

INPLASY PROTOCOL

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Review Stage at time of this submission: The review has not yet started.

Conflicts of interest:
The authors declare that they have no competing interests.

INTRODUCTION

Review question / Objective: Do CD44,TLR4,BIRC5 gene polymorphisms have any associations with a higher lung cancer risk?

Condition being studied: Lung cancer; model of inheritance; network meta-analysis; susceptibility.

A comprehensive assessment of single nucleotide polymorphisms associated with lung cancer risk: a protocol for systematic review and network meta-analysis

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Review question / Objective: Do CD44,TLR4,BIRC5 gene polymorphisms have any associations with a higher lung cancer risk?

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Information sources: The databases retrieved in this study include: PubMed, Web of Science, Embase, Cochrane Library, China National Knowledge Infrastructure (CNKI) Science and Technology Periodical Database (VIP) and Wanfang databases, with no language limits. All those studies published through April 2020. The search terms we studied are as follows: single nucleotide polymorphism, SNP, lung cancer and lung tumor.

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 28 May 2020 and was last updated on 28 May 2020 (registration number INPLASY202050105).

METHODS

Participant or population: Participants affected by lung cancer and was taken serum samples before prior chemoradiotherapy will be included.

Intervention: Associated with lung cancer gene polymorphisms.

Comparator: Noncancer controls may be healthy or have non-malignant diseases.No restrictions were placed on age, gender, country, or tumor stage.

Study designs to be included: Case-control studies.

Eligibility criteria: This study will include RCTs and case-control study that comparing the risk of different gene polymorphisms for patients with lung cancer.

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Main outcome(s): Lung cancer risk comparisons.

Quality assessment / Risk of bias analysis: The methodological quality of data was assessed based on the STREGA statement. Two reviewers(ZY and LL) conducted the rating independently and a third reviewer (JZ) was consulted for consensus if disagreement occurred.

Strategy of data synthesis: StataMP14.0 software will be used to analyse these data. We use the value of 95% confidence interval (CIs) to select the mixed odds ratio (or) under the condition of fixed effect or random effect, and according to the result of its heterogeneity, we carry out different

genetic models Model, homozygous model, heterozygous model, explicit model, recessive model).

Subgroup analysis: We will conduct a subgroup analysis of the SNPs most associated with pancreatic cancer, according to race, type of virus infection, age, sex, etc.

Sensibility analysis: Sensitivity analysis will be conducted to check the robustness and reliability of pooled outcome results.

Country(ies) involved: China.

Keywords: Lung cancer; model of inheritance; network meta-analysis; susceptibility.

Contributions of each author:

Author 1 - Li-juan Li.

Author 2 - M. Meda.

Author 3 - Yuan-yuan Zhao.

Author 4 - M.Medb.

Author 5 - Jing-hui Zheng.