INPLASY PROTOCOL

To cite: Li. A comprehensive assessment of single nucleotide polymorphisms associated with lung cancer risk: a systematic review and network meta-analysis of protocols. Inplasy protocol 202240018. doi: 10.37766/inplasy2022.4.0018

Received: 04 April 2022

Published: 04 April 2022

Corresponding author:
li lijuan

alilijuan@163.com

Author Affiliation:
Hong Kong Baptist University.

Support: **Hong Kong Baptist University.**

Review Stage at time of this submission: **Completed but not published.**

Conflicts of interest:
None declared.

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

Li, LJ[1].

Review question / Objective: **Single nucleotide polymorphisms associated with lung cancer risk: A protocol of systematic review and network meta-analysis.**
Condition being studied: **Single nucleotide polymorphisms (SNPs) have been inconsistently associated with lung cancer risk. This meta-analysis aimed to synthesize relevant data on SNPs associated with lung cancer.**
Information sources: **Search the database to identify SNP-LC related research published from PubMed's database as of December 2021, Web of Science, Embase, Cochrane Library, China National Knowledge Infrastructure (CNKI), the Chinese Science and Technology Periodical Database (VIP) and Wan fang databases.Network meta-analysis and Thakkinstian's algorithm were used to select the most appropriate genetic model, along with false positive report probability (FPRP) for noteworthy associations. The methodological quality of data was assessed based on the STREGA statement and Stata 14.0 will be used for systematic review.**

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 04 April 2022 and was last updated on 04 April 2022 (registration number INPLASY202240018).

INTRODUCTION

Review question / Objective: **Single nucleotide polymorphisms associated with lung cancer risk: A protocol of systematic review and network meta-analysis.**

Condition being studied: **Single nucleotide polymorphisms (SNPs) have been inconsistently associated with lung cancer risk. This meta-analysis aimed to synthesize relevant data on SNPs associated with lung cancer.**

METHODS

Participant or population: **all over the world.**

Intervention: Hardy-Weinberg equilibrium.

Comparator: Lung cancer control group.

Study designs to be included: The objective of this study was to comprehensively evaluate significant SNPs associated with lung cancer susceptibility. Moreover,we aim to indicate which genetic model is most appropriate to identify associations of SNPs with lung cancer .Search the database to identify SNP-LC related research published from PubMed's database as of December 2021, Web of Science, Embase, Cochrane Library, China National Knowledge Infrastructure (CNKI), the Chinese Science and Technology Periodical Database (VIP) and Wan fang databases.Network meta-analysis and Thakkinstian's algorithm were used to select the m.

Eligibility criteria: The methods of this systematic review conducted in accordance with the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines.

Information sources: Search the database to identify SNP-LC related research published from PubMed's database as of December 2021, Web of Science, Embase, Cochrane Library, China National Knowledge Infrastructure (CNKI), the Chinese Science and Technology Periodical Database (VIP) and Wan fang databases.Network meta-analysis and Thakkinstian's algorithm were used to select the most appropriate genetic model, along with false positive report probability (FPRP) for noteworthy associations. The methodological quality of data was assessed based on the STREGA statement and Stata 14.0 will be used for systematic review.

Main outcome(s): Case-control study related to the susceptibility of the SNPs to the lung cancer, will be incorporated in our review. Repeat report, conference report, thesis, review paper, or animal study, or study has insufficient data for genotyping distribution calculation or which SNPs demonstrated a departure from Hardy-Weinberg equilibrium (HWE) in controls were excluded.

Quality assessment / Risk of bias analysis: Data extracted from individual papers include: author, year of publication, country, sample size, the value of HWE, sex composition, age of diagnosis, and details of target SNPs, including genotyping methods, frequencies of genotypes.The methodological quality of data was assessed based on the STREGA statement11. Two reviewers(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 calculated fixed- or random-effects pooled odds ratio (OR) with 95% confidence intervals (CIs) for pairwise meta-analysis, depending on degree of heterogeneity under different genetic models (allele contrast model, homozygous model, heterozygous model, dominant model, recessive model).

Subgroup analysis: We further compared genetic models to select the most appropriate model using the algorithm by Thakkinstian et al13. To assess the noteworthiness of the normally significant SNPs under the most appropriate genetic model determined by network meta-analysis or Thakkinstian' algorithm, false positive report probability (FPRP) was calculated assuming three levels of prior probabilities (low: 0.1; moderate: 0.01; high: 0.001) and an OR of 1.5, as previously described14,15. Significant SNPs with a FPRP value < 0.2 were considered noteworthy4. Diagnostic meta-analysis was conducted to determine sensitivity and specificity of SNPs in predicting lung cancer risk using the Meta-DiSc software16.

Sensitivity analysis: Diagnostic meta-analysis was conducted to determine sensitivity and specificity of SNPs in predicting lung cancer risk using the Meta-DiSc software16.

Language: English.

Country(ies) involved: China.

Keywords: lung cancer, single nucleotide polymorphisms.

Contributions of each author:
Author 1 - Li Lijuan.