INPLASY PROTOCOL

To cite: Chen et al. The Correlation of MDM4(rs4245739, rs1563828, rs11801299, rs10900598 and rs1380576) polymorphisms with cancer susceptibility: A meta-analysis. Inplasy protocol 2021110083. doi: 10.37766/inplasy2021.11.0083

Received: 23 November 2021

Published: 23 November 2021

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Support: **There was no external funding.**

Review Stage at time of this submission: **Preliminary searches.**

Conflicts of interest:
None declared.

The Correlation of MDM4(rs4245739, rs1563828, rs11801299, rs10900598 and rs1380576) polymorphisms with cancer susceptibility: A meta-analysis

Chen, J[1]; Xiong, H[2]; Liu, R[3]; Liu, Z[4].

Review question / Objective: **The connection between MDM4 polymorphisms and tumor risk has been investigated by several studies and yielded different results. Therefore, we are going to perform a meta-analysis to assess synthetically the association of MDM4(rs4245739, rs1563828, rs11801299, rs10900598 and rs1380576) polymorphisms with the susceptibility of cancers.**
Eligibility criteria: **(a) Studies for cancers and MDM4 gene polymorphisms (including rs4245739, rs1563828, rs11801299, rs10900598 and rs1380576). (b) Case-control studies with a case group of patients with pathologically confirmed malignancies and a control group of healthy individuals without tumors. (c) Ability to access complete available data.**

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 23 November 2021 and was last updated on 23 November 2021 (registration number INPLASY2021110083).

INTRODUCTION

Review question / Objective: **The connection between MDM4 polymorphisms and tumor risk has been investigated by several studies and yielded different results. Therefore, we are going to perform a meta-analysis to assess synthetically the association of MDM4(rs4245739, rs1563828, rs11801299, rs10900598 and rs1380576) polymorphisms with the susceptibility of cancers.**

Condition being studied: **The connection between MDM4 polymorphisms and tumor risk has been investigated by several studies and yielded different results.**

METHODS

Search strategy: The studies included in this meta-analysis will be obtained from five databases we searched (Pubmed, Web of Science, Cochrane Library, CNKI and Wan Fang Database) . The search terms is: (Neoplasm or tumor or cancer or carcinoma) and (Mouse double minute 4 or MDM4 or rs4245739 or rs1563828 or rs11801299 or rs10900598 or rs1380576) and (polymorphism or SNP or allele or variation). We will find articles with high relevance to our study based on the cited literature of the included articles.

Participant or population: Case group and control group were extracted from previous case-control studies on the relationship between MDM4(rs4245739, rs1563828, rs11801299, rs10900598 and rs1380576) polymorphisms and tumors.

Intervention: Patients of different races with tumors.

Comparator: Healthy persons.

Study designs to be included: Case-control studies, tumor patients will be included in the case group and healthy people in the control group.

Eligibility criteria: (a) Studies for cancers and MDM4 gene polymorphisms (including rs4245739, rs1563828, rs11801299, rs10900598 and rs1380576). (b) Case-control studies with a case group of patients with pathologically confirmed malignancies and a control group of healthy individuals without tumors. (c) Ability to access complete available data.

Information sources: The studies included in this meta-analysis will be obtained from five databases we searched (Pubmed, Web of Science, Cochrane Library, CNKI and Wan Fang Database).

Main outcome(s): The Correlation of MDM4(rs4245739, rs1563828, rs11801299, rs10900598 and rs1380576) polymorphisms with cancer susceptibility.

Quality assessment / Risk of bias analysis: Both researchers will assess the quality of the included experiments based on Newcastle-Ottawa Scale (NOS). Publication bias will be assessed by funnel plot and egger's test.

Strategy of data synthesis: We will use the Cochran's Q test ($P < 0.05$ is statistically significant) and the I2 statistic in forest plots to assess the level of heterogeneity between the original studies. P values less than 0.05 and/or I2 greater than 50% will be considered to have heterogeneity. A fixed-effects model will be used for merging ORs to assess the association of individual models with tumor risk in cases where heterogeneity is not significant; otherwise, a random-effects model will be used. Meta-regression analysis will be used to explore sources of heterogeneity.

Subgroup analysis: To further investigate the association of single nucleotide polymorphisms in MDM4 with cancer risk, we will perform subgroup analysis regarding ethnicity, cancer-type and sources of controls for SNPs that were included in more studies.

Sensitivity analysis: Sensitivity analysis will be performed by the leave-one-out method to assess the stability of the outcomes for single nucleotide polymorphisms with the number of included studies greater than or equal to 10.

Language: No restriction.

Country(ies) involved: China.

Keywords: single-nucleotide polymorphisms, MDM4, meta-analysis, cancer susceptibility.

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