INPLASY PROTOCOL

To cite: Lyu et al. Vitamin D receptor gene polymorphisms and multiple myeloma: evidence from a systematic review and meta-analysis. Inplasy protocol 202330076. doi: 10.37766/inplasy2023.3.0076

Received: 21 March 2023

Published: 21 March 2023

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Support: **ZR2020KH023.**

Review Stage at time of this submission: **Completed but not published.**

Conflicts of interest:
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: **Our meta-analysis was based on systematic collected studies relating to VDR gene polymorphisms andMM.**
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.**

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 21 March 2023 and was last updated on 21 March 2023 (registration number INPLASY202330076).

INTRODUCTION

Review question / Objective: **Our meta-analysis was based on systematic collected studies relating to VDR gene polymorphisms andMM.**

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.

METHODS

Participant or population: The case group included patients meet the diagnostic criteria of MM.

Intervention: N/A.

Comparator: The control group included healthy individuals.

Study designs to be included: case-control study.

Eligibility criteria: The numbers of each genotype in case and control groups were sufficient to calculate Odds ratios (OR) and 95% confidence intervals (95% CI). The genotype distributions of the control group followed the Hardy–Weinberg equilibrium (HWE).

Information sources: PubMed, Web of Science, Medline, Embase, CNKI, WANFANG databases were retrieved.

Main outcome(s): The frequency distribution of genotypes examined for the cases and the controls.

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-Weinburg 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 I2 were used. According to whether the homogeneity was low ($P \geq 0.10$, $I2 \leq 50\%$) or high (P 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.

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

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