INPLASY PROTOCOL

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Conflicts of interest:
The authors declare no conflicts of interest in this work.

The potential diagnostic value of exosomal long non-coding RNAs in solid tumours: a meta-analysis and systematic review

Wu, Z[1]; Xu, Z[2]; Yu, B[3]; Zhang, JT[4].

Review question / Objective: **P: 1)all types of solid tumor patients. 2)All solid tumor patients must be diagnosed by clinical histopathology; I: no intervention because this is a systematic review of observational studies (diagnostic meta); C: are shown in the included criteria: healthy people; O: Sensitivity, Specificity, diagnostic likelihood ratio negative, the diagnostic likelihood ratio positive, Higgin's I2, Cochran's Q test.**
Condition being studied: **Exosomal lncRNA in solid tumor.**
Information sources: **Web of science, EMBASE, PubMed.**

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 22 June 2020 and was last updated on 22 June 2020 (registration number INPLASY202060083).

INTRODUCTION

Review question / Objective: **P: 1)all types of solid tumor patients. 2)All solid tumor patients must be diagnosed by clinical histopathology; I: no intervention because this is a systematic review of observational studies (diagnostic meta); C: are shown in the included criteria: healthy people; O: Sensitivity, Specificity, diagnostic likelihood ratio negative, the diagnostic likelihood ratio positive, Higgin's I2, Cochran's Q test.**

Condition being studied: **Exosomal lncRNA in solid tumor.**

METHODS

Search strategy: ((((((((((((((((((((((((((RNA, Long Noncoding[Title/Abstract]) OR Noncoding RNA, Long[Title/Abstract]) OR lncRNA[Title/Abstract]) OR Long ncRNA[Title/Abstract]) OR ncRNA, Long[Title/Abstract]) OR RNA, Long Non-Translated[Title/Abstract]) OR Long Non-Translated RNA[Title/Abstract]) OR Non-Translated RNA, Long[Title/Abstract]) OR RNA, Long Non Translated[Title/Abstract]) OR Long Non-Coding RNA[Title/Abstract]) OR Long Non Coding RNA[Title/Abstract]) OR Non-Coding RNA, Long[Title/Abstract]) OR RNA, Long Non-Coding[Title/Abstract]) OR Long Non-Protein-Coding RNA[Title/Abstract]) OR Long Non-Protein-Coding RNA[Title/Abstract]) OR Long Non Protein Coding RNA[Title/Abstract]) OR Non-Protein-Coding RNA, Long[Title/Abstract]) OR RNA, Long Non-Protein-Coding[Title/Abstract]) OR Long Noncoding RNA[Title/Abstract]) OR RNA, Long Untranslated[Title/Abstract]) OR Long Untranslated RNA[Title/Abstract]) OR Untranslated RNA, Long[Title/Abstract]) OR Long ncRNAs[Title/Abstract]) OR ncRNAs, Long[Title/Abstract]) OR Long Intergenic Non-Protein Coding RNA[Title/Abstract]) OR Long Intergenic Non Protein Coding RNA[Title/Abstract]) OR LincRNAs[Title/Abstract]) OR LINC RNA[Title/Abstract]) AND ((((((((((((((((Neoplasms[Title/Abstract]) OR Neoplasia[Title/Abstract]) OR Neoplasias[Title/Abstract]) OR Neoplasm[Title/Abstract]) OR Tumors[Title/Abstract]) OR Tumor[Title/Abstract]) OR Cancer[Title/Abstract]) OR Cancers[Title/Abstract]) OR Malignancy[Title/Abstract]) OR Malignancies[Title/Abstract]) OR Malignant Neoplasms[Title/Abstract]) OR Malignant Neoplasm[Title/Abstract]) OR Neoplasm, Malignant[Title/Abstract]) OR Neoplasms, Malignant[Title/Abstract]) OR Benign Neoplasms[Title/Abstract]) OR Neoplasms, Benign[Title/Abstract]) OR Benign Neoplasm[Title/Abstract]) OR Neoplasm, Benign[Title/Abstract]) AND(exosomes[Title/Abstract]) OR exosome[Title/Abstract].

Participant or population: 1)all types of solid tumor patients. 2)All solid tumor patients must be diagnosed by clinical histopathology.

Intervention: No intervention because this is a systematic review of observational studies (diagnostic meta).

Comparator: Are shown in the included criteria: healthy people.

Study designs to be included: Sensitivity, Specificity, diagnostic likelihood ratio negative, the diagnostic likelihood ratio positive, Higgin's I2, Cochran's Q test.

Eligibility criteria: 1) include all types of solid tuomorcancer patients. 2) All solid tumor patients must be diagnosed by clinical histopathology. 3)include healthy people as a control group. 43) provide the expression levels of exosomal lncRNA 5)provide the method to testify to the existence of related exosomes. 64) evaluated a liquid sample type. 75) include data about the diagnostic significance of exosomes in all types of cancer patients. 86) include sample size, control group size, and sensitivity, specificity. The following studies were excluded: 1) Duplicate literature. 2) Insufficient data. 3) meta-analysis, letter, animal experiment, review. 4) non-cancer research. 5) The article did not verify the presence of exosomes. 6) The article does not have diagnostic significance data related to the exosomal lncRNA. 7) control group that did not meet the requirements.

Information sources: Web of science, EMBASE, PubMed.

Main outcome(s): Sensitivity, Specificity, diagnostic likelihood ratio negative (DLR-), diagnostic likelihood ratio positive (DLR+), AUC value.

Additional outcome(s): Higgin's I 2 and Cochran's Q test.

Quality assessment / Risk of bias analysis: According to Quality Assessment of

Diagnosis Accuracy Studies QUADAS-2 criteria, we evaluated the quality of the involved studies by using RevMan 5.3 software. Futhermore, we plotted the Deek's funnel plot asymmetry test to perform the publication bias.

Strategy of data synthesis: Statistical analysis was performed by Stata 14.0 software (Stata, College Station, TX, USA). We applied the bivariate random-effects regression model to combine the effect values of all included studies. The analysis includes sensitivity, Specificity, diagnostic likelihood ratio negative (DLR-), diagnostic likelihood ratio positive (DLR+) with corresponding 95%CI32, the Higgin's I 2 and Cochran's Q test also included in the analysis33. Moreover, we utilized the kappa statistic to analysis the concordance between diagnosis on exosomal lncRNA and clinical histopathology. Furthermore, we plotted the bivariate boxplot to roughly assess the heterogeneity of the study. And we plotted the SROC curve to calculate the pooled under the curve (AUC) value34.

Subgroup analysis: To further explore the potential heterogeneity between the included studies, we performed a subgroup analysis by Stata software 14.0. The included studies are divided into six subgroups based on tumor type, number of samples, and exosomes isolation.

Sensibility analysis: The analysis model will not be changed.

Country(ies) involved: China, Iran.

Keywords: Solid tumours; Diagnosis; Exosome; Long non-coding RNAs; Meta-analysis.

Contributions of each author:
Author 1 - Zilong Wu - Author1 provide the study materials, analysis and interpretate the data, write the manuscript.
Author 2 - Zihao Xu - Author 2 provide the materials of study, analysis and interpretate the data, write manuscript.
Author 3 - Boyao Yu - Author 3 collect and assess the data.
Author 4 - Jing tao Zhang - Author 4 provide the support of administrative and write the manuscript.
Author 5 - Bentong Yu - Author 5 concept and design the study, provide the support of administration.