles were finally included in meta-analysis, including gastric cancer[14, 20], hepatocellular carcinoma[15, 16], lung adenocarcinoma cancer[21], colorectal cancer[22, 23], breast cancer[24], prostate cancer[25], Ovarian cancer[26], melanoma[27], tongue squamous cell carcinoma[28], and renal cell carcinoma[18].

The main characteristics of the qualified articles were summarized in Table 1. All included studies were performed in China and published between 2017 and 2022. The expression level of lncRNA SNHG17 was detected by qRT-PCR, and all patients were divided into high expression and low expression groups. All 13 studies, 2 recorded the HR and 95% CI of OS, and the OS data of the other 11 studies were indirectly calculated by Kaplan -Meier curve.

Table 1 The characteristic details of included studies.

Authors	Year	Country	Tumor type	Sample size	Follow-up months	Detection method	Survival analysis	HR calculation method	NOS
Chen, L.	2019	China	GC	157	60	qRT-PCR	OS PFS	K-M	8
Gao, H.	2019	China	melanoma	148	60	qRT-PCR	OS	K-M	7
Pan, X.	2020	China	Ovarian cancer	90	100	qRT-PCR	OS	K-M	7
Du Y	2020	China	BRCA	58	60	qRT-PCR	OS	K-M	6
Ma, Z	2017	China	colorectal cancer	56	40	qRT-PCR	OS	K-M	7
Liu, X	2020	China	TSCC	56	60	qRT-PCR	OS	K-M	8
Luo, Y.	2021	China	HCC	364	120	qRT-PCR	OS DFS	K-M	8
Zhang, Z	2021	China	LUAD	50	150	qRT-PCR	OS	K-M	7
Wu, J	2021	China	RCC	84	120	qRT-PCR	OS RFS	Directly	7
Zhu, X.	2021	China	HCC	58	60	qRT-PCR	OS	Directly	7
Zhao, H	2021	China	prostate cancer	58	70	qRT-PCR	OS	K-M	6
Bian, Z.	2021	China	colorectal cancer	214	180	qRT-PCR	OS DFS	K-M	8
ZHANG, X	2021	China	GC	99	80	qRT-PCR	OS	K-M	7

Tags: GC: gastric cancer, BRCA: breast cancer, TSCC: tongue squamous cell carcinoma, LUAD: lung adenocarcinoma, RCC: renal cell carcinoma, HCC: hepatocellular carcinoma.

Association of SNHG17 expression with OS

Thirteen studies were included in the meta-analysis of OS[14-16, 18, 20-28]. As shown in Figure 2A, a fixed effect model was adopted because there was no heterogeneity (I^2 = 0%, P=0.97) in the included studies. The results indicated that the patients with high expression of lncRNA SNHG17 was closely related to the shorter OS of patients (HR = 1.78, 95%CI = 1.50-2.10, P < 0.01). Besides, we performed subgroup analysis based on cancer type (Figure 2B) sample size (Figure 2C), and follow-up time (Figure 2D), showing that SNHG17 expression levels correlated with the prognosis of cancer patients, with high expression predicting poorer OS, which further validates our results. More details can be found in in Table 2.

Table 2: The results of subgroup analyses of OS.

Subgroup	Studies	HR and 95%CI	P	I^2	Model
Sample size	13	1.78(1.50-2.10)	0.97	0	Fixed
<90	7	2.04(1.49-2.80)	0.99	0	Fixed
≥90	6	1.69(1.39-2.05)	0.75	0	Fixed
Cancer type	13	1.78(1.50-2.10)	0.97	0	Fixed
Colorectal cancer	2	2.14(1.24-3.68)	0.99	0	Fixed
Gastric cancer	2	2.00(1.35-2.97)	0.50	0	Fixed
Hepatocellular carcinoma	2	1.60(1.23-2.06)	0.52	0	Fixed
Other	7	1.82(1.35-2.46)	0.97	0	Fixed
Follow-up months	13	1.78(1.50-2.10)	0.97	0	Fixed
≤60	7	1.79(1.45-2.21)	0.78	0	Fixed
>60	6	1.76(1.31-2.31)	0.94	0	Fixed

Association of SNHG17 expression with DFS, RFS and PFS

See Figure 3 for illustration, among all the included studies, two articles introduced DFS[15, 23], and one article reported PFS[20] and RFS[18] respectively, which were included into meta-analysis. The results showed that the DFS (HR = 1.36, 95%CI = 1.06-1.74, P < 0.05, I2=0%), RFS (R = 2.49,95%CI = 1.13-5.49, P < 0.01) and PFS (R = 2.02, 95%CI = 1.24–3.28, P < 0.05) of cancer patients with high expression of lncRNA SNHG17 were significantly shorter (Figure 3A). The funnel plot means that there is no obvious bias (Figure 3B).

Association of SNHG17 expression with clinical characteristics

The clinical data of 10 articles were extracted and included in meta-analysis[14, 16, 20-22, 24-28].The correlation between age, gender, tumor size, clinical stage, LNM, distant metastasis and differentiation and SNHG17 expression was analyzed. As listed in Table 3, there was no distinct relationship between lncRNA SNHG17 expression and age (P = 0.84)，gender (P = 0.28) and tumor size (P =0.47) (Supplement Figure 1(A-C)). However, high lncRNA SNHG17 expression was significantly related to advanced clinical stage (HR = 3.25, 95%CI = 1.77-5.97, P < 0.01) (Figure 4A), earlier lymph node metastasis (HR = 2.94, 95%CI = 2.15-4.02, P < 0.01) (Figure 4B), worse differentiation (HR = 1.41, 95%CI = 0.82-2.45, P < 0.01) (Figure 4C) and earlier metastasis (HR = 2.33, 95%CI = 1.30-4.19, P < 0.01) (Figure 4D).

Table 3: Meta analysis of the relationship between the expression of SNHG17 and clinical parameters.

Subgroup	studies	participants	OR and 95%CI	P	I^2	Model
Age (old vs young)	10	830	1.26(0.94-1.69)	0.84	0	Fixed
Gender (male vs female)	7	598	1.20(0.86-1.69)	0.28	0	Fixed
Tumor size (large vs small)	8	533	2.80(1.94-4.05)	0.47	0	Fixed
Clinical stages(/ vs /)	10	830	3.25(1.77-5.97)	0.0002	72	Random
LNMyes vs no	9	780	2.94(2.15-4.02)	0.00001	0	Fixed
Differentiationpoor vs good	2	215	1.41(0.82-2.45)	0.22	16	Fixed
Metastasisyes vs no	2	215	2.33(1.30-4.19)	0.005	21	Fixed

SNHG17 expression in TCGA pan-cancer dataset

TCGA pan-cancer dataset was explored to further verified our conclusions. SNHG17 aberrant expression in cancer tissue were found in Cholangiocarcinoma (CHOL), colon adenocarcinoma (COAD), Lymphoid Neoplasm Diffuse Large B-cell Lymphoma (DLBC), Glioblastoma multiforme (GBM), Brain Lower Grade Glioma (LGG), Pancreatic adenocarcinoma (PAAD), Rectum adenocarcinoma (READ), Testicular Germ Cell Tumors (TGCT), Thymoma (THYM) and Stomach adenocarcinoma (STAD). (Figure 5(A-J)). Furthermore, K-M survival curves suggested that high SNHG17 expression was associated with poorer OS and DFS. (Figure 5(K-L)), in which indicated that SNHG17 could be a novel prognostic biomarker for human multiple cancers.

Publication bias and sensitivity analysis

The absence of publication bias in the 13 papers included was demonstrated by funnel plots as well as the begg's test. The funnel plots were clearly symmetrical and begg's test (P = 0.200) also showed no publication bias (Figure 6A). Sensitivity analysis confirmed the robustness of the obtained results (Figure 6B).

Discussion

Long non-coding RNAs (lncRNAs) refers to RNA with a length of more than 200 bases and does not encode protein, Studies have reported that lncRNA have been proved to be the main regulator of gene expression. It plays a key role in cancer and various biological functions and diseases[29]. Recent studies have shown that SNHG17 is highly expressed in many cancers and is closely related to the poor prognosis and progression of cancer patients, such as colorectal cancer[22, 23], gastric cancer[14, 20], breast cancer[24], and hepatocellular carcinoma[15, 16]. Whether lncRNA SNHG17 can be used as a potential biomarker to predict cancer prognosis has attracted scholars' attention. Due to the insufficient sample size of current basic and clinical trials, we cannot get strong evidence to prove the prognostic value of SNHG17 in clinical application. Therefore, we conduct a systematic meta-analysis on the expression level of SNHG17, the prognosis of various cancer patients and clinicopathological parameters.

A total of 13 studies and 1492 patients were included in this meta-analysis. We found that patients with high expression of SNHG17 had worse OS, PFS, DFS and RFS than those with low expression of SNHG17, this strongly proves that the overexpression of SNHG17 is associated with poor prognosis and can be used as a biomarker of

poor prognosis in cancer patients. Secondly, we also evaluated the relationship between the expression of SNHG17 and clinicopathological parameters, our analysis showed that SNHG17 overexpression was significantly correlated with the degree of differentiation, distant metastasis, LNM and TNM stage. In addition, we further verified our conclusion in TGCA database. We found that SNHG17 was highly expressed in CHOL, COAD, DLBC, GBM, LGG, PAAD, READ, TGCT, THYM and other cancer species, and plotted K-M survival curve, we found that SNHG17 was significantly correlated with worse OS and DFS. To sum up, our results fully illustrate that SNHG17 is a favorable prognostic biomarker for multiple human cancer.

At present, although many studies have demonstrated the relationship between SNHG17 expression and cancer, the potential mechanism of SNHG17 is still uncertain. More and more studies have shown that SNHG17 can inhibit the function of miRNA as a competitive endogenous RNA (ceRNA). For instance, Chen et al.[30] found that SNHG17 as ceRNA accelerates ESCC progression by sponging miR-338-3P to regulate SOX4 expression Li et al.[31] and Zhang et al.[32] found that SNHG17 promote LUAD by suppressing miR-485-5p and miR-193a-5p expression. Subsequently, SNHG17 overexpression was reported to significantly enhance the migration and invasive ability of tumor cells, and SNHG17 may regulate H2AX signaling through competitive inhibition of miR-328-3p in renal cell carcinoma[33]. Pan et al.[26] observed that SNHG17 regulates cell cycle progression and proliferation of ovarian cancer cells via the miR-214-3p/CDK6 axis. Therefore, more convincing clinical trials are needed to verify the role of SNHG17 in cancer.

Our meta-analysis also has some limitations. Firstly, we included 13 literatures, The sample size of the study was small and involved few cancer species. Secondly, all the documents we include are in English, and the research area is China, which may cause some differences in demography. The later research should be oriented to more countries and people. Finally, because most studies cannot directly extract the value of HR from the original study, some HRs were calculated from K–M curves, which may introduce possible deviations.

In conclusion, abnormal expression of SNHG17 is strongly correlated with adverse OS, PFS, DFS, RFS, clinical stage, LNM, tumor differentiation, and metastasis. Therefore, SNHG17 may be a novel prognostic biomarker in multiple human cancers. However, more multicenter studies with larger sample sizes are needed to validate the results of this study.

Abbreviations

SNHG17
Long non-coding RNA Small nucleolar RNA host gene 17
OR
Odds ratio
HR
Hazard ratio
95% CI
95% confidence interval
TCGA
The Cancer Genome Atlas
TNM
Tumor node metastasis
NOS

Newcastle Ottawa scale
K-M curve
Kaplan-Meier curve
OS
Overall survival
DFS
Disease-free survival
RFS
Relapse-free survival
PFS
Progress-free survival
qRT-PCR
Quantitative real-time polymerase chain reaction.

Declarations

Supplementary Information

Additional file 1: Figure S1. Forest plot of enrolled studies for association between SNHG17 expression and other clinical parameters. (A) age, (B) gender, (C) tumor size.

Additional file 2: Table S1. PRISMA checklist

Acknowledgements

We are grateful to all researchers of enrolled studies.

Authors' contributions

SNX, SYM, LDY, JWH and YCG conceived and designed the study. Performed the experiments: SNX, and SYM. Analyzed the data: LDY and JWH. Contributed analysis tools/materials: YK, WJM, LHL and WJM. Wrote the paper: SNX, SYM and LHL. All authors have read and approved the final manuscript.

Funding

The study was supported by the Natural Science Foundation of Shandong Province, Grant/Award Number: ZR2019MH033; and the Introduction Plan of Young Creative Talents in Colleges and Universities of Shandong Province, Grant/Award Number: 205.

Availability of data and materials

All data analyzed during this study are included in this published article. GEPIA database is publicly available at (http://gepia.cancer-pku.cn/api.html)

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they do not have any competing interests.

Author details

1 College of Nursing, Weifang Medical University, Weifang, Shandong 261053, China

2 Medicine Research Center, Weifang Medical University, Weifang, Shandong 261053, China

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Figures

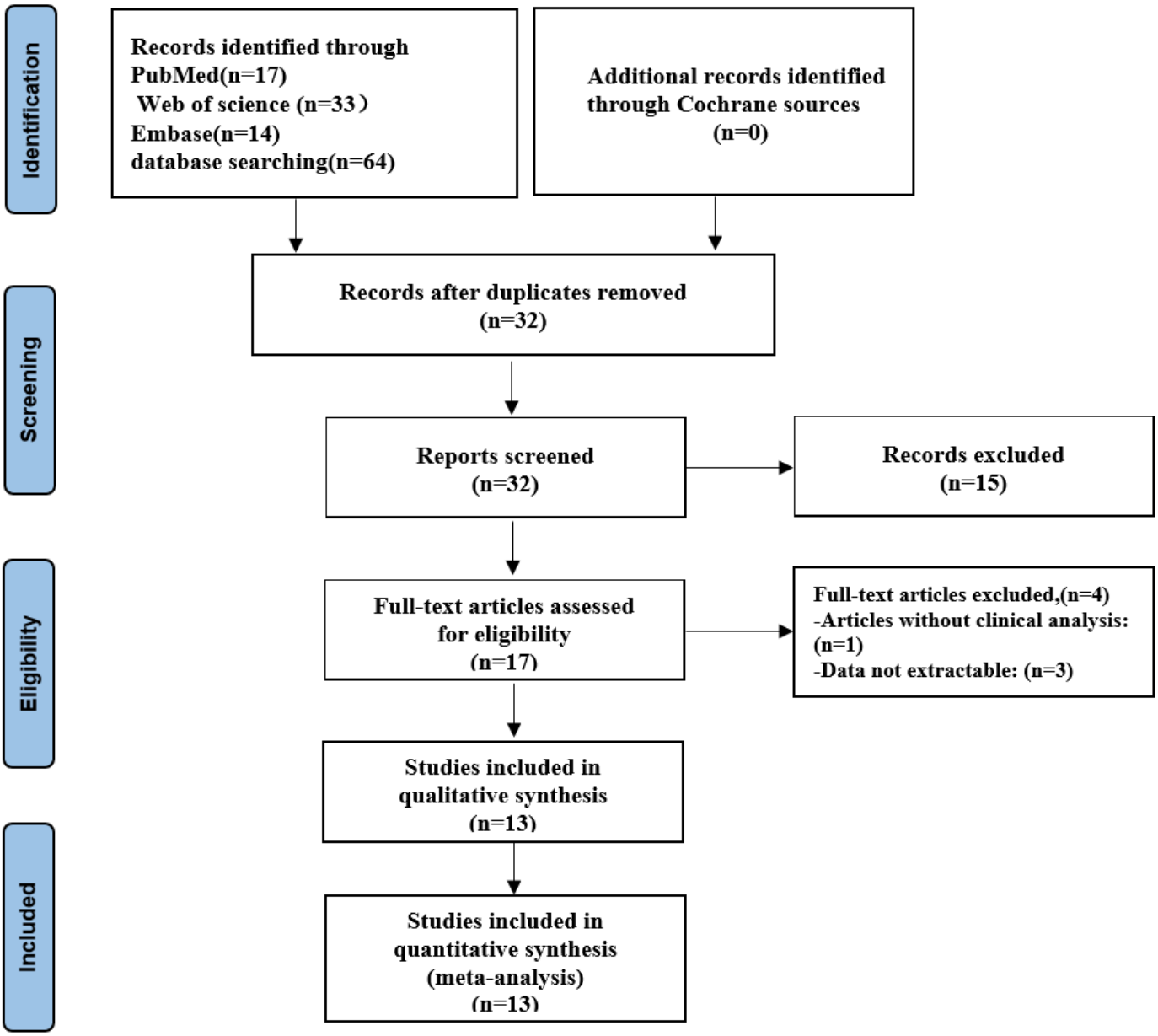

Figure 1

Flow diagram of the literature selection process

Figure 2

Evaluation of lncRNA SNHG17 expression levels for overall and subgroup analysis of OS in hazard ratios forest plots. (A), All enrolled studies (B), tumor type (C), sample size (D), follow-up time.

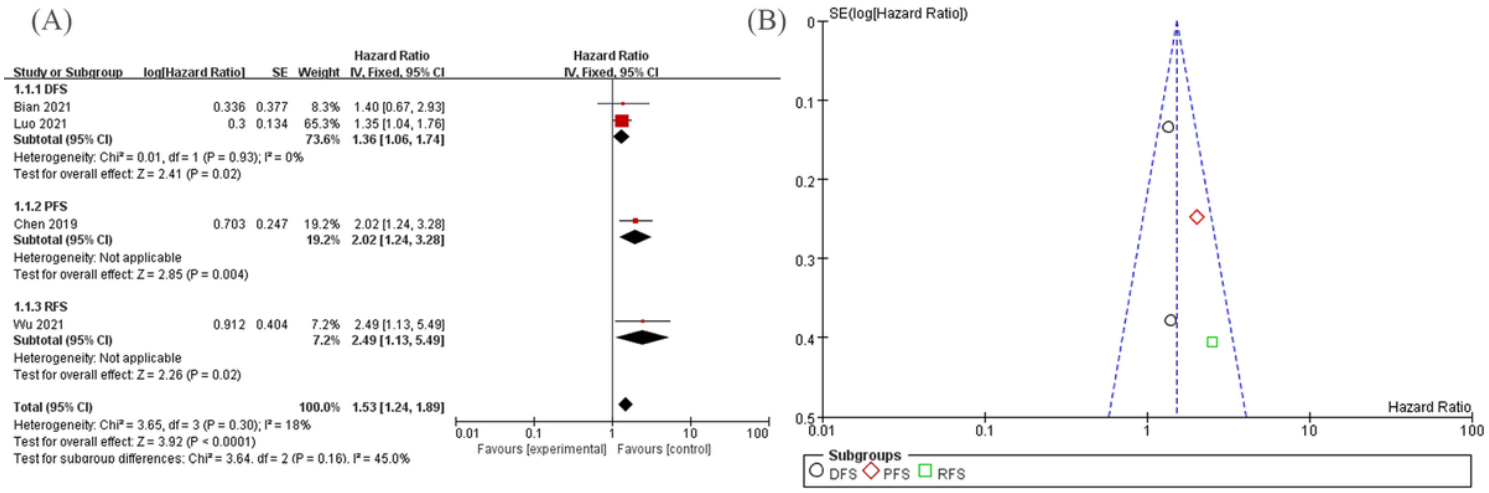

Figure 3

Association of SNHG17 expression with DFS, RFS and PFS. (A), Forest plot for the meta-analysis of DFS, RFS and PFS (B), Funnel plot for the meta-analysis of DFS, RFS and PFS.

Figure 4

Forest plot of enrolled studies for association between SNHG17 expression and other clinical parameters. (A), clinical stages (B), lymph node metastasis (C), differentiation (D), metastasis.

Figure 5

SNHG17 expression in cancer and clinical outcomes in TCGA dataset. (A-J) The box plots showed the expression in cancerous tissues and normal tissues. (K-L) The Kaplan Meier-plotters revealed the association between SNHG17 expression levels and overall survival and disease-free survival.

Figure 6

Publication bias and sensitivity analysis for OS in this meta-analysis. (A) Begg's funnel plot for the meta-analysis of overall survival. (B) Sensitivity analysis for the meta-analysis of overall survival.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- SupplementFigure1.tif
- PRISMA2020checklist.docx