INPLASY PROTOCOL

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Review Stage at time of this submission: **Data extraction.**

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

A comprehensive evaluation of single nucleotide polymorphisms associated with osteosarcoma risk: a protocol for systematic review and network meta analysis

Ye, Z[1]; Luo, M[2]; Zheng, J[3]; Zhang, C[4]; Tang, Y[5].

Review question / Objective: **Do MATP,IL-6,CTLA-4 gene polymorphisms have any associations with a higher pancreatic cancer risk?**
Condition being studied: **Osteosarcoma,SNPs,gene polymorphism.**
Information sources: **As of January 2020, we have obtained articles on the study of SNPs frequency differences between OS patients and non-cancer control groups from various well-known paper websites. These sites are Embase, PubMed, Web of Science, Cochrane Library, the Chinese Science and Technology Periodical Database (VIP), China National Knowledge Infrastructure (CNKI). Get related articles by searching for keywords in this study and keywords included: "single nucleotide polymorphism", "SNP", "osteosarcoma" and "osteogenic sarcoma".**

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 22 April 2020 and was last updated on 22 April 2020 (registration number INPLASY202040141).

INTRODUCTION

Review question / Objective: **Do MATP,IL-6,CTLA-4 gene polymorphisms have any associations with a higher pancreatic cancer risk?**

Condition being studied: **osteosarcoma,SNPs,gene polymorphism.**

METHODS

Participant or population: **Participants affected by OS and was taken**

serumsamples before prior chemoradiotherapy will be included.

Intervention: Associated with osteosarcoma 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 study, published in either English or Chinese that concern the susceptibility of the SNPs to the OS, will be integrated into this review.

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

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Main outcome(s): Osteosarcoma risk comparisons.

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

Strategy of data synthesis: A random-effects network meta-analysis within a Bayesian framework was conducted using the GeMTC software (v 0.14.3)(15). 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. A pairwise meta-analysis was performed using stata to assess the consistency of each model, and whether the models are consistent with each other or not, we can obtain consistent results from the model. When $P<0.5$, it means that there is a significant deviation, we use the inconsistent model, otherwise we adopt the consistent model. In the network analysis, we made a probabilistic sequence diagram of the relevant models and genes based on the Bayesian method.

Subgroup analysis: If the data are sufficient, we will proceed a subgroup analysis of the SNPs associated with OS by race, age, type, gender, etc.

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

Country(ies) involved: China.

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