

Contents lists available at ScienceDirect

IJC Heart & Vasculature



journal homepage: www.sciencedirect.com/journal/ijc-heart-and-vasculature

Causal relationship between serum uric acid and cardiovascular disease: A Mendelian randomization study



Yujun Zhang^a, Qiufang Lian^c, Yanwu Nie^b, Wei Zhao^{c,*}

^a Yan'an University Xianyang Hospital, Data Management Center, Xianyang, China

^b School of Public Health, Nanchang University, Nanchang, China

^c Department of Cardiology, Xianyang Hospital, Yan'an University, Xianyang, China

ARTICLE INFO	A B S T R A C T		
Keywords: Cardiovascular disease Uric acid Mendelian randomization Causality Single nucleotide polymorphism	<i>Background:</i> Observational studies have established an association between serum uric acid and cardiovascular disease (CVD). However, these studies are susceptible to uncontrolled confounders and reverse causality bias. To overcome these challenges, we employed a two-sample Mendelian randomization (MR) approach to investigate the causal link between serum uric acid and CVD. <i>Methods:</i> We utilized Genome-wide association study (GWAS) data for serum uric acid and six CVD: coronary artery disease (CAD), hypertension, myocardial infarction (MI), heart failure (HF), angina, and coronary heart disease (CHD). MR analyses employed inverse variance weighting (IVW), MR-Egger, weighted median, and weighted model. Sensitivity analyses were conducted to assess result reliability, including Cochrane's Q test, MR-Egger intercept, MR-PRESSO, and the leave-one-out approach. <i>Results:</i> IVW analysis revealed that a genetic predisposition to elevated serum uric acid levels significantly in creases the risk of CVD, with higher odds ratios (ORs) observed for CAD (OR: 1.227; 95 % CI: 1.107–1.360, $P = 0.0002$), hypertension (OR: 1.138, 95 %CI: 1.184–1.466, $P = 2.13E-06$), MI (OR: 1.184, 95 %CI: 1.1074–1.231, $P = 0.0002$) and CHD (OR: 1.158, 95 %CI: 1.072–1.276, $P = 0.0005$). Sensitivity analysis research results have robustness. <i>Conclusion:</i> This MR study robustly demonstrates a significant causal relationship between genetically elevated serum uric acid and various cardiovascular diseases, suggesting that higher levels may enhance the risk of cardiovascular events. Consequently, patients with elevated uric acid levels warrant early and aggressive interventions to mitigate cardiovascular risks.		

1. Introduction

Cardiovascular disease (CVD) is a pathology affecting the heart and blood vessels, encompassing conditions like hypertension, coronary heart disease, myocardial infarction, and heart failure [1]. As the global population ages, the incidence of CVD has been progressively increasing. According to the World Health Organization, CVD is the leading cause of mortality among non-communicable diseases, claiming approximately 17.8 million lives annually, which constitutes one-third of global deaths. This trend significantly threatens human life and health [2,3]. Therefore, understanding the factors influencing the development of cardiovascular diseases is crucial for their early prevention, diagnosis, and treatment. Uric acid is considered a biologically inactive waste product resulting from purine metabolism, and it was identified as the cause of gout [4]. Many Observational studies have linked uric acid with increased incidence and mortality rates of CVD, which might contribute to CVD through inflammatory responses, oxidative stress, Renin-Angiotensin System (RAS) activation, and endothelial dysfunction [5–7]. Chen et al. [8] indicated that patients with high uric acid levels face a 1.5 to 3.0 times greater risk of CVD compared to those with normal levels. In a cohort study that included 25,284 Chinese people, Tian et al. [9] found that the risk of cardiovascular disease increased with elevated uric acid levels in individuals without hyperuricemia or other traditional cardiovascular disease risk factors. However, observational studies are inherently limited by reverse causation and confounding factors, leading

https://doi.org/10.1016/j.ijcha.2024.101453

Received 22 May 2024; Received in revised form 21 June 2024; Accepted 25 June 2024 Available online 29 June 2024 2352-9067/© 2024 The Authors. Published by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/bync-nd/4.0/).

^{*} Corresponding author at: Department of Cardiology, Xianyang Hospital, Yan'an University, Xianyang, China. *E-mail address:* iewoahz1120@126.com (W. Zhao).

to potential bias that obscures the true relationship. Meta-analyses of the effects of uric acid on cardiovascular disease provide estimates of the increased risk of cardiovascular disease, Miao et al. [10] showed that Serum uric acid is positively associated with the risk of adverse events in chronic heart failure patients. Zuo et al. [11] found that uric acid levels were prognostically associated with coronary heart disease mortality, with a 9% increase in mortality for every 1 mg/dL increase in uric acid. The studies evaluated in the meta-analysis can introduce bias to the findings due to the high risk of bias in the quality assessment section and the different thresholds for high and low uric acid in different studies. And, similar to observational studies, a causal relationship could not be fully established. Therefore, the causal relationship between uric acid levels and CVD remains unknown, and it is important to reveal the potential impact of uric acid levels on the initiation of CVD and its progression, which will help to reduce the risk of CVD by monitoring and regulating uric acid levels.

Mendelian randomization (MR) is an analytical method employing single nucleotide polymorphisms (SNPs) as instrumental variables (IVs) to assess causal relationships between exposures and outcomes [12]. As genetic variants are assigned randomly at conception, MR circumvents confounding factors and reverse causality, common issues in traditional observational studies [13–14]. In this study, we used two-sample MR analysis to investigate the causal relationship between serum uric acid and cardiovascular disease (CVD), contributing novel insights for CVD prevention.

2. Materials and methods

2.1. Study design

We conducted a two-sample MR analysis using public GWAS summary data (https://gwas.mrcieu.ac.uk/). In this analysis, serum uric acid was considered the "exposure", while coronary artery disease (CAD), hypertension, myocardial infarction (MI), heart failure (HF), angina, and coronary heart disease (CHD) were the "outcomes." This approach evaluated the causal relationship between serum uric acid levels and CVD. We assessed heterogeneity through Cochran's Q test and verified causality reliability using sensitivity analyses, including pleiotropy and "leave-one-out" analyses. Informed consent and ethical approval were obtained in the original publications and publicly available databases. The MR Analysis rested on three critical assumptions: (1) IVs are strongly associated with serum uric acid levels. (2) There is no association between IVs and confounding factors. (3) IVs influence CVD solely through serum uric acid (Fig. 1).

2.2. Data sources

Our systematic analysis utilized GWAS summary statistics from a comprehensive cohort to determine a causal link between serum uric acid and CVD. The serum uric acid dataset (GWAS ID: ebi-a-GCST90018977) comprised 343,836 participants with 19,041,286 SNPs. The analysis included six CVDs: CAD (42,096 cases and 361 controls), hypertension (55,917 cases and 162,837 controls), MI (14,825 cases and 44,000 controls), HF (47,309 cases and 93,0014 controls), angina (30,025cases and 440,906 controls) and CHD (60,801 cases and 123,504 controls). To minimize population heterogeneity bias, only aggregated data from European populations were included. For detailed information on the GWAS dataset, refer to Table 1.

2.3. Selection of the instrumental variables (IVs)

To elucidate the causal relationship between serum uric acid and seven CVDs, we identified IVs for serum uric acid. In this study, single nucleotide polymorphisms (SNPs) were selected as IVs based on the



Fig. 1. Flow chart of the MR Study between serum uric acid and 6 cardiovascular diseases.

Table 1

Summary of serum uric acid and cardiovascular disease gwas dataset.

Trait	GWAS ID	Participants	nSNPs	PMID	Ethnicity
serum uric acid coronary artery disease hypertension myocardial infarction heart failure angina	ebi-a-GCST90018977 ebi-a-GCST003116 finn-b-19_HYPTENS ebi-a-GCST011365 ebi-a-GCST009541 ebi-a- GCST90018793	343,836 individuals 42,096 cases and 361 controls 55,917 cases and 162,837 controls 14,825 cases and 44,000 controls 47,309 cases and 930,014 controls 30,025 cases and 440,906 controls	19,041,286 8,597,751 16,380,466 8,106,745 7,773,021 470,931	34,594,039 26,343,387 NA 33,532,862 31,919,418 34,594,039	European European European European European
coronary heart disease	ieu-a-7	60,801 cases and 123,504 controls	9,455,779	26,343,387	European

following criteria: (1) SNPs significantly associated with serum uric acid $(P < 5 \times 10^{-8})$ were extracted [15]; (2) To ensure SNP independence, those in linkage disequilibrium (LD) ($r^2 = 0.0001$, kb = 10000) were excluded [16]; (3) SNPs closely related to the seven CVD were eliminated $(P > 5 \times 10^{-5})$ [17]; (4) SNPS that were missing or palindromic with moderate allele frequency were removed from the outcome data [18]; (5) The F statistic was calculated for each SNP to assess weak instrumental variable influence, discarding those with F < 10 [19]. $F = \frac{R^2(n-2)}{1-R^2}$, where n is the exposure sample size, and R^2 is the proportion of variation in the exposure database explained by SNPs. R² is calculated as follows: $R^2 = 2 \times$ (1-MAF) \times (MAF $\times \beta^2$) where MAF is the minor allele frequency and β is the allele effect value; (6) SNPs associated with potential confounders (BMI, blood lipid level, diabetes, alcohol consumption) were identified and removed using the PhenoScanner V2 database (https://www.phenoscanner.medschl.cam.ac.uk/) [20]; (7) An MR-PRESSO outlier test was conducted to eliminate anomalous SNP [21]. Subsequently, MR Analysis was performed with the included SNPs.

2.4. Mendelian randomization (MR) analysis

Four distinct methods were employed to estimate the causal effect between serum uric acid and CVD: inverse variance weighting (IVW), MR-Egger, weighted median (WM), and weighted model [22]. These methods address varying levels of horizontal pleiotropy, thereby thoroughly assessing the causal relationship between serum uric acid and CVD: (1) IVW, assuming no horizontal pleiotropy among SNPs, amalgamates Wald ratio estimates from each SNP to yield a combined causality estimate with optimal statistical power [23]; (2) MR-Egger accounts for the presence of horizontal pleiotropy and provides consistent results under the Instrument Strength Independent of Direct Effect (InSIDE) assumption [24]; (3) WM aggregates data from multiple genetic variants into a singular causal estimate, offering consistent effect estimation even if up to 50 % of the data originates from invalid IVs [25]; (4) The weighted model assigns causal estimates to each genetic variant inversely proportional to its variance [26]. Thus, IVW analysis serves as the primary MR method, complemented by the other three techniques to enhance result reliability. Additionally, we applied False Discovery Rate (FDR) correction, establishing statistical significance at an adjusted P-value threshold of 0.05.

2.5. Sensitivity analysis

To ensure a robust MR Estimate, several sensitivity analyses were conducted:

The Cochran's Q test, applied to both the IVW and MR-Egger methods, assessed heterogeneity. A P-value greater than 0.05 indicated an absence of heterogeneity. Additionally, potential heterogeneity was visually appraised using funnel plots [27]. (2) The MR-Egger-intercept test evaluated horizontal pleiotropy, with P > 0.05 suggesting no such pleiotropy [21]. (3) A leave-one-out analysis was performed by sequentially excluding each SNP to determine if a single SNP biased the IVW estimate results [28].

2.6. Statistical analysis

All analyses were conducted using R software (version 4.3.0), employing the "Two-Sample-MR" (version 0.5.6), "MR-PRESSO" (version 1.2), and "MendelianRandomization" (version 0.4.3) R packages for Mendelian randomization.

3. Results

3.1. Identification of instrumental variables (IVs)

A comprehensive description of all SNPs used in this study is presented in Supplementary Table 1. All SNPs met the established screening criteria. The selected SNPs exhibited F statistics above 10, indicating no weak tool bias and robustly predicting the causal effect of serum uric acid on CVD in MR Analyses.

3.2. Causal effects of serum uric acid on cardiovascular diseases

Fig. 2 illustrates the genetic association between serum uric acid and various cardiovascular diseases. The primary analysis using the IVW method revealed that genetically predicted serum uric acid increases the risk of cardiovascular diseases, including CAD (OR: 1.155; 95 % CI: 1.074–1.242, P = 0.0002), hypertension (OR: 1.318, 95 %CI: 1.184–1.466, P = 2.13E-06), MI (OR: 1.184, 95 %CI: 1.108–1.266, P = 2.13E-06), HF (OR: 1.158, 95 %CI: 1.066–1.258, P = 2.13E-06), angina (OR: 1.150, 95 %CI: 1.074–1.231, P = 0.0002) and CHD (OR: 1.170, 95 %CI: 1.072–1.276, P = 0.0005). Complementary MR statistical models, including MR-Egger, weighted median, and weighted model, yielded effect estimates directionally consistent with the IVW approach.

3.3. MR sensitivity analysis

The results of the sensitivity analysis are presented in Table 2. Cochran's Q test revealed no heterogeneity among SNPs in the analysis of CAD's causal effect (Q_pval_{IVW} = 0.2095, Q_Pval_{MR-Egger} = 0.2099), leading to the use of a fixed-effect IVW model for analysis. Conversely, in analyses of other causal effects, including hypertension(Q_pval_{IVW} = 6.35E-31,Q_pval_{MR-Egger} = 2.52E-30), MI (Q_pval_{IVW} = 1.64E- 05, Q_pval_{MR-Egger} = 1.35E-05), HF (Q_pval_{IVW} = 1.23E-07, Q_pval_{MR-Egger} = 9.64E-08), angina (Q_pval_{IVW} = 3.69E-24, Q_pval_{MR-Egger} = 7.50E-24), and CHD (Q_pval_{IVW} = 1.50E-08, Q_pval_{MR-Egger} = 1.17E-08), heterogeneity among SNPs was observed, necessitating the use of a random-effects IVW model for analysis. Furthermore, the symmetry of the points represented by each SNP in the funnel plot corresponded to the results of Cochran's Q test (Supplementary Fig. 1).

Employing the MR-Egger intercept test, we evaluated whether genetic variations related to serum uric acid could contribute to CVD through alternative pathways. The results, as shown in Table 3, indicate no horizontal pleiotropy in our MR analysis (P > 0.05), suggesting that the study's conclusions are stable and reliable (Supplementary Fig. 2). Furthermore, the leave-one-out approach reveals that the inferred causal relationship between serum uric acid and CVD risk is not attributable to any single SNP (Supplementary Figure 3).

Exposure	No.of SNP	Method		OR(95% CI)	Р
coronary artery disease	215	IVW	; 	1.16 (1.07 to 1.24)	< 0.001
		MR Egger		1.23 (1.07 to 1.41)	0.029
		Weighted median	↓ →	1.20 (1.05 to 1.36)	0.015
		Weighted mode	⊢ →→	1.19 (1.04 to 1.36)	0.015
hypertension	226	IVW		1.32 (1.18 to 1.47)	< 0.001
		MR Egger	⊢ →	1.14 (0.93 to 1.41)	0.212
		Weighted median	⊢→	1.19 (1.04 to 1.36)	0.018
		Weighted mode	\mapsto	1.16 (1.00 to 1.34)	0.052
myocardial infarction	218	IVW		1.18 (1.11 to 1.27)	< 0.001
		MR Egger	⊢ →→	1.19 (1.05 to 1.36)	0.029
		Weighted median		1.11 (1.00 to 1.24)	0.067
		Weighted mode	⊢	1.17 (1.05 to 1.30)	0.015
heart failure	200	IVW		1.16 (1.07 to 1.26)	0.001
		MR Egger	→	1.15 (0.96 to 1.39)	0.191
		Weighted median	→	1.21 (1.08 to 1.35)	0.006
		Weighted mode	⊢ →	1.22 (1.05 to 1.41)	0.015
angina	256	IVW		1.15 (1.07 to 1.23)	< 0.001
		MR Egger	1	1.09 (0.99 to 1.21)	0.146
		Weighted median		1.06 (0.98 to 1.15)	0.162
		Weighted mode		1.10 (1.03 to 1.17)	0.015
coronary heart disease	230	IVW	→	1.17 (1.07 to 1.28)	0.001
		MR Egger	<u>⊷</u> →	1.17 (0.99 to 1.39)	0.146
		Weighted median	⊢ →	1.20 (1.05 to 1.36)	0.015
		Weighted mode	0.70.80.9 1 1.11.21.3	1.20 (1.05 to 1.36)	0.015

Fig. 2. Forest plot of MR analysis results serum uric acid and cardiovascular diseases.

Table 2 The results of heterogeneity analysis for serum uric acid on cardiovascular diseases.

Traits (outcome)	Methods	Q	Q-dif	Р
coronary artery disease	IVW	230.4616	213	0.209488
	MR-Egger	229.392	214	0.209892
hypertension	IVW	563.0569	225	6.35E-31
	MR-Egger	566.9734	224	2.52E-30
myocardial infarction	IVW	314.5666	217	1.64E-05
	MR-Egger	314.5448	216	1.35E-05
heart failure	IVW	319.5367	199	1.23E-07
	MR-Egger	319.5343	198	9.46E-08
angina	IVW	553.5222	255	3.69E-24
	MR-Egger	549.4822	254	7.50E-24
coronary heart disease	IVW	368.0202	229	1.50E-08
	MR-Egger	368.0195	228	1.17E-08

Table 3

MR-Egger intercept analysis of horizontal pleiotropy between serum uric acid and cardiovascular disease.

Traits (outcome)	Egger_Intercept	se	Р
coronary artery disease hypertension myocardial infarction heart failure angina	-0.00157 0.0036 -0.00018 7.53E-05 0.00186	0.001571 0.002301 0.001442 0.001944 0.001361	0.320091 0.119187 0.902801 0.969163 0.172972
coronary heart disease	-4.02E-05	0.001863	0.982812

4. Discussion

We conducted a two-sample MR analysis using four analytical methods to evaluate the causal relationship between genetically predicted serum uric acid and CVD. Our findings indicate a causal association between higher serum uric acid levels and an increased risk of CAD, hypertension, MI, HF, angina, and CHD. The sensitivity analysis demonstrated the absence of horizontal pleiotropy, affirming the robustness of the effect estimates and confirming that none of the instrumental variables significantly influenced the outcome variables. Therefore, early detection and management of high serum uric acid are crucial in preventing the onset and progression of cardiovascular diseases.

Given the widespread prevalence of hyperuricemia and the high incidence of CVD globally, understanding the role of hyperuricemia in CVD is crucial. Numerous observational studies over recent decades have indicated an association between uric acid and increased risk of CVD outcomes. In our Mendelian Randomization (MR) analysis, we specifically examined the causal relationship between serum uric acid and six prevalent types of CVD. Kleber et al. [29] reported that each 1 mg/dl increase in uric acid raised the risk of CVD mortality by 0.77 times. Kojima et al. [30], utilizing the Japanese Acute Coronary Syndrome Research Database to assess 1,124 patients, found that the mortality rate in acute myocardial infarction (MI) patients with low uric acid levels was only a quarter of that in the high uric acid group. A study involving 21,386 participants identified elevated uric acid as an independent risk factor for HF [31]. Research in the general elderly female population revealed that uric acid levels exceeding 404.6 µmol/L tripled the risk of hypertension [32]. A cohort study of 16,063 Chinese patients

showed a 14 % increase in the risk of CHD in middle-aged and elderly individuals for every 100 μ mol/L increase in serum uric acid levels [33]. Ma et al. [34] found higher uric acid levels in patients with angina compared to a control group. These findings align with our MR analysis, suggesting uric acid as a contributing risk factor in the development of CVD.

There are multiple potential mechanisms explaining the causal link between serum uric acid and CVD. High uric acid levels can lead to the formation of urate crystals, depositing in vascular endothelium and causing endothelial damage through oxidative stress. This process activates platelets and increases blood viscosity, potentially resulting in local thrombosis [35]. Uric acid can also exacerbate the oxidation of low-density lipoprotein, lipid peroxidation, and the production of oxygen free radicals. This stimulates the adherence of white blood cells to endothelial cells, initiating an oxidative stress response. The uptake of uric acid by endothelial cells can rapidly induce nuclear factor-kappa B (NF-KB) activation, stimulating chemokine and adhesion factor production, and promoting mononuclear cell migration and adherence to endothelial cells, ultimately leading to atherosclerosis [36]. Normal endothelial function, crucial for maintaining vasoconstriction and diastolic stability, is impaired by elevated uric acid levels, which can reduce nitric oxide (NO) availability, resulting in vascular endothelial dysfunction [37].

Our research has several advantages. Firstly, the sample size of this study significantly exceeds that of prior observational studies, thereby providing ample statistical power. Secondly, we employed five MR analysis methods and conducted sensitivity analyses, where the consistency of results across these methods enhanced the study's credibility. Finally, compared with previous MR Studies, we used MR to analyze the causal association between serum uric acid and 6 types of CVDs in the study design. More stringent criteria were used to screen SNPs associated with serum uric acid, which not only excluded SNPS associated with confounders, but also used "MR-PRESSO" to remove outlier SNPS. To ensure authenticity of the findings, we used an adjusted P value <0.05 as a condition for a causal association between serum uric acid and cardiovascular disease. However, this study also has limitations: (1) All data were derived from the European population, which, while reducing bias due to racial differences, limits the generalizability of the results. Further studies are needed with corresponding GWAS datasets for other ethnic groups; (2) The data from the GWAS database are aggregated statistics, lacking individual-level detail, thus precluding statistical subgroup analysis; (3) Heterogeneity among SNPs may introduce bias into the study results. Nonetheless, the use of a random effects model in our study makes this heterogeneity acceptable [38].

In conclusion, this study systematically explored the potential causal relationship between serum uric acid and six types of CVD using a twosample MR approach. The findings suggest that serum uric acid is a risk factor for CVD, indicating that correcting high serum uric acid levels may help prevent the onset of CVD. Therefore, further in vivo and in vitro experiments are necessary to understand the complex interplay between serum uric acid and CVD and to elucidate its underlying biological mechanisms, with the aim of reducing the incidence and prevalence of CVD.

Sources of funding

This research was funded by the key research and development Plan of Shaanxi Province (grant numbers: 2023-YBSF-636 and 2021SF-396), and the Shaanxi Province Traditional Chinese Medicine Research Project (grant number: 2021-ZZ-JC042).

CRediT authorship contribution statement

Yujun Zhang: Data curation. Qiufang Lian: Supervision. Yanwu Nie: Methodology. Wei Zhao: Software.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

We extend our sincere gratitude to all researchers who contributed statistical data for serum uric acid, CAD, hypertension, MI, HF, AF, angina, and CHD for GWAS analysis.

Appendix A. Supplementary material

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ijcha.2024.101453.

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