

INPLASY PROTOCOL

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None declared.

Association between Toll-like receptor gene polymorphisms and risk of Helicobacter pylori infection: A protocol for systematic review and meta-analysis

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Review question / Objective: Do Toll-like receptor gene polymorphism associated with Helicobacter pylori infection risk?

Condition being studied: Toll-like receptor, gene polymorphisms, Helicobacter pylori infection.

Information sources: We searched the following seven databases: PubMed, EMBASE, Web of science, Cochrane library, China National Knowledge Infrastructure (CNKI), China Biology Medicine (CBM), Wan Fang Database for Chinese Technical Periodicals and VIP Database, all the Database were searched from inception to December 2020. Our search terms included: #1: (“Helicobacter pylori”[Mesh] OR “H. pylori”[Title/Abstract], #2:(“Toll-Like Receptors” [Mesh] OR “TLR” [Title/Abstract]), #3(“Polymorphism, Genetic” [Mesh] OR “variant” [Title/Abstract] OR “genotype” [Title/Abstract]), the search strategy was:#1 AND #2 AND #3,all the databases were searched by the way of subject words combined with free words.

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 03 March 2021 and was last updated on 03 March 2021 (registration number INPLASY202130009).

INTRODUCTION

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METHODS

Participant or population: Participants affected by Helicobacter pylori infection was taken serum samples will be included in the meta-analysis.

Intervention: Associated with Toll-like receptor gene polymorphisms.

Comparator: Healthy population.

Study designs to be included: Case-control studies performed the association between TLR gene Polymorphisms and the correlation of H. pylori infection.

Eligibility criteria: This study will include case-control study that TLR gene Polymorphisms and the correlation of H. pylori infection.

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Main outcome(s): H. pylori infection risk comparisons.

Quality assessment / Risk of bias analysis: The quality of included studies was assessing by the Newcastle-Ottawa scale (NOS). We assessing it from the selection, the comparability, and the exposure in both cases and controls, the NOS score vary from zero to nine, in which (score 0-5) was low quality study and (score 6-9) was high quality study.

Strategy of data synthesis: For pairwise meta-analysis, OR with the corresponding 95% CI were presented as associations between certain TLR genetic polymorphism and the risk of H. pylori infection in the allele, codominant, dominant and recessive models, the significance was determined by Z-test, with a P value<0.05 as significant

level. The heterogeneity assumption was checked by Q-test and I² statistics, when P value of Q test was greater than 0.1 or I² was less than 50%, fixed effects model was used for meta-analysis, otherwise, random effects model was carried out.All statistical analyses were performed by Review Manager 5.2 version software (The Cochrane Collaboration, Software Update, Oxford, United Kingdom).

Subgroup analysis: Subgroup analyses were subsequently conducted by ethnicity or country of participants.

Sensitivity analysis: Sensitivity analysis was performed by deletion of each single study in the meta-analysis to reflect the influence of the individual data-set on the pooled OR.

Country(ies) involved: China.

Keywords: Helicobacter pylori; Toll-like receptor; Gene polymorphisms; Meta-analysis.

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