INPLASY PROTOCOL

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

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

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

Ye,Z[1]; Li,L[2]; Zheng,J[3]; Zhang,C[4]; Lu,Y[5]; Tang,Y[6].

Review question / Objective: **Do XPC,ERCC2,ABO,COX-2 gene polymorphisms have any associations with a higher pancreatic cancer risk?**
Condition being studied: **Pancreatic cancer,SNPs,gene polymorphism.**
Information sources: **We will search for relevant studies in the following databases: PubMed, Web of Science, Embase, Cochrane Library, China National Knowledge Infrastructure (CNKI), the Chinese Science and Technology Periodical Database (VIP) and Wanfang databases, with no language limits.All those studies published through January 2020. The search strategy was based on the following search terms: "single nucleotide polymorphism", "SNP", "pancreatic cancer", and "pancreatic carcinoma".**

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 04 April 2020 and was last updated on 04 April 2020 (registration number INPLASY202040023).

INTRODUCTION

Review question / Objective: **Do XPC,ERCC2,ABO,COX-2 gene polymorphisms have any associations with a higher pancreatic cancer risk?**

Condition being studied: **Pancreatic cancer,SNPs,gene polymorphism.**

METHODS

Participant or population: **Participants affected by PC and was taken serum**

samples before prior chemoradiotherapy will be included in the meta-analysis.

Intervention: Associated with pancreatic cancer gene polymorphisms.

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

Study designs to be included: Case-control study related to the susceptibility of the SNPs to the PC, will be incorporated in our review. Repeat report, conference report, thesis.

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

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Main outcome(s): pancreatic 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 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). Heterogeneity was quantified with the I2 statistic and P value; a I2 statistic < 50% and a P > 0.1 indicated low heterogeneity between studies, in which case the fixed-effect model was employed.For significant SNPs with evidence of heterogeneity in meta-analysis, assessment of sources of heterogeneity was employed using subgroup analysis if sufficient data existed. A random-effects network meta-analysis within a Bayesian framework was conducted using the GeMTC software (v 0.14.3)(21). Four parallel Markov chain Monte Carlo simulations were run for a 20,000-stimulation burn-in phase and an additional 50,000-stimulation phase. Convergence was satisfied with a potential scale reduction factor (PSRF) value of 1.0 as the cut-off value. Consistency, referring to agreement between direct and indirect comparisons in terms of effect estimates, was evaluated by comparing consistency model with inconsistency model in terms of standard deviation of the random effect. Theinconsistency model was used when an obvious deviation was detected; otherwise, the consistency model was used. This Bayesian approach was used to rank the probability of each genetic model for risk assessment for PC and corresponding rank probability plots were generated.

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.

Countries involved: China

Keywords: pancreatic cancer; case-control study; model of inheritance; network meta-analysis; susceptibility.