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Quantitative assessment of the association between TNF- α gene polymorphism and angina risk

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ADMINISTRATIVE INFORMATION

Support - The author(s) received no specific funding for this work.

Review Stage at time of this submission - The review has not yet started.

Conflicts of interest - None declared.

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Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 30 July 2024 and was last updated on 30 July 2024.

INTRODUCTION

Review question / Objective Previous investigations into the correlation between tumor necrosis factor- α (TNF- α) gene polymorphism and susceptibility to angina have produced a range of results. This study aims to clarify the potential significance of TNF- α polymorphism as a contributing factor to the onset of angina.

Condition being studied Previous investigations into the correlation between tumor necrosis factor- α (TNF- α) gene polymorphism and susceptibility to angina have produced a range of results.

METHODS

Participant or population Case-control studies investigating the relationship between TNF- α rs1800629 -308 G/A polymorphism and the risk of angina.

Intervention / Comparator The inclusion criteria were precisely defined: (a) case-control studies investigating the relationship between TNF-a rs1800629 -308 G/A polymorphism and the risk of angina; Other types of studies are not allowed to be included, including randomized controlled trials, cohort studies, reviews and case report. (b) studies providing sufficient data. (c) Studies must investigate the population of angina. The studies were not enrolled if they investigate other cardiovascular diseases including myocardial infarction, ischemic heart disease, stroke, cardiomyopathy, rheumatic heart disease, hypertensive heart disease, and endocarditis. On the contrary, the exclusion criteria were set to omit (a) studies not adhering to a case-control design; (b) studies lacking adequate data for the computation of OR and 95% CI computation; and (c) studies where the primary subjects were animals, ensuring that the focus remained on human-related research.

Study designs to be included case-control studies investigating the relationship between TNF- α rs1800629 -308 G/A polymorphism and the risk of angina.

Eligibility criteria The inclusion criteria were precisely defined: (a) case-control studies investigating the relationship between TNF-a rs1800629 -308 G/A polymorphism and the risk of angina; Other types of studies are not allowed to be included, including randomized controlled trials, cohort studies, reviews and case report. (b) studies providing sufficient data. (c) Studies must investigate the population of angina. The studies were not enrolled if they investigate other cardiovascular diseases including myocardial infarction, ischemic heart disease, stroke, cardiomyopathy, rheumatic heart disease, hypertensive heart disease, and endocarditis. On the contrary, the exclusion criteria were set to omit (a) studies not adhering to a case-control design; (b) studies lacking adequate data for the computation of OR and 95% CI computation; and (c) studies where the primary subjects were animals, ensuring that the focus remained on human-related research.

Information sources A systematic search was carried out by two independent authors in a selection of major databases. This search spanned from the inception of each database up to March 2024, ensuring a thorough inclusion of relevant literature. The keywords used for this extensive search encompassed "polymorphism" or "polymorphisms," "angina," "TNF- α ," and "tumor necrosis factor- α ," with a focus on the literature published in PubMed to maximize the scope of our research.

Main outcome(s) To determine the distribution differences among TNF-a polymorphism genotypes and alleles of the TNF- polymorphism, the chi-square test (X2) based Q test was used. If p 50% of heterogeneity test, suggesting the existence of heterogeneity, a random-effects model (the DerSimonian and Laird method) was applied to count the summary ORs; otherwise, If p >=0.1 and I2<=50% of heterogeneity test, suggesting no existence of heterogeneity, the fixed-effects model (the Mantel-Haenszel method) was applied.

Quality assessment / Risk of bias analysis The data and pertinent information were meticulously extracted and evaluated by the first and second authors, strictly adhering to the established inclusion and exclusion criteria. Essential elements extracted included the name of the literature,

genotyping methods, control sources, and Newcastle-Ottawa Scale (NOS) scores. In instances of disagreement between the two authors, a discussion was initiated with the corresponding author to reach a consensus. Given the nature of this meta-analysis, which involves the aggregation of existing data, the requirement for ethics approval and patient consent was deemed unnecessary.

Strategy of data synthesis Odds ratios (OR) and 95% confidence intervals (CI) were performed using logistic regression modeling, providing a measure of the strength of the association between TNF-α polymorphism and angina risk.

Subgroup analysis The meta-regression and subgroup analysis were applied to find the source of heterogeneity. The characteristics were enrolled as covariates in the meta-regression including genotyping methods (TaqMan vs. PCR-RFLP), ethnicity (Caucasian vs. Asian), source of controls (HB vs. PB), quality scores (High-quality vs. Lowquality) and HWE conformity (Yes vs. No).

Sensitivity analysis Sensitivity analysis and the evaluation of publication bias were performed following protocols established in previous meta-analyses.

Country(ies) involved China.

Keywords angina, TNF-α, gene polymorphism, Meta-analysis.

Contributions of each author

Author 1 - Sen Xu, performed the data collection, extraction, analyzed the data and interpreted and reviewed the data and drafts. Email: xsxsxsxs112@126.com

Author 2 - Jielei Zhou performed the data collection, extraction and analyzed thedata. Email: zilwmu025@163.com

Author 3 - Yunzhu Zhang conceived study design, conceived the content concept and reviewed the final draft.

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