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The Association between Obstructive Sleep Apnea and Venous Thromboembolism: A Bidirectional Two-Sample Mendelian Randomization Study

Zhihai Huang^{1,*} Zhenzhen Zheng^{2,*} Lingpin Pang^{1,*} Kaili Fu² Junfen Cheng² Ming Zhong¹ Lingyue Song¹ Dingyu Guo¹ Qiaoyun Chen¹ Yanxi Li¹ Yongting Lv¹ Riken Chen² Xishi Sun¹

1 Emergency Medicine Center, Affiliated Hospital of Guangdong Medical University, Zhanjiang, Guangdong, China 2Respiratory and Critical Care Medicine, The Second Affiliated

Hospital of Guangdong Medical University, Zhanjiang, Guangdong, China

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Address for correspondence Riken Chen, MD, Respiratory and Critical Care Medicine, The Second Affiliated Hospital of Guangdong Medical University, Zhanjiang, 524003, Guangdong, China (e-mail: chenriken@126.com).

Xishi Sun, MM, Emergency Medicine Center, Affiliated Hospital of Guangdong Medical University, Zhanjiang, 524000, Guangdong, China (e-mail: [109721368@qq.com\)](mailto:109721368@qq.com).

Abstract Background Despite previous observational studies linking obstructive sleep apnea (OSA) to venous thromboembolism (VTE), these findings remain controversial. This study aimed to explore the association between OSA and VTE, including pulmonary embolism (PE) and deep vein thrombosis (DVT), at a genetic level using a bidirectional two-sample Mendelian randomization (MR) analysis.

> Methods Utilizing summary-level data from large-scale genome-wide association studies in European individuals, we designed a bidirectional two-sample MR analysis to comprehensively assess the genetic association between OSA and VTE. The inverse variance weighted was used as the primary method for MR analysis. In addition, MR– Egger, weighted median, and MR pleiotropy residual sum and outlier (MR-PRESSO) were used for complementary analyses. Furthermore, a series of sensitivity analyses were performed to ensure the validity and robustness of the results.

> Results The initial and validation MR analyses indicated that genetically predicted OSA had no effects on the risk of VTE (including PE and DVT). Likewise, the reverse MR

Keywords

- ► obstructive sleep apnea
- ► venous thromboembolism
- ► Mendelian randomization \blacktriangleright association

analysis did not find substantial support for a significant association between VTE (including PE and DVT) and OSA. Supplementary MR methods and sensitivity analyses provided additional confirmation of the reliability of the MR results. Conclusion Our bidirectional two-sample MR analysis did not find genetic evidence supporting a significant association between OSA and VTE in either direction.

These authors contributed equally to this study.

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Introduction

Obstructive sleep apnea (OSA) is a prevalent sleep disorder characterized by the recurrent partial or complete obstruction and collapse of the upper airway during sleep, leading to episodes of apneas and hypoventilation.^{1,2} Research studies have reported that the prevalence of OSA in the adult population ranges from 9 to 38%, with a higher prevalence observed in males (13–33%) compared to females (6–19%). Moreover, the prevalence of OSA tends to increase with age and is closely associated with the prevalence of obesity.^{3,4}

There is mounting evidence indicating that OSA serves as an independent risk factor for several cardiovascular diseases, including hypertension,⁵ stroke,⁶ pulmonary hypertension, $⁷$ and heart failure.⁸ Venous thromboembolism</sup> (VTE), including deep vein thrombosis (DVT) and pulmonary embolism (PE), is recognized as the third most common cardiovascular disease worldwide.⁹ There is evidence suggesting that OSA may also be linked to an increased risk of VTE.¹⁰ For instance, a prospective study involving 15,664 subjects (1,424 subjects with OSA) observed a twofold higher incidence of VTE in patients with OSA compared to non-OSA patients.¹¹ Similarly, findings from a national retrospective cohort study conducted by Peng and his colleagues indicated that patients with OSA had a 3.50-fold higher risk of DVT and a 3.97-fold higher risk of PE compared to the general population.¹² However, the results of observational studies remain somewhat controversial. A 5-year prospective study involving 2,109 subjects concluded that OSA did not increase the risk of VTE recurrence.¹³ Another retrospective analysis involving 1,584 patients, of which 848 were women, revealed an intriguing discovery suggesting that OSA may serve as an independent risk factor for VTE solely in women,

rather than in men.¹⁴ Moreover, patients with VTE were found to have a higher prevalence of OSA, 15 suggesting a potential bidirectional relationship.

Although previous observational studies have investigated the potential association between OSA and VTE, elucidating aspects of the association from these studies is challenging due to the limitations of potential confounders and reverse causality bias. Mendelian randomization (MR) is a genetic epidemiological methodology that utilizes genetic variants, such as single-nucleotide polymorphisms (SNPs), as instrumental variables (IVs) to infer the genetic association between exposure and outcome.¹⁶ The advantage of MR analysis lies in the random assignment of genetic variants during meiosis, which effectively circumvents the effects of potential confounders and reverse causality encountered in classical epidemiologic studies.¹⁷

At present, the nature of the association between OSA and VTE remains inconclusive, and there is a dearth of pertinent studies comprehensively exploring the genetic association between OSA and VTE. Therefore, this study aimed to conduct a bidirectional two-sample MR analysis using publicly available summary statistics from large-scale genome-wide association studies (GWAS) to genetically assess the exact association between OSA and VTE, including PE and DVT.

Methods

Study Design

MR utilizes genetic variants, primarily SNPs, as IVs to investigate the genetic association between exposure and outcome. MR is based on three fundamental assumptions: (1) genetic variants exhibit a high correlation with exposure; (2) genetic variants are independent of potential confounders; (3) genetic variants solely affect outcomes through exposure. IVs are deemed valid only when these assumptions are met.

This study employed a bidirectional two-sample MR analysis to evaluate the genetic association between OSA and VTE. Initially, SNPs associated with OSA were utilized to examine their effects on VTE. Subsequently, to investigate the possibility of reverse association, eligible IVs were employed to quantify the implications of VTE on OSA.

Data Source and Selection of Instrumental Variables

OSA was defined based on subjective symptoms, clinical examination, and sleep registration applying apnea–hypopnea index $>5/h$ our or respiratory event index $>5/h$ our.

Summary-level data for OSAwere obtained from the GWAS study conducted by Jiang et al on European individuals, which included 2,827 cases and 453,521 controls, covering 11,831,932 SNPs. 18 To ensure the robustness of the findings, additional datasets for OSA were acquired from a GWAS metaanalysis conducted by Campos and colleagues, comprising 25,008 cases of European ancestry and 337,630 controls, involving 9,031,949 SNPs for validation analysis.¹⁹ The study conducted a meta-analysis of GWAS datasets from five cohorts in the United Kingdom, Canada, Australia, the United States, and Finland. These summary-level GWAS statistics for OSA can be accessed from the GWAS Catalog [\(https://www.ebi.ac.](https://www.ebi.ac.uk/gwas/downloads) [uk/gwas/downloads](https://www.ebi.ac.uk/gwas/downloads)). VTE was defined as a condition comprising PE (blockage of the pulmonary artery or its branches by an embolus) and DVT (formation of a blood clot in a deep vein). The GWAS datasets for VTE (19,372 cases and 357,905 controls), PE (9,243 cases and 367,108 controls), and DVT (9,109 cases and 324,121 controls) were derived from the FinnGen consortium (Release 9, [https://r9.](https://r9.finngen.fi/)finngen.fi/). Detailed information regarding the data sources is provided in ►Table 1.

The selection criteria for IVs were as follows: (1) the threshold for genome-wide significant SNPs for VTE (including PE and DVT) was set at $p < 5.0 \times 10^{-8}$, while the threshold for OSA was adjusted to $p < 1 \times 10^{-5}$ due to the inability to detect OSA-associated SNPs using a significance level of p $<$ 5.0 \times 10⁻⁸. (2) SNPs with linkage disequilibrium effects $(r^2$ < 0.001 within a 10,000-kb window) were excluded to ensure the independence of the selected IVs. (3) The strength of the association between IVs and exposure was measured using the F-statistic [F-statistic $=$ (Beta/SE)²].²⁰ SNPs with Fstatistics >10 were retained to avoid the effects of weak instrumental bias. (4) During the harmonization process, SNPs that did not match the results were removed, along with palindromic SNPs with ambiguous allele frequencies $(0.42-0.58)$ ²¹ (5) Previous studies have demonstrated obesity as an established risk factor for OSA and VTE.^{22,23} SNPs associated with body mass index were queried and excluded by Phenoscanner (http://www.phenoscanner.medschl.cam. ac.uk/). The flowchart of IV selection is shown in \blacktriangleright Fig. 1.

Statistical Analysis

This study employed the multiplicative random-effects inverse variance weighted (IVW) method as the primary approach for conducting MR analysis to evaluate the genetic association between OSA and VTE. The IVW method metaanalyzes the Wald ratio estimates for each SNP on the outcome, providing precise estimates of causal effects when all selected SNPs are valid IVs. 24 However, the estimates of causal effects from the IVW method may be biased by the influence of pleiotropic IVs. To ensure the validity and robustness of the results, sensitivity analyses were implemented using three additional MR methods, namely MR–Egger, weighted median, and MR pleiotropy residual sum and outlier (MR-PRESSO). The MR–Egger method is able to generate reliable causal estimates even in situations where all IVs are invalid. Additionally, MR– Egger offers an intercept test to detect horizontal pleiotropy, with a significance threshold of $p < 0.05$ indicating the presence of horizontal pleiotropy.²⁵ In comparison to the IVW and MR–Egger methods, the weighted median method demonstrates greater robustness and provides consistent estimates of causal effects, even when up to 50% of the IVs are invalid instruments.²⁶ The MR-PRESSO method identifies outliers with potential horizontal pleiotropy and provides estimates after removing the outliers, where $p < 0.05$ for the global test indicates the presence of outliers with horizontal pleiotropy. 27 Furthermore, the Cochran Q test was utilized to examine heterogeneity, with a significance threshold of $p < 0.05$ indicating significant heterogeneity.

All statistical analyses were carried out using the "TwoSampleMR" and "MRPRESSO" packages in R software (version 4.2.1).

Trait	Sample size	Case	Control	No. of SNPs	Participates	PMID/Link
OSA (Jiang et al)	456.348	2,827	453,521	11,831,932	European ancestry	34737426
OSA (Campos et al)	362,638	25,008	337,630	9.031.949	European ancestry	36525587
VTE	377,277	19,372	357.905	20,170,236	European ancestry	FinnGen consortium (https://www.finngen.fi/fi)
PE	376,351	9.243	367,108	20,170,202	European ancestry	FinnGen consortium (https://www.finngen.fi/fi)
DVT	333.230	9.109	324.121	20,169,198	European ancestry	FinnGen consortium (https://www.finngen.fi/fi)

Table 1 Information on data sources

Abbreviations: DVT, deep vein thrombosis; OSA, obstructive sleep apnea; PE, pulmonary embolism; SNPs, single-nucleotide polymorphisms; VTE, venous thromboembolism.

Fig. 1 The flowchart of instrumental variables selection. LD, linkage disequilibrium; SNPs, single-nucleotide polymorphisms; BMI, body mass index; VTE, venous thromboembolism; PE, pulmonary embolism; DVT, deep vein thrombosis; OSA, obstructive sleep apnea; ①, represents OSA (Jiang et al) as the outcome; ②, represents OSA (Campos et al) as the outcome.

Results

Instrumental Variable Selection

As previously outlined, a total of 13 and 28 SNPs were identified through a rigorous screening process to evaluate the effects of OSA on VTE, PE, and DVT. In the reverse MR analysis, 23, 14, 18, 19, 11, and 13 SNPs were identified to assess the implications of reverse association, respectively. Additional details regarding these genetic variants utilized for MR analysis are provided in ►Tables 2 and 3.

Effects of OSA on VTE

► Fig. 2 shows the estimates of the effects for OSA on VTE, PE, and DVT. In the initial MR analysis using the OSA (Jiang et al) dataset, the random-effects IVW method revealed no significant association between OSA and the risk of VTE (odds ratio [OR]: 0.964, 95% confidence interval [CI]: 0.914-1.016, $p = 0.172$), PE (OR: 0.929, 95% CI: 0.857-1.006, $p = 0.069$), PE (OR: 0.929, 95% CI: 0.857–1.006, $p = 0.069$), and DVT (OR: 1.001, 95% CI: 0.936-1.071, $p = 0.973$). No heterogeneity was observed using the Cochran Q test (all $p^* > 0.05$). The MR-Egger intercept test (all $p^{**} > 0.05$) and the MR-PRESSO global test (all $p^{***} > 0.05$) failed to detect any evidence of pleiotropy.

The validation analysis using genetic variants of OSA (Campos et al) yielded similar results. Notably, heterogeneity was observed in the sensitivity analysis for OSA (Campos et al) and VTE ($p^* = 0.018$). However, considering the random-effects IVW model employed, the level of heterogeneity was deemed acceptable.²⁸ Despite the presence of outliers suggested by the MR-PRESSO global test ($p = 0.015$), no significant association between OSA and VTE (OR: 1.071,

95% CI: 0.917–1.251, $p = 0.396$) was found after excluding an outlier (rs7106583). In addition, none of the three complementary MR methods supported a genetic association between OSA and VTE.

Effects of VTE on OSA

We conducted reverse MR analysis to further evaluate the effects of VTE (including PE and DVT) on OSA. Both MR analyses yielded consistent results, indicating no significant effects of VTE, PE, and DVT on OSA (see ►Fig. 3). Moreover, the Cochran Q test revealed no heterogeneity (all $p^* > 0.05$), and both the MR–Egger intercept test and the MR-PRESSO global test found no evidence of pleiotropy (all $p^{**} > 0.05$ and p^{***} > 0.05, respectively) (see \blacktriangleright Fig. 3). In summary, a range of sensitivities confirmed the reliability of the MR results.

Discussion

In this study, we conducted a comprehensive two-sample MR analysis to explore the genetic association between OSA and VTE. Our MR findings did not yield evidence of a significant association between OSA and VTE from a genetic standpoint.

Our findings contradict some previous observational studies suggesting a link between susceptibility to OSA and an increased risk of VTE.²⁹⁻³²

However, these studies were hindered by inadequate consideration of confounding factors, particularly obesity, along with methodological flaws and small sample sizes. Obesity is widely recognized as a significant risk factor for both OSA³³ and VTE.³⁴ Therefore, it is crucial not to overlook the impact of obesity in striving for a deeper understanding of the potential association between OSA and VTE. Notably, a

Fig. 2 The genetic association of OSA with VTE/PE/DVT. OSA, obstructive sleep apnea; VTE, venous thromboembolism; PE, pulmonary embolism; DVT, deep vein thrombosis; MR, mendelian randomization; IVW, inverse variance weighted; PRESSO, pleiotropy residual sum and outlier; P*, represents P for heterogeneity test; P**, represents P for MR-Egger intercept; P***, represents P for MR-PRESSO global test.

cohort study involving 31,309 subjects indicated a higher likelihood of VTE development among patients with more severe OSA. Yet, this association disappeared upon adjusting for confounders, notably obesity levels.³⁵ Thus, it is plausible that the observed association between OSA and VTE could be attributed to obesity confounding. Additionally, Aman and his colleagues' report yielded consistent results, suggesting that OSA does not elevate the risk of VTE after adjusting for obesity confounding.³⁶

MR is a robust analytical method that employs genetic variation as IVs to deduce the genetic association between exposure and outcome. Consequently, it effectively controls for confounders induced by environmental factors and mitigates reverse causality bias. In this study, we meticulously screened genetic variants and thoroughly accounted for the effects of obesity levels to procure reliable IVs for inferring the genetic association between OSA and VTE. To mitigate bias and enhance the reliability of our MR findings, we devised initial and validation MR analyses supplemented by a series of sensitivity analyses, drawing upon datasets sourced from various origins. Notably, neither MR analysis provided evidence supporting a genetic association between OSA and VTE. Moreover, a succession of sensitivity analyses served to bolster the robustness of our MR results. These findings indicate that, although diverging from some previous observational studies, our results are reliable and corroborate the conclusions drawn from the MR study.

While our MR study did not find evidence supporting a genetic association between OSA and VTE, it remains possible that OSA could influence the onset or progression of VTE. Virchow's triad depicts three major factors inducing VTE: endothelial injury, venous stasis, and hypercoagulability.³⁷ The pathophysiologic mechanism linking OSA and VTE remains unknown but may be associated with OSA's capacity to affect the three classical mechanistic pathways of Virchow's triad.³⁸ Intermittent hypoxia, a signature feature of OSA, can induce oxidative stress and activate inflammatory markers, further damaging the vascular endothelium.^{39,40} OSA-associated hemodynamic alterations and reduced physical activities may result in venous stasis. 41 A growing number of studies have demonstrated a strong correlation between OSA and hypercoagulability. A retrospective cohort study aimed at assessing coagulation in patients with OSA suggested that patients with moderate to severe OSA experienced elevated markers of blood coagulability, primarily evidenced by shortened prothrombin time, compared to healthy individuals.⁴² Two additional studies of thrombotic parameters found that patients with OSA possessed higher levels of the thrombin-antithrombin complex.^{43,44} Furthermore, several coagulation factors, such as fibrinogen, coagulation factor VII, coagulation factor XII, and vascular hemophilic factor, which play a crucial role in the coagulation process, are elevated in patients with OSA.⁴⁵ Collectively, this evidence supports that patients with OSA are in a state of hypercoagulability, facilitating our understanding of the

Table 2 Genetic variants used in the MR analysis Table 2 Genetic variants used in the MR analysis

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polymorphism; VTE, venous thromboembolism.
Note: F-statistic = (Beta/SE)², represents the strength of each instrumental variable polymorphism; VTE, venous thromboembolism.

Note: F-statistic = $(Beta/SE)^2$, represents the strength of each instrumental variable

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Table 3 (Continued)

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Abbreviations: DVT, deep vein thrombosis; EA, effect allele; MR, Mendelian randomization; OA, other allele; OSA, obstructive sleep apnea; PE, pulmonary embolism; SE, standard error; SNP, single-nucleotide ╗ polymorphism; VTE, venous thromboembolism.

Note: F-statistic = $(Beta/SE)^2$, represents the strength of each instrumental variable.

Fig. 3 The genetic association of VTE/PE/DVT with OSA, OSA, obstructive sleep apnea; VTE, venous thromboembolism; PE, pulmonary embolism; DVT, deep vein thrombosis; MR, mendelian randomization; IVW, inverse variance weighted; PRESSO, pleiotropy residual sum and outlier; P*, represents P for heterogeneity test; P**, represents P for MR-Egger intercept; P***, represents P for MR-PRESSO global test.

underlying pathophysiologic mechanisms between OSA and VTE. Considering these potential mechanisms, future largescale studies are necessary to thoroughly explore the potential association between OSA and VTE, delving into greater depth.

The greatest strength of this study is that the bidirectional two-sample MR analysis designed based on summary data from large-scale GWAS was used for the first time to investigate the genetic association between OSA and VTE. Furthermore, to bolster the robustness of the findings and mitigate bias, we conducted initial and validated MR analyses using two independent OSA GWAS datasets. Subsequently, a series of sensitivity analyses provided further validation and affirmed the robustness of the results. However, our study also has several limitations. First, it was exclusively centered on European individuals, thereby constraining the generalizability of our findings to other ethnicities or ancestries. Second, the lack of individual-level data in the summary-level statistics prevented us from stratifying the study population by important factors such as age or sex. Lastly, there is a possibility of sample overlap between the exposure and outcome datasets, but the Fstatistics of the IVs selected in the MR analysis were sufficiently strong to mitigate the potential effects of weak instrumental bias.

Conclusion

In conclusion, our MR study did not uncover genetic evidence supporting an association between OSA and VTE, including DVT and PE. This implies that the association between OSA and VTE reported in some previous observational studies may rely on alternative pathways to function, rather than being directly linked to the diseases themselves.

What is known about this topic?

- Previous studies have linked obstructive sleep apnea (OSA) and venous thromboembolism (VTE).
- Existing studies regarding the association between OSA and VTE are somewhat controversial.
- The various aspects of the association between OSA and VTE remain to be evaluated.

What does this paper add?

- There were no significant effects of OSA on VTE.
- Similarly, VTE also had no significant effects on OSA. • The association between OSA and VTE may arise
- through pathways other than the diseases themselves.

Data Availability Statement

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation.

Authors' Contribution

All authors listed have made a substantial, direct, and intellectual contribution to the work, and approved it for publication.

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Conflict of Interest

None declared.

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