

# INPLASY

INPLASY202370016

doi: 10.37766/inplasy2023.7.0016

Received: 04 July 2023

Published: 04 July 2023

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## The relationship between the hOGG1 rs1052133 polymorphism and the susceptibility to the nasopharyngeal carcinoma: a systematic review and meta-analysis

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## ADMINISTRATIVE INFORMATION

**Support** - None.

**Review Stage at time of this submission** - Piloting of the study selection process.

**Conflicts of interest** - None declared.

**INPLASY registration number:** INPLASY202370016

**Amendments** - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 04 July 2023 and was last updated on 04 July 2023.

## INTRODUCTION

**Review question / Objective** There is no unified conclusion on the relationship between hOGG1 rs1052133 polymorphisms and the occurrence of nasopharyngeal carcinoma. Different studies have drawn different conclusions. To clarify the relationship, we conducted a systematic evaluation and meta-analysis.

**Condition being studied** Nasopharyngeal cancer is the common head and neck malignant tumor in China, and its incidence is related to EB virus infection, genetic factors, and environmental factors. More and more studies have shown that gene polymorphism is closely related to the occurrence of nasopharyngeal carcinoma. Recent studies have found that the occurrence of nasopharyngeal carcinoma is related to the polymorphism of the DNA repair gene, and hOGG1(human 8-oxoguanine DNA glycosylase 1) in the BER(base excision repair) pathway may be

related to the occurrence of nasopharyngeal carcinoma. Exon 7 of the hOGG1 gene can change from C to G, resulting in amino acid substitutions from Ser(C) to Cys(G) at codon 326(rs1052133). However, there is no unified conclusion on the relationship between hOGG1 rs1052133 polymorphisms and the occurrence of nasopharyngeal carcinoma. Different studies have drawn different conclusions. To clarify it, we conducted a systematic review and meta-analysis.

## METHODS

**Participant or population** This study will include adult patients diagnosed with nasopharyngeal carcinoma through endoscopic biopsy.

**Intervention** The intervention group took peripheral blood samples from each patient and extracted DNA samples for hOGG1 rs1052133 polymorphism analysis.

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**Comparator** The control group took peripheral blood samples from normal individuals and extracted DNA samples for hOGG1 rs1052133 polymorphism analysis.

**Study designs to be included** Randomized clinical trials will be included in this study.

**Eligibility criteria** Inclusion criteria: (1) After nasopharyngeal biopsy, the pathological diagnosis was confirmed as nasopharyngeal carcinoma and no any anti-tumor treatment was received before genetic analysis. (2) Patients were greater than 18 years old. (3) Patients had no serious cardio-cerebral-vascular disease, diabetes, mental disease, blood disease. (4) Patients agreed to take blood samples and conduct genetic testing. Exclusion criteria: (1) Other nasopharyngeal malignancies. (2) Patients were less than 18 years old.

**Information sources** Pubmed, Cochrane, Web of science.

**Main outcome(s)** We will integrate the odds ratios of all studies to obtain the overall odds ratio and further draw conclusions.

**Quality assessment / Risk of bias analysis** We will use the Newcastle Ottawa Scale to evaluate bias.

**Strategy of data synthesis** The results will be analyzed by using Stata 17.0 statistical software. The forest plot will be drawn at first by using the fixed effect model. For the consistency evaluation of the study, the traditional statistical test (Cochran's Q test) will be first used for evaluation, and then the  $I^2$  test will be used for verification. If the  $I^2$  value is greater than 75%, it indicates that there is great heterogeneity, so further sensitivity analysis will be needed to identify the source of heterogeneity and the randomized effect model will be used for integrating the odds ratios of all studies. For the evaluation of publication bias, Begg and Egger's tests will be used for validation.  $P < 0.05$  means that the results are statistically significant.

**Subgroup analysis** We will conduct subgroup analysis based on different genotypes.

**Sensitivity analysis** If the conclusion has significant heterogeneity, we will conduct sensitivity analysis to identify the source of heterogeneity.

**Language restriction** None.

**Country(ies) involved** China.

**Keywords** hOGG1; rs1052133; polymorphisms; nasopharyngeal carcinoma.

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