

INPLASY PROTOCOL

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Conflicts of interest:
None declared.

Prognostic role of long noncoding RNA NEAT1 expression in oral squamous cell carcinoma: A protocol for systematic review and meta-analysis

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Review question / Objective: This systematic review and meta-analysis is performed to determine the prognostic role of lncRNA NEAT1 expression in oral squamous cell carcinoma (OSCC), and we speculate that high lncRNA NEAT1 expression predicts the worse prognosis in OSCC.

Condition being studied: Oral squamous cell carcinoma.

Information sources: The comprehensive literature search will be performed in the following common databases: EMBASE, Cochrane Library, PubMed, and Web of Science. The following key words will be used to retrieve the relevant studies: “long noncoding RNA”, “lncRNA”, “nuclear paraspeckle assembly transcript 1”, “NEAT1”, “oral squamous cell carcinoma”, and “OSCC”. To avoid missing relevant studies, the following databases will be also searched: Google Scholar and NIH clinical registry ClinicalTrials.gov. All retrieved studies will be evaluated using the above mentioned eligibility criteria.

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 30 March 2022 and was last updated on 30 March 2022 (registration number INPLASY202230171).

INTRODUCTION

Review question / Objective: This systematic review and meta-analysis is performed to determine the prognostic role of lncRNA NEAT1 expression in oral squamous cell carcinoma (OSCC), and we

speculate that high lncRNA NEAT1 expression predicts the worse prognosis in OSCC.

Condition being studied: Oral squamous cell carcinoma.

METHODS

Participant or population: Patients with OSCC.

Intervention: Patients with high lncRNA NEAT1 expression.

Comparator: Patients with low lncRNA NEAT1 expression.

Study designs to be included: Randomized clinical trials.

Eligibility criteria: Studies meeting the following criteria are included into this systematic review and meta-analysis: (1) participants: patients diagnosed as OSCC; (2) intervention: the expression of lncRNA NEAT1; (3) outcomes: overall survival (OS), and clinicopathological parameters, such as clinical stage; and (4) study design: randomized clinical trials (RCTs). The language of included studies is restricted to English. Following studies will be directly excluded from this systematic review and meta-analysis: cell or animal experiments, reviews, case reports, and studies with duplicated patients. Two authors evaluated the eligibility of all included studies obtained from the databases independently using the eligibility criteria. Discrepancies during the process of study selection between two authors will be resolved through group discussion.

Information sources: The comprehensive literature search will be performed in the following common databases: EMBASE, Cochrane Library, PubMed, and Web of Science. The following key words will be used to retrieve the relevant studies: “long noncoding RNA”, “lncRNA”, “nuclear paraspeckle assembly transcript 1”, “NEAT1”, “oral squamous cell carcinoma”, and “OSCC”. To avoid missing relevant studies, the following databases will be also searched: Google Scholar and NIH clinical registry ClinicalTrials.gov. All retrieved studies will be evaluated using the above mentioned eligibility criteria.

Main outcome(s): The association of lncRNA NEAT1 expression with overall

survival (OS) and clinicopathological parameters, such as clinical stage.

Quality assessment / Risk of bias analysis: For each included study, the risk of bias will be evaluated using the Cochrane Collaboration Risk of Bias (ROB2.0), which consists of seven parts: random sequence generation, allocation concealment, blinding of participants and personnel, blinding of outcome assessment, incomplete outcome data, selective reporting, and other (analysis for intention to treat and compliance). For each part, the study will be assigned with a value of “high,” “low,” or “unknown” risk of bias. The risk of bias will be evaluated by two authors independently, and any disagreement in the evaluation process will be resolved through group discussion.

Strategy of data synthesis: The Stata 12.0 software is used to synthesize and analyze the data. Study results for the association between the expression of NEAT1 and prognosis of multiple cancers are reported as odds ratio (OR) / hazard ratio (HR) value with 95% confidence interval (CI). In details, the association of NEAT1 expression with OS is assessed using the HR with corresponding 95%CI, and the association of NEAT1 expression with clinicopathological parameters is assessed using the OR with corresponding 95%CI.

Subgroup analysis: To comprehensively assess the relationship between NEAT1 expression and OS in OSCC, subgroup analyses will be performed according to different grouping standards, such as ethnicity and sample size.

Sensitivity analysis: When applicable, a sensitivity analysis will be performed to reflect the effect of an individual study on the pooled results.

Country(ies) involved: China.

Keywords: nuclear paraspeckle assembly transcript 1; oral squamous cell carcinoma; prognosis; overall survival; meta-analysis.

Contributions of each author:

Author 1 - Hui Zhan.

Author 2 - Jiayuan Zou.

Author 3 - Shaolin Deng.