

INPLASY PROTOCOL

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submission:** Data extraction -
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None declared.

INTRODUCTION

Review question / Objective: Polymorphism of fucosyltransferase 3 (FUT3) gene is associated with inflammatory bowel disease (IBD) - a systematic review and Meta-analysis.

Condition being studied: This study collected relevant literatures and analyzed the relationship between the polymorphism

Polymorphism of fucosyltransferase 3 (FUT3) gene is associated with inflammatory bowel disease (IBD) – a systematic review and Meta-analysis

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Review question / Objective: Polymorphism of fucosyltransferase 3 (FUT3) gene is associated with inflammatory bowel disease (IBD) – a systematic review and Meta-analysis.

Condition being studied: This study collected relevant literatures and analyzed the relationship between the polymorphism of the FUT3 genes at rs3745635, rs3894326, and rs28362459 to the IBD with Meta-analysis, in order to further explore the possible mechanism of the polymorphism of the FUT3 gene and IBD.

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 01 March 2022 and was last updated on 01 March 2022 (registration number INPLASY202230001).

of the FUT3 genes at rs3745635, rs3894326, and rs28362459 to the IBD with Meta-analysis, in order to further explore the possible mechanism of the polymorphism of the FUT3 gene and IBD.

METHODS

Search strategy: "Inflammatory bowel disease, IBD, Crohn* disease, ulcerative colitis, CD, UC, fucosyltransferase3, FUT3,

rs3745635, G508A, rs3894326, T1067A, rs28362459, T59G" were applied as key words to search corresponding English literature from PubMed database. Chinese literatures were searched from China Knowledge Network, Wanfang, Weipu database using "inflammatory bowel disease, Crohn's disease, ulcerative colitis, FUT3, fucosyltransferase 3" in Chinese as key words.

Participant or population: Enrolled in studies of inflammatory bowel disease screening will be eligible for this review, with no exclusions based on ethnicity or age. This article finally collected 1,712 patients with IBD (1,165 patients with UC and 547 patients with CD) and 1903 controls.

Intervention: rs3745635[(GA + AA),(GG + GA),GG,A], rs3894326[(TA + AA), (TT + TA), TT , A], rs28362459[(TG+GG), (TT+TG), TT), G].

Comparator: rs3745635[GG,AA,G], rs3894326[(TT ,AA , T], rs28362459[TT,GG, T]

Study designs to be included: Case-control study.

Eligibility criteria: Inclusion criteria: ① study design belonged to case-control study; ② the case group was patients with clinical diagnosis of IBD disease (UC or CD patients), the control group was healthy people or other patients without IBD diseases, in addition to both groups of the research subjects being comparable through baseline comparison; ③phenotype was in line with Hardy-Weinberg balance; ④ the content of the literature included the correlative study of polymorphism of the FUT3 gene and IBD; ⑤ the literature data was sufficient to calculate OR value.

Information sources: Pub Med database,China Knowledge Network, China Wanfang database, China Weipu database.

Main outcome(s): "Inflammatory bowel disease" OR IBD OR "Crohn* disease" OR "Ulcerative colitis" OR CD OR UC) AND (Fucosyltransferase3 OR FUT3 OR rs3745635 OR G508A OR rs3894326 OR T1067A OR rs28362459 OR T59G).

Quality assessment / Risk of bias analysis: Two reviewers evaluated the quality of each document by using the NOS bias risk assessment standard. Once there were different results, the final decision was reached based on the consensus after the two sides have resolved the differences. If the two sides still have disputes, a third reviewer would be invited to participate to discuss and decide.

Strategy of data synthesis: RevMan 5.3 software was applied for Meta-analysis of dominant gene model, recessive gene model, co-dominant gene model, and allele frequency of the FUT3.

Subgroup analysis: If the heterogeneity test $P \leq 0.1$ or $I^2 \geq 50\%$, random effect model was applied for the Meta-analysis after excluding the effects of obvious clinical heterogeneity. OR and 95% confidence interval (CI) effect size were used as indicators of binary qualitative variable data.

Sensitivity analysis: Sensitivity analysis was performed by eliminating each original study one by one. Stata12.0 software was applied for Egger's test to analyze the publication bias.

Country(ies) involved: China.

Keywords: Inflammatory bowel disease (IBD); fucosyltransferase 3 (FUT3); polymorphism; genotype; Meta-analysis.

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