

INPLASY PROTOCOL

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None declared.

Vitamin D receptor gene polymorphisms and multiple myeloma: evidence from a systematic review and meta-analysis

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Review question / Objective: We applied a comprehensive meta-analysis to explore the association between genetic models of VDR polymorphism and MM susceptibility.

Condition being studied: Polymorphism in the vitamin D receptor (VDR) gene has been shown to alter VDR functions that affect vitamin D activity. Recent studies suggest a link between VDR gene (BsmI rs1544410, FokI rs2228570, TaqI rs731236, and ApaI rs7975232) polymorphism and multiple myeloma (MM), but the published data are conflicting.

Eligibility criteria: 1. Study type: case-control study. 2. Study population: the case group included patients meet the diagnostic criteria of MM, and the control group included healthy individuals. 3. The numbers of each genotype in case and control groups were sufficient to calculate Odds ratios (OR) and 95% confidence intervals (95% CI). 4. The genotype distributions of the control group followed the Hardy-Weinberg equilibrium (HWE).

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 30 October 2022 and was last updated on 30 October 2022 (registration number INPLASY2022100119).

INTRODUCTION

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multiple myeloma (MM), but the published data are conflicting.

METHODS

Participant or population: Multiple myeloma patients.

Intervention: N/A.

Comparator: Healthy population.

Study designs to be included: case-control study.

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Information sources: PubMed, Web of Science, Medline, Embase, CNKI, WANFANG databases were retrieved from the construction of the database to October, 2022.

Main outcome(s): SNP.

Quality assessment / Risk of bias analysis: Literature quality evaluation Newcastle-Ottawa quality Assessment scale (NOS) was adopted to evaluate the quality of the included studies. The NOS consists of three aspects of evaluation: selection, comparability and outcomes between the case group and the control group. The full score was 9 stars, and high quality was defined as a study with ≥ 7 stars.

Strategy of data synthesis: Data for meta-analysis and sensitivity analysis using the software Comprehensive Meta-Analysis (CMA, version 3.0). All SNPs were in conformation with Hardy-Weinberg equilibrium in control subjects, and trim and fill method was used to test publication bias, which was constructed by using

STATA 12.0 (STATA Corporation, Texas, USA). For the assessment of interstudy heterogeneity, the chi-square test and I^2 were used. According to whether the homogeneity was low ($P \geq 0.10$, $I^2 \leq 50\%$) or high ($P < 0.10$, $I^2 > 50\%$), we used a fixed- or random-effects model in the meta-analysis. The odds ratio (OR) was used as a summary statistic for dichotomous variables. A confidential interval of 95% (95%CI) was calculated for all mean values. P values that were > 0.05 were considered insignificant.

Subgroup analysis: N/A.

Sensitivity analysis: To explore the source of heterogeneity among studies included in the review, leave-one-out sensitivity analysis was employed in this study. This sensitivity analysis involves conducting a meta-analysis on each subset of the studies obtained by leaving out exactly one study. Publication bias was tested using Begg and Egger tests. If $P > 0.05$, there is no publication bias, whereas publication bias exists. If publication bias was indicated, the trim and fill method procedure was performed to identify and correct the publication bias.

Country(ies) involved: China (Affiliated Hospital of Shandong University of Traditional Chinese Medicine).

Keywords: multiple myeloma, gene polymorphism, vitamin D receptor, VDR, meta-analysis.

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