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# [Causal association between type](https://www.frontiersin.org/articles/10.3389/fendo.2024.1407503/full) [2 diabetes mellitus and acute](https://www.frontiersin.org/articles/10.3389/fendo.2024.1407503/full) [suppurative otitis media: insights](https://www.frontiersin.org/articles/10.3389/fendo.2024.1407503/full) [from a univariate and](https://www.frontiersin.org/articles/10.3389/fendo.2024.1407503/full) [multivariate Mendelian](https://www.frontiersin.org/articles/10.3389/fendo.2024.1407503/full) [randomization study](https://www.frontiersin.org/articles/10.3389/fendo.2024.1407503/full)

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Background: Type 2 diabetes mellitus (T2DM) and hearing loss (HL) constitute significant public health challenges worldwide. Recently, the association between T2DM and HL has aroused attention. However, possible residual confounding factors and other biases inherent to observational study designs make this association undetermined. In this study, we performed univariate and multivariable Mendelian Randomization (MR) analysis to elucidate the causal association between T2DM and common hearing disorders that lead to HL.

Methods: Our study employed univariate and multivariable MR analyses, with the Inverse Variance Weighted method as the primary approach to assessing the potential causal association between T2DM and hearing disorders. We selected 164 and 9 genetic variants representing T2DM from the NHGRI-EBI and DIAGRAM consortium, respectively. Summary-level data for 10 hearing disorders were obtained from over 500,000 participants in the FinnGen consortium and MRC-IEU. Sensitivity analysis revealed no significant heterogeneity of instrumental variables or pleiotropy was detected.

Results: In univariate MR analysis, genetically predicted T2DM from both sources was associated with an increased risk of acute suppurative otitis media (ASOM) (In NHGRI-EBI: OR = 1.07, 95% CI: 1.02-1.13, P = 0.012; In DIAGRAM: OR = 1.14, 95% CI: 1.02-1.26,  $P = 0.016$ ). Multivariable MR analysis, adjusting for genetically predicted sleep duration, alcohol consumption, body mass index, and smoking, either individually or collectively, maintained these associations. Sensitivity analyses confirmed the robustness of the results.

Conclusion: T2DM was associated with an increased risk of ASOM. Strict glycemic control is essential for the minimization of the effects of T2DM on ASOM.

#### KEYWORDS

acute suppurative otitis media (ASOM), type 2 diabetes mellitus (T2DM), hearing loss (HL), causal relationship, Mendelian randomization (MR)

### 1 Introduction

Hearing loss (HL) is a prevalent sensory impairment disease that affects approximately 430 million people around the world [\(1,](#page-8-0) [2\)](#page-8-0). Acute otitis media (AOM) is one of the common hearing disorders facing general practitioners and otolaryngologists [\(3\)](#page-8-0). Although AOM mostly occurs in children, the incidence rate of AOM in adults is around 5/1000 person-years ([4](#page-8-0)). Acute suppurative otitis media (ASOM) is a subtype of AOM ([5](#page-8-0)). ASOM often presents with fever, otalgia, ear purulence, tympanic membrane congestion, and tympanic perforation ([6](#page-8-0)). Persistent ASOM can turn into chronic suppurative otitis media (CSOM) and cause HL ([7\)](#page-8-0). Untreated patients with CSOM may also develop further serious complications, including potentially lethal otitic meningitis and brain abscess ([8](#page-8-0), [9\)](#page-8-0).

Diabetes mellitus (DM) is a metabolic disease characterized by hyperglycemia ([10](#page-8-0)). Long-term hyperglycemia can lead to chronic damage and dysfunction of various organs, especially kidneys, blood vessels, nerves, and eyes [\(11\)](#page-8-0). It is reported that the number of DM patients worldwide will increase to 783 million by 2045 as the escalating global prevalence of DM ([12](#page-8-0)–[14](#page-8-0)). Type 2 diabetes mellitus (T2DM) accounts for 90%-95% of DM patients. T2DM results from a complex inheritance-environment interaction along with other risk factors such as age, obesity, and physical inactivity ([15](#page-8-0)– [17\)](#page-8-0). T2DM is characterized by hyperglycemia, insulin resistance, and insulin secretion disorders [\(18,](#page-8-0) [19](#page-8-0)). Patients with T2DM are always complicated with cardiovascular and cerebrovascular diseases and digestive tract dysfunction due to metabolic disorders and decreased resistance, which seriously affect the quality of life of patients [\(20\)](#page-8-0).

Previous studies have highlighted a greater incidence of HL in DM patients compared to nondiabetic patients, and revealed a direct correlation between the severity of DM and the extent of HL ([21](#page-8-0)–[23\)](#page-8-0). Patients with T2DM have shown both HL and vestibular dysfunction ([24](#page-8-0)). It has also been shown that the insulin/glucose signaling pathology in T2DM can lead to inner ear pathology and accompanying HL [\(25\)](#page-8-0). However, other studies suggested that the association between DM and HL does not exist when age, sex, and hypertension were taken into account [\(23\)](#page-8-0). The causal associations between T2DM and HL remain ambiguous.

Mendelian randomization (MR) is a type of instrumental variables (IVs) analysis, which has been increasingly used in observational studies in recent years. MR uses independent single nucleotide polymorphisms (SNPs) with strong associations with exposure as IVs, facilitating to estimate of causal associations between exposure and outcomes ([26](#page-8-0)). This effectively minimizes the potential residual confounding factors and other biases inherent in studies with an observational design.

In this study, we investigated the association between T2DM and 10 distinct types of HL disorders (conductive HL, sensorineural HL, mixed conductive and sensorineural HL, otitis externa (OE), otitis media (OM), ASOM, nonsuppurative OM, perforation of the tympanic membrane, hearing difficulty/problems with background noise, and sudden idiopathic HL) with T2DM. Univariate and multivariate MR analysis was used to examine the association between T2DM from two databases and 10 common types of HL disorders.

### 2 Materials and methods

#### 2.1 Genetic instrumental variables selection

The overall design of the MR analysis in this study is shown in [Figure 1.](#page-2-0) This MR study utilized GWAS data for T2DM in European populations, categorized according to the ICD-10 standards, from the consortium NHGRI-EBI, for first validation. The data originated from a cross-population GWAS meta-analysis of genetic associations across 220 human phenotypes [\(27](#page-8-0)). We further repeated verification through DIAGRAM consortium data, a GWAS study that performed a meta-analysis of genetic variants in T2DM involving nearly 150,000 people, the vast majority of whom were of European ancestry ([28\)](#page-8-0). More information about the exposure is presented in [Table 1](#page-3-0).

In this MR analysis, we employed SNPs that exhibit robust associations (defined by a genome-wide significance threshold of P<  $5\times10^{-8}$ ) with T2DM as IVs [\(29\)](#page-8-0). We meticulously selected these IVs to ensure minimal linkage disequilibrium, setting the correlation coefficient threshold to  $r^2$ < 0.001 and adopted a clumping window exceeding 10,000kb to guarantee the independence of the IVs [\(26\)](#page-8-0). To address potential confounders — namely sleep patterns, alcohol consumption, smoking, and body mass index — which could impact exposure or outcomes [\(30](#page-8-0)–[36\)](#page-8-0), we utilized the PhenoScanner tool ([http://www.phenoscanner.medschl.cam.ac.uk/\)](http://www.phenoscanner.medschl.cam.ac.uk/) to identify and subsequently exclude any SNPs linked to these confounding factors ( $P$ < 5×10<sup>-8</sup>). During the statistical harmonization process

<span id="page-2-0"></span>

between exposure and outcome data, we meticulously removed palindromic SNPs incompatible with our analysis and SNPs directly associated with the outcomes under study. Additionally, we excluded SNPs with available exposure data but lacking corresponding outcome information. To address and minimize the potential bias from weak IVs, we calculated the F-statistic for each IV using the formula  $F_{exposure} = \frac{Beta_{exposure}^2}{SE_{exposure}^2}$  ([37](#page-8-0)). IVs exhibiting F-statistics less than 10 were systematically excluded from our analysis to mitigate the risk of bias associated with weak IVs [\(38\)](#page-8-0).

### 2.2 Data sources of hearing disorders

Details of the outcomes (10 types of hearing disorders) can be found in [Table 1.](#page-3-0) Data on nine of these hearing disorders were sourced from the FinnGen database, an extensive public-private consortium dedicated to the amalgamation and analysis of genetic

and health data from approximately 500,000 participants in Finnish biobanks ([39\)](#page-8-0). The data on "hearing difficulty/problems with background noise" as one of the types of HL disorders came from the Medical Research Council Integrated Epidemiology Unit (MRC-IEU). Participants in this study were asked on an ACE touchscreen, "Do you find it difficult to hear conversations if there is background noise, such as from a television, radio, or children playing?" [\(https://](https://biobank.ndph.ox.ac.uk/showcase/field.cgi?id=2257) [biobank.ndph.ox.ac.uk/showcase/](https://biobank.ndph.ox.ac.uk/showcase/field.cgi?id=2257)field.cgi?id=2257).

### 2.3 Data sources for confounders

Analyses were adjusted for sleep duration, alcohol consumption, body mass index, and smoking status by applying multivariate MR (MVMR). Adjustments for sleep duration were based on summarylevel statistics derived from a comprehensive genome-wide association study encompassing over 120,000 individuals ([40\)](#page-8-0).

#### <span id="page-3-0"></span>TABLE 1 Details of exposure and outcome GWAS datasets.



GWAS, genome-wide association study; NHGRI-EBI, National Human Genome Research Institute-European Bioinformatics Institute; DIAGRAM, DIAbetes Genetics Replication And Metaanalysis; MRC-IEU, Medical Research Center-Integrative Epidemiology Unit; MR, mendelian randomization; NA, not applicable.

Summary-level data for alcohol consumption were obtained from MRC-IEU [\(41\)](#page-8-0). Summary-level data for body mass index were extracted from a large multiethnic genome-wide association study of adult body mass index to identify novel loci [\(42\)](#page-8-0). Summary-level data for smoking status were available from a mixed-model association study for biobank-scale datasets from more than 450,000 European samples ([43](#page-8-0)). More information is presented in Table 1.

#### 2.4 Statistical analyses

In our analysis, we applied the Inverse-Variance Weighted (IVW) approach as the principal analytical method ([44\)](#page-8-0). The selection between fixed-effect (IVW-FE) and random-effect (IVW-RE) models was contingent on Cochrane's Q heterogeneity test outcomes: IVW-RE was used in cases of detected heterogeneity (P< 0.05) to provide conservative estimates, while the IVW-FE model was employed in the absence of such heterogeneity ([45](#page-8-0)).

Additionally, our analysis incorporated two supplementary MR methodologies: MR-Egger and weighted median, to bolster result credibility and ascertain causality direction. MR-Egger was used when assuming substantial horizontal pleiotropy among over half of the IVs, whereas the weighted median approach assumes less extensive pleiotropy [\(46,](#page-8-0) [47](#page-8-0)). Causality was inferred only when consistent effects were observed across all employed MR methods, supplemented by significant findings from IVW analysis, thus ensuring a robust and concise evaluation of the studied associations.

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Furthermore, for sensitivity analysis, horizontal pleiotropy was assessed using the MR-Egger intercept's P-value ([46,](#page-8-0) [48\)](#page-8-0). The significance of the intercept was determined by its P-value, which indicates whether there is a pattern of pleiotropy that could bias the causal estimates. Also, we incorporated the MR-PRESSO distortion test to check the consistency of MR estimates after excluding potential pleiotropic outliers ([48\)](#page-8-0). This test identified and corrected for outliers in the IVs analysis that could be attributed to pleiotropy and the subsequent recalculations, thereby ensuring the robustness of our findings against such biases. A leave-one-out sensitivity analysis was conducted to determine the impact of each individual SNP on the overall MR estimation, which involves recalculating the causal effect with one SNP removed at a time. Significant alterations in MR estimates upon SNP exclusion suggest potential biases, whereas stable results across variations indicate robust findings.

Multivariable Mendelian Randomization (MVMR) extends the conventional MR analysis to enable the simultaneous assessment of multiple exposures on an outcome, proving invaluable for adjusting potential confounders and exploring the collective impact of several exposures [\(49](#page-8-0)). In this study, we considered four significant confounders: sleep duration, alcohol consumption, body mass index, and smoking status.

Upon compiling GWAS summary datasets for T2DM and the aforementioned confounders, we verified that each IV maintained a strong association ( $P$ <  $5x10^{-8}$ ) with at least one exposure or confounder. To mitigate the effects of linkage disequilibrium, SNPs were pruned within a 10,000 kb window with an  $r^2$ threshold of< 0.001. The IVW method was then utilized to discern the causal effects, post exclusion of palindromic SNPs and those absent in the outcome data, while accounting for the identified confounders, ensuring a refined and methodologically sound approach to our MVMR analysis.

Statistical significance was set at a threshold of P< 0.05. The outcomes of the causal relationships were expressed in terms of odds ratios (OR) with 95% confidence intervals (95% CI). These procedures were implemented using the "TwoSampleMR" (version 0.5.6) and "MRPRESSO" (version 1.0) [\(50,](#page-8-0) [51](#page-8-0)) tools in R software (version 4.2.3), ensuring a concise yet comprehensive analysis.

### 3 Results

Eligible 164 and 9 SNPs were screened out from the T2DM GWAS data sets of NHGRI-EBI and DIAGRAM respectively as IVs. Selected SNPs' characteristics were detailed in [Supplementary Table](#page-7-0) [S1](#page-7-0), indicating minimal risk of weak instrument bias, with F statistics ranging between 29.61 and 1066.63. The confounder information was detailed in [Supplementary Table S2](#page-7-0). IVW results of univariable and multivariable MR analysis were shown in Figures 2 and [3](#page-5-0).

### 3.1 Univariable MR analysis results

The analysis of T2DM from NHGRI-EBI has identified heterogeneity in the assessment of sensorineural HL, hearing difficulty/problems with background noise, and mixed conductive and sensorineural HL ( $P_{heterogeneity}$ < 0.05; [Table 2](#page-5-0)). Therefore, the IVW-RE model was used as the primary MR method for analysis in these cases. For other analyses, the IVW-FE model was employed.

Genetically predicted T2DM was associated with an increased risk of ASOM (In NHGRI-EBI: OR = 1.07, 95%CI: 1.02-1.13,  $P =$ 0.012; In DIAGRAM: OR = 1.14, 95%CI: 1.02-1.26,  $P = 0.016$ ) in the univariable MR analysis (Figure 2). Also for genetically predicted T2DM, there was an association with an increased risk of conductive HL (OR= 1.12, 95%CI: 1.01-1.25,  $P = 0.032$ ) as derived from the NHGRI-EBI, and an association with an increased risk of OE (OR= 1.19, 95%CI: 1.04-1.35, P = 0.010), hearing difficulty/problems with background noise (OR= 1.01, 95%) CI: 1.00-1.01,  $P = 0.004$ ), and sudden idiopathic HL (OR= 1.33, 95% CI: 1.10-1.60,  $P = 0.003$ ) as derived from DIAGRAM (Figure 2). MR-Egger and weighted median analysis shown a consistent direction of effect ([Supplementary Table S3](#page-7-0)-[4\)](#page-7-0). Beyond the above, the analysis shown no significant association between T2DM and other hearing disorders.

In our sensitivity analysis, we found no evidence of pleiotropy in the MR-Egger regression (P for Egger intercept > 0.05) and the MR-PRESSO Global Test ( $P > 0.05$ ) when examining the impact of T2DM on ASOM, utilizing data from NHGRI-EBI and DIAGRAM ([Table 2\)](#page-5-0). Furthermore, the leave-one-out sensitivity analysis



Associations between genetically predicted T2DM and hearing disorders based on the IVW approach. OR, odds ratio; CI, indicates confidence interval.

<span id="page-5-0"></span>

FIGURE 3 Multivariable MR analysis: Assessing the impact of T2DM on hearing disorders with adjustments for sleep, alcohol consumption, body mass index, and smoking. OR, odds ratio; CI, indicates confidence interval.

affirmed the consistency of our MR findings, indicating that no individual SNP disproportionately influenced the results (details provided in [Supplementary Figures S1,](#page-7-0) [S2\)](#page-7-0).

EBI: OR = 1.09, 95%CI: 1.03-1.16,  $P = 0.005$ ; In DIAGRAM: OR = 1.12, 95%CI: 1.03-1.22,  $P = 0.010$ ). Notably, this association was more pronounced than those identified through univariate MR analyses, underscoring a robust link between T2DM and ASOM.

### 3.2 MVMR analysis result

To deepen our understanding of the causal connections between T2DM and various hearing disorders, we conducted an additional MVMR analysis. In multivariable MR analyses adjusting for sleep duration, alcohol consumption, body mass index and smoking alone ([Supplementary Tables S5-](#page-7-0)8) or together (Figure 3), we found only ASOM to be associated with T2DM from both databases (In NHGRI-

Previous studies have identified DM as a potential risk factor for

4 Discussion

HL ([21,](#page-8-0) [22](#page-8-0)). However, there are different types of HL, which are often classified by anatomical deficit as conductive, sensorineural, or mixed [\(1](#page-8-0)). The disorders of HL are also diverse, such as OE, OM, ASOM, nonsuppurative OM, perforation of the tympanic





(Continued)

#### TABLE 2 Continued



NHGRI-EBI, National Human Genome Research Institute-European Bioinformatics Institute; DIAGRAM, DIAbetes Genetics Replication and Meta-analysis; IVW, inverse-variance weighted; SNP, single nucleotide polymorphism.

NA, not applicable.

membrane, hearing difficulty/problems with background noise, sudden idiopathic HL, etc. In this study, to delve deeper into the associations between common hearing disorders and T2DM, we selected 10 common hearing disorders as outcomes. The univariate MR analysis from the NHGRI-EBI and DIAGRAM consortium supports a significant causal association between T2DM and an elevated risk for ASOM. Furthermore, multivariable MR analyses, adjusted for genetically predicted sleep duration, alcohol consumption, body mass index, and smoking, continue to demonstrate a positive causal relationship between T2DM and ASOM. However, a causal link between T2DM and other hearing disorders was either observed only in analyses from a single source or not detected at all. Our study is the first to reveal the relationship between ASOM and T2DM with causal evidence.

It has been reported that in the process of DM and its complications, the body will produce a persistent inflammatory response due to immune cell dysfunction and inflammatory pathway activation [\(52](#page-8-0)–[54\)](#page-9-0). Patients with DM have hyperglycemia for a long time, which leads to increased plasma osmolarity and inhibition of leukocyte activity ([55\)](#page-9-0). In the middle ear (ME) of diabetic patients, inhibition of leukocyte activity leads to a decrease in the internal killing, phagocytosis, and adhesion of leukocytes, which increases the risk of infection. In addition, T2DM is often accompanied by microangiopathy, which is characterized by structural alterations of the capillary walls including thickening of the basement membrane and increased permeability of capillary vessels [\(56](#page-9-0)–[58](#page-9-0)). The thickened basement membrane of the capillary wall reduces blood flow to certain areas [\(59](#page-9-0), [60\)](#page-9-0). Capillary damage leads to tissue ischemia and hypoxia, and metabolic disorder. Reducing

the normal intake of calories and proteins impairs immune function and reduces antibody production, which in turn inhibits the ability to clear invading pathogens and increases the risk of infection. This may be one of the reasons why T2DM increases the risk of ASOM.

ASOM is a purulent lesion caused by pyogenic bacteria invading the tympanic mucosa through the eustachian tube (ET). ET is a complex structure connecting the middle ear cavity to the nasopharynx ([61\)](#page-9-0), and eustachian tube dysfunction (ETD) is considered to be associated with most ME pathologies, although the mechanism of its role in ME diseases is still unclear ([62](#page-9-0), [63\)](#page-9-0). Recently, the important functions of surfactant protein (SP) in the body have received increasing attention from different specialists. Studies have confirmed the presence of surfactant proteins A and D (SP-A and SP-D) in the human ET [\(64](#page-9-0)–[66\)](#page-9-0). As the major protein component of surfactant, SP-A plays an important role in innate and acquired immune processes [\(67](#page-9-0)). When inflammation occurs, SP-A can promote the recruitment of inflammatory cells, the activation of phagocytic cells, or directly kill pathogens, thereby preventing pathogen infection, regulating allergic reactions, and alleviating inflammation ([68](#page-9-0)–[70](#page-9-0)). This suggests that SP-A may enhance the resistance of ET to infection by participating in immune defense. In adult gerbils and mice, intranasal application of aerosolized metered dose inhaler surfactant reduced the severity and duration of ME infections ([71\)](#page-9-0). In addition, SP-A plays a key role in the working process of ET. ETD impairs the clearance of inflammatory products and secretions in the ME and ET by affecting the mucociliary system of ET ([62\)](#page-9-0). Recent studies have also shown that SP-D gene polymorphism (rs721917) was associated with gestational DM ([72\)](#page-9-0), and the serum SP-D was found to have negative association with <span id="page-7-0"></span>extra-pulmonary infections in T2DM patients ([73](#page-9-0)). Therefore, it can be speculated that if the expression of SP in the ET changes, it may lead to the exacerbation of ASOM. This may be another potential mechanism by which T2DM increases the risk of ASOM. However, current studies only shown changes in the expression of SP. The associations between SP, ASOM and ET function have not been investigated. More experimental models are needed to demonstrate the possible mechanisms by which T2DM promotes the development of ASOM by affecting SP.

Our study shows several predominant strengths. Firstly, the causal relationship between T2DM and ASOM was revealed by MR for the first time. MR analysis design can avoid the influence of reverse causation and residual confounding in the process of exploring the causal association between T2DM and ASOM. In addition, the GWAS summary data of T2DM were obtained from two independent European populations, this non-overlapping exposure can avoid the possible bias. Finally, sensitivity analyses with various approaches support the robustness of our MR results. However, there are several certain limitations in our study. The GWAS data of the majority of participants in our study came from European, which makes our results avoid population heterogeneity while also may not be entirely applicable to subjects in other populations. Second, because of the limitations of summarized GWAS data, stratified analyses based on common factors (such as age, sex, hypertension, etc.) could not be performed in our study.

Our findings provide important insights into understanding and preventing diabetes-related complications, particularly ear infections. These findings offer significant insights into understanding and preventing T2DM complications, particularly in the realm of ear infections. They also provide valuable reference information for public health strategies and individual medical decision-making, highlighting the importance and necessity of considering T2DM as a potential risk factor in managing and preventing such complications.

## 5 Conclusion

In summary, our study is the first to reveal the relationship of T2DM and ASOM with causal evidence. The univariate MR analysis from the NHGRI-EBI and DIAGRAM consortium supports a causal association between T2DM and an increased risk of ASOM. MVMR analyses adjusted for confounders continue to demonstrate this association. However, a causal link between T2DM and other hearing disorders was either observed only in analyses from a single source or not detected at all. To further confirm and elucidate the biological mechanisms underpinning the association between T2DM and ASOM, more experimental models are need to perform in future studies.

# Data availability statement

The original contributions presented in the study are included in the article/Supplementary Material. Further inquiries can be directed to the corresponding author.

# Author contributions

LK: Conceptualization, Data curation, Methodology, Writing – original draft, Writing – review & editing. CD: Data curation, Formal Analysis, Software, Writing – original draft. JW: Data curation, Software, Validation, Visualization, Writing – original draft, Writing – review & editing. FZ: Formal Analysis, Funding acquisition, Resources, Writing – original draft. BY: Data curation, Formal Analysis, Methodology, Writing – original draft. ZW: Data curation, Formal Analysis, Methodology, Writing – original draft. MY: Data curation, Formal Analysis, Investigation, Methodology, Writing – original draft. CX: Data curation, Formal Analysis, Investigation, Methodology, Writing – original draft. PQ: Conceptualization, Methodology, Supervision, Writing – review & editing, Writing – original draft.

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# Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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# Supplementary material

The Supplementary Material for this article can be found online at: [https://www.frontiersin.org/articles/10.3389/fendo.2024.](https://www.frontiersin.org/articles/10.3389/fendo.2024.1407503/full#supplementary-material) [1407503/full#supplementary-material](https://www.frontiersin.org/articles/10.3389/fendo.2024.1407503/full#supplementary-material)

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