INPLASY PROTOCOL

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Corresponding author:
Xuejun Liang

liangxj1027@126.com

Author Affiliation:
Jinling Hospital Affiliated to Southern Medical University

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None declared.

Clinicopathological significance and prognostic value of long noncoding RNA MIAT in human Cancers: a meta-analysis

Liang, X[1]; Zhu, H[2]; Tang, G[3]; LI, W[4]; Ye, L[5]; Shi, S[6].

Review question / Objective: **LncRNA MIAT was discovered in various carcinomas, such as cervical cancer, pancreatic cancer, but limited sample size and controversial conclusions lead us to think that further analysis is necessary. Is there a potential role for MIAT and the clinicopathological characteristics of tumors? Does the expression of LncRNA MIAT affect the prognosis of patients? We aim to evaluate the significance of LncRNA MIAT in the clinicopathological characters and prognosis of human cancers and lay the foundation for the clinical application of LncRNA MIAT.**
Condition being studied: **Long noncoding RNA myocardial infarction associated transcript (MIAT), which was thought to confers risk of myocardial infarction, is located in human chromosome 22q12.1. LncRNA MIAT performs a variety of cellular functions through different molecular mechanisms., including diabetic retinopathy, cancer. The increasing number of studies had identified that aberrant MIAT expression definitely interacted with clinicopathologic prognostic outcomes in many kinds of malignancies. However, most individual studies are restricted by controversial and small sample sizes. A comprehensive understanding of the role of MIAT in human cancers may provide more useful information for the doctor about the disease to formulate a better treatment schedule for the patients.**

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 23 September 2021 and was last updated on 23 September 2021 (registration number INPLASY202190076).

INTRODUCTION

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METHODS

Search strategy: #1 ("Myocardial infarction associated transcript") OR ("MIAT") | #2 ("Neoplasms"[Mesh]) OR ("cancer") OR ("tumor") OR ("neoplasia") OR ("malignancy") OR ("carcinoma") | #3 ("prognosis" [Mesh]) OR (prognos*) | #4 ("survival" [Mesh]) OR ("Mortality" [Mesh]) OR ("outcome") OR ("recurrence"[Mesh]) OR ("relapse") | #5 ("pathology" [Mesh]) OR (pathology*) | #6 #3 OR #4 OR #5 | #7 #1 AND #2 AND #6.

Participant or population: Human with diagnosed cancer.

Intervention: High expression of MIAT.

Comparator: Low or no expression of MIAT.

Study designs to be included: A case-control or cohort study.

Eligibility criteria: Inclusion criteria:(1) Study the roles of MIAT in human cancer, (2) Detected the expression levels of MIAT in cancer tissues, (3) Divided patients into two dichotomous groups according to the specific criteria of MIAT expression level, (4) Reported data were related to prognostic information or one of the following pathological characteristics: clinical stage, tumor size, histological grade, lymph node metastasis, and distant metastasis, (5)it should be a case-control or cohort study.(1) Study the roles of MIAT in human cancer, (2) Detected the expression levels of MIAT in cancer tissues, (3) Divided patients into two dichotomous groups according to the specific criteria of MIAT expression level, (4) Reported data were related to prognostic information or one of the following pathological characteristics: clinical stage, tumor size, histological grade, lymph node metastasis, and distant metastasis.

Information sources: We will search from 1948 to August 2021, the following databases for relevant English language literature: PubMed (MEDLINE), Web of Science, EMBASE, and The Cochrane Library. The searched keywords were as follows: "MIAT", "cancer", "prognosis", "pathology". Synonyms of these words will also be searched, and searched in different combinations. The reference lists of included studies were also checked to identify potentially relevant papers.

Main outcome(s): Relationship between clinicopathological characteristics and MIAT expression.

Additional outcome(s): Overall survival.

Quality assessment / Risk of bias analysis: The quality of included studies was evaluated by using the Newcastle-Ottawa Scale standard, which included selection (4 points), comparability (2 points), and outcome (3 points) with a score range of 0–

9. Studies with higher or equal to 6 points could be considered as high quality.

Strategy of data synthesis: The effect of MIAT expression on clinicopathological characteristics was described as a combined odds ratio (OR) and a matched 95% CI. A pooled HR with a corresponding 95% CI was used to estimate the relationship between MIAT expression and patient prognosis. Cochran's Q and I^2 tests are used to check the heterogeneity of results. A P value 50% indicates significant heterogeneity. When there are homogeneous data, the fixed-effects framework is adopted, otherwise, the random-effects model is adopted. In addition, possible publication biases were quantified by performing Begg's test and Egger's test, respectively. A sensitivity analysis was also performed to study the stability of the cumulative results. All analyses were performed using Revman 5 software. P value<0.05 is considered statistically significant.

Subgroup analysis: We will consider subgroups such as cancer type, tumor size.

Sensitivity analysis: After excluding a low-quality study, re-analyze the combined effect size and compare the new combined result with the combined result before the exclusion. If there is no major change between the two, it means that the sensitivity is low. The result of the meta-analysis is robust and credible; on the contrary, if the merged result after the exclusion is quite different from the original merged result or even the opposite conclusion is obtained, it indicates that the sensitivity is high, and the robustness of the results of this meta-analysis is low. At this time, we should be very cautious, and we need to further clarify the source of bias factors.

Language: English.

Country(ies) involved: China.

Keywords: long noncoding RNA MIAT; cancer; clinicopathology; prognosis.

Contributions of each author:

Author 1 - Xuejun Liang.
Email: liangxj1027@126.com
Author 2 - Hanlong Zhu.
Email: hanlongzhu0319@126.com
Author 3 - Guoxing Tang.
Email: 1392946798@qq.com
Author 4 - Wencai LI.
Email: liwencai2021@163.com
Author 5 - Lei Ye.
Email: 1256555640@qq.com
Author 6 - Shaopei Shi.
Email: 15151822814@163.com