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ORIGINAL ARTICLE

Clinicopathological and Prognostic Value of Long Noncoding RNA SNHG15 in Human Cancers: a Meta-Analysis and Bioinformatics

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SUMMARY

Background: Recently, accumulating evidence has suggested that the long noncoding RNA small nucleolar RNA host gene 15 (lncRNA SNHG15) was elevated in various malignancies and correlated to poor clinical outcome of patients. However, the prognosis value of SNHG15 in tumors remains not well understood.

Methods: The PubMed, Web of Science, Embase, Ovid, Cochrane Library databases were used to search for eligible articles. Stata MP14.0 software was applied in the systematic meta-analysis. The Cancer Genome Atlas (TCGA) dataset was adopted to verify the results.

Results: A total of 13 studies including 1,190 patients were enrolled in this meta-analysis. SNHG15 high expression predicted shorter overall survival (OS) (hazard ratio (HR) = 2.34, 95% confidence interval (CI): 1.75 - 3.12, p < 0.001) with no statistical heterogeneity, which was validated by the data of TCGA. The subgroup analyses stratified according to OS analysis method, cancer type, sample size, and follow-up time showed similar results. Additionally, SNHG15 expression was positively associated with TNM stage (III + IV vs. I + II, odds ratio (OR) = 2.23, 95% CI: 1.14 - 4.38, p = 0.020) and poor differentiation (low + undifferentiated vs. well + moderate, OR = 2.89, 95% CI: 1.89 - 4.42, p < 0.001).

Conclusions: IncRNA SNHG15 may act as a useful and potential biomarker for prognosis and clinical parameters in human cancers.

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Supplemental Tables

Tuble 51, Reporting recommendations for tumor marner prognostic studies (REAMINING) encember	Table S1. R	eporting recomn	nendations for tumo	r marker progno	stic studies	(REMARK)	checklist.
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	INTRODUCTION
1	State the marker examined, the study objectives, and any pre-specified hypotheses
	MATERIALS AND METHODS
Patients	
2	Describe the characteristics (for example, disease stage or co-morbidities) of the study patients, including their source and inclusion and exclusion criteria
3	Describe treatments received and how chosen (for example, randomized or rule-based)
Specimen characteristics	
4	Describe type of biological material used (including control samples) and methods of preservation and storage
Assay methods	
5	Specify the assay method used and provide (or reference) a detailed protocol, including specific reagents or kits used, quality control procedures, reproducibility assessments, quantitation methods, and scoring and reporting protocols. Specify whether and how assays were performed blinded to the study endpoint
Study design	
6	State the method of case selection, including whether prospective or retrospective and whether stratification or matching (for example, by stage of disease or age) was used. Specify the time period from which cases were taken, the end of the follow-up period, and the median follow-up time
7	Precisely define all clinical endpoints examined
8	List all candidate variables initially examined or considered for inclusion in models
9	Give rationale for sample size; if the study was designed to detect a specified effect size, give the target power and effect size
Statistical analysis methods	
10	Specify all statistical methods, including details of any variable selection procedures and other model-building issues, how model assumptions were verified, and how missing data were handled
11	Clarify how marker values were handled in the analyses; if relevant, describe methods used for cutpoint determination
	RESULTS
Data	
12	Describe the flow of patients through the study, including the number of patients included in each stage of the analysis (a diagram may be helpful) and reasons for dropout. Specifically, both overall and for each subgroup extensively examined report the number of patients and the number of events
13	Report distributions of basic demographic characteristics (at least age and sex), standard (disease-specific) prognostic variables, and tumor marker, including numbers of missing values
Analysis and presentation	
14	Show the relation of the marker to standard prognostic variables
15	Present univariable analyses showing the relation between the marker and outcome, with the estimated effect (for example, hazard ratio and survival probability). Preferably provide similar analyses for all other variables being analyzed. For the effect of a tumor marker on a time-to-event outcome, a Kaplan-Meier plot is recommended
16	For key multivariable analyses, report estimated effects (for example, hazard ratio) with confidence intervals for the marker and, at least for the final model, all other variables in the model

RESULTS									
17	Among reported results, provide estimated effects with confidence intervals from an analysis in which the marker and standard prognostic variables are included, regardless of their statistical significance								
18	If done, report results of further investigations, such as checking assumptions, sensitivity analyses, and internal validation								
	DISCUSSION								
19	Interpret the results in the context of the pre-specified hypotheses and other relevant studies; include a discussion of limitations of the study								
20	Discuss implications for future research and clinical value								

Table S1.	Reporting	recommendations f	or tumor marke	r prognostic studies	(REMARK)	checklist (continued)
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Table S2. Assessing the quality of included studies based on reporting recommendations for tumor marker prognostic studies (REMARK) guideline.

Study	Q 1	Q 2	Q 3	Q 4	Q 5	Q 6	Q 7	Q 8	Q 9	Q 10	Q 11	Q 12	Q 13	Q 14	Q 15	Q 16	Q 17	Q 18	Q 19	Q 20	Total (%)
Chen 2015 [15]	1	1	1	1	1	x	х	x	x	x	~	1	1	x	1	1	1	1	1	1	70
Zhang 2016 [16]	1	1	1	1	1	x	x	x	x	x	1	1	1	x	1	1	1	1	1	1	70
Kong 2017 [18]	1	1	1	1	1	х	х	x	x	x	1	1	1	x	1	x	1	1	1	1	65
Ma 2017 [19]	1	1	1	1	1	х	х	x	x	x	~	1	1	x	x	x	1	1	1	1	60
Cui 2018 [23]	1	1	1	1	1	х	х	x	x	x	1	1	1	x	1	x	1	1	1	1	65
Dong 2018 [22]	1	1	1	1	1	х	х	x	x	x	>	1	1	x	1	x	1	1	1	1	65
Du 2018 [24]	1	1	~	1	1	х	х	x	x	x	>	1	1	x	x	x	1	1	1	-	60
Guo 2018 [20]	1	1	1	1	1	х	x	x	x	x	1	1	1	x	1	1	1	1	1	1	70
Huang 2018 [25]	1	1	1	1	1	х	х	x	x	x	1	1	1	x	1	1	1	1	1	1	70
Jin 2018 [21]	1	1	1	1	1	x	х	x	x	x	1	1	1	x	1	x	1	1	1	1	65
Liu 2018 [26]	1	1	1	1	1	x	x	x	x	x	1	1	1	x	x	x	1	1	1	1	60
Wu 2018 [27]	1	1	1	1	1	x	x	x	x	x	1	1	1	x	1	x	1	1	1	1	65
Dai 2019 [17]	1	1	1	1	1	x	x	x	x	x	1	1	1	x	x	x	1	1	1	1	60