

The impact of growth differentiation factor 15 on the risk of cardiovascular disease: evidence from Mendelian randomization study

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Research article

Keywords: Cardiovascular Diseases, GDF-15, Mendelian randomization, atrial fibrillation, cardioembolic stroke

Posted Date: May 20th, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-29531/v1>

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Version of Record: A version of this preprint was published on October 28th, 2020. See the published version at <https://doi.org/10.1186/s12872-020-01744-2>.

Abstract

Background: Growth differentiation factor 15(GDF-15) concentration is apparently associated with cardiovascular disease, but whether there is a causal relationship has not been testified.

Methods: We utilized Mendelian randomization to assess the function of GDF-15 in incidence of cardiovascular disease. The single-nucleotide polymorphism-GDF-15 association evaluations came from meta-analysis of genome-wide association study (GWAS). Besides inverse-variance weighted, MR-Egger test and weighted median method were applied to examine sensitivity.

Results: Base on the instruments, GDF-15 level linked to increased risk of cardioembolic stroke (1.06, OR 1.09 per SD increase, 95% CI 1.01, 1.19) and atrial fibrillation (OR 1.03 per SD increase, 95% CI 1.0, 1.06). However, the significant causal relationship between GDF-15 and the other cardiovascular diseases was not found in our work.

Conclusions: The result suggested that GDF-15 is causally associated with the risk of cardioembolic stroke and atrial fibrillation, providing conceivable strategies to alleviate the burden of cardiovascular disease.

Introduction

Leading morbidity and mortality worldwide, cardiovascular disease(CVD) cost more than \$200 billion every year in the United States despite advanced therapy [1]. Burgeoning works demonstrated metformin, an extraordinarily classical and first-line glucose-lowering drug, was beneficial to diabetic individuals with CVD [2]. Furthermore, Growth differentiation factor 15(GDF-15), the potential downstream of metformin, may play a crucial role in the process[3]. GDF-15 is a stress-responsive protein, involving in oxidative stress, inflammation and tissue hypoxia[4] [5], which could be an effective predictor and promising therapeutic targets for CVD. In PARADIGM-HF trial, Bouabdallaoui N, et al. manifested that GDF-15 independently provided prognostic information in patients with heart failure with reduced ejection fraction(HFrEF) in which higher baseline and incremental GDF-15 levels were obviously relevant to mortality and all cardiovascular events, even after adjusting NT-proBNP and high-sensitivity cTnT [6]. Similar results was observed in acute coronary syndrome (ACS)[7], stable coronary artery disease(CAD)[8], folks with CVD risks[9],and acute pulmonary embolism[10]. However, argument that GDF15 was uncorrelated to cardiometabolic outcomes was raised by a large genome-wide association study (GWAS)[11]. It remains intricate whether GDF-15 links to the pathogenesis of CVD since those observational works arduously avoid some confounding (where some factors associated with GDF-15 actually result in the disease) and reverse causality bias (where some patients with CVD may be more likely to higher GDF-15). Mendelian randomization (MR) is a robust tool for causal deduction to complement observational trials[12]. Illuminating the value of GDF-15 in CVD can feasibly provide another perspective to improve diagnosis and prognosis of CVD.

Hence, in this article, we focus on the GDF-15 in seven kinds of CVDs cardiovascular diseases including any ischemic stroke, cardioembolic stroke, large artery stroke, small vessel stroke, atrial fibrillation, heart failure and nonischemic cardiomyopathy through the method of two sample MR to assess their causal correlation.

Methods

Instrument Selection

Circulating GDF-15 level was predicted by the exposure genetically. A meta-analysis of GWAS which including 5440 individuals of European ancestry from four community-based cohorts (the mean age was 62 years and 53% were women) was utilized to obtain GDF-15 genetic associations[13], as the previous work did[14]. The selected single-nucleotide polymorphism (SNP) was associated with GDF-15 concentration at the genome-wide threshold ($p < 5 \times 10^{-8}$). All the SNPs were on chromosome 19 containing the PGPEP1 and MIC-1/GDF15 genes. LD-Link (<https://ldlink.nci.nih.gov/>) was applied to test linkage disequilibrium between two loci in the same chromosome based on European ancestry. Every targeted SNP was searched in the PhenoScanner (www.phenoscanter.medschl.cam.ac.uk) for the known effects of restricting the potential pleiotropy.

Data for Outcomes

The summary statistics for the selected SNPs with stroke were extracted from a large-scale meta-analysis of GWAS of 446696 subjects of European ancestry (40585 cases; 406111 controls), conducted by the MESTROKE consortium[13]. Specifically, any

ischemic stroke (AIS) cases were divided into three subtypes: cardioembolic stroke (CES), large artery stroke (LAS) and small vessel stroke (SVS). Genetic associations with atrial fibrillation (AF) were obtained from the largest meta-analysis of GWAS conducted by the Atrial Fibrillation consortium[15]. The study sample included 537409 individuals of European ancestry. Summary statistics of heart failure (HF) and nonischemic cardiomyopathy (NICM) were extracted from a meta-analysis of GWAS of 488010 European participants in the UK Biobank (6504 HF cases; 1816 NICM cases)[16].

Statistical Analyses

Two sample MR method was performed to access the causality between genetic-predicted circulating GDF-15 concentration and stroke, AF, HF and NICM. The casual effect estimates of SNP instruments on CVD outcomes were calculated using the Wald Estimator[17], with standard error obtained using Delta method[18]. Then, odds ratios(OR) for each disease were meta-analyzed with the inverse-variance weighted (IVW) method to establish all SNPs valid or not.[19]. Sensitivity analyses were conducted with the weighted median method and the MR-Egger method. The weighted median method allows half of the information comes from invalid instrumental variables[20]. The MR-Egger method not only detects pleiotropy with regression intercept but also tests all unbalanced directional pleiotropy[21]. All statistical analyses were performed by R version 3.6.1 (R Foundation for Statistical Computing, Vienna, Austria) and the MR package.

Results

There were nine SNPs identified from the GWAS, and 4 SNPs were discarded for rs1054564, rs3746181, rs1363120 were high linkage disequilibrium (LD) ($r^2 \geq 0.8$) and and rs16982345 had not reach the genome-wide threshold ($p \text{ value} > 5 \times 10^{-8}$). The rest SNPs (rs1227731, rs3195944, rs17725099, rs888663, rs749451) coming from chromosome 19 and containing the PGPEP1 and GDF15 genes displayed in STable 1.

Figure 1 shown the relationship between GDF-15 and the seven kinds of CVD containing AIS, CES, LAS, SVS, AF, HF, NICM. Increment of GDF-15 resulted in augmenting incidence of CES (OR 1.09 per SD increase, 95% confidence interval(CI)1.01, 1.19) and AF (OR 1.03 per SD increase, 95% CI 1.0, 1.06). However, the significant relation couldn't been reached between GDF-15 and AIS (OR 1.02 per SD increase, 95% CI 0.98, 1.07), LAS (OR 0.99 per SD increase, 95% CI 0.89, 1.11), SVS (OR 0.96 per SD increase, 95% CI 0.87, 1.06), HF (OR 1.04 per SD increase, 95% CI 0.97, 1.12), NICM (OR 1.12 per SD increase, 95% CI 0.98, 1.29).

Validation and sensitivity analyses of relation of GDF-15 concentration and outcomes conducted by IVW, MR-Egger test and weighted median method shown in Table 1. We did not find strong evidence against the hypothesis of pleiotropy of the gene of GDF-15 in patients with CES and patients with AF using MR-Egger ($P = 0.30$, $P = 0.67$ respectively) while SNPs were valid proved by IVW ($P = 0.035$, $P = 0.043$ respectively).

Table 1
Examination of the relationship of GDF-15 and outcomes.

Outcome	IVW			Weighted median			MR-Egger				
	Estimate	SE	P-value	Estimate	SE	P-value	Estimate	SE	P-value	Intercept	P-value
CES	0.091	0.043	0.035	0.111	0.053	0.036	0.154	0.150	0.304	-0.017	0.660
AIS	0.024	0.022	0.268	0.022	0.027	0.409	0.104	0.077	0.175	-0.021	0.279
LAS	-0.007	0.055	0.898	-0.013	0.062	0.829	-0.033	0.189	0.862	0.007	0.886
SVS	-0.037	0.051	0.464	-0.037	0.057	0.523	0.030	0.177	0.864	-0.018	0.689
AF	0.031	0.016	0.043	0.032	0.018	0.078	0.024	0.054	0.661	0.002	0.884
HF	0.040	0.038	0.294	-0.004	0.048	0.926	0.131	0.133	0.326	-0.024	0.477
NICM	0.117	0.072	0.102	0.106	0.084	0.204	0.207	0.249	0.406	-0.024	0.708

Examination of the relationship of GDF-15 and outcomes. Data are reported as OR and 95% CI. SE (Std Error), AIS (any ischemic stroke), CES (cardioembolic stroke), LAS (large artery stroke), SVS (small vessel stroke), AF (atrial fibrillation), HF (heart failure), NICM (nonischemic cardiomyopathy).

Discussion

We used two-sample Mendelian Randomization to evaluate the association between GDF-15 level and CVD, including AIS, CES, LAS, SVS, AF, HF. It was suggested GDF-15 level could impact on the incidence of CES and AF whereas an obvious relation could not be concluded when coming to other CVDs. Therefore, our works maybe support a causal relation between GDF-15 and the incident of CES and AF and further indicated a crucial role for GDF-15 -targeted interventions to lessen the epidemic of CVD. However, the evidence was not straightforward since MR-Egger did not refuse the null hypothesis.

Our result corresponds to a slice of previous randomized and observational studies. In community-based Individuals[22], postoperative patients[23] and hypertrophic cardiomyopathy (HCM) folks[24] who had a higher GDF-15 level were more vulnerable to AF than those remaining lower level. In contrast, Santema BT, et al. and Lamprea-Montealegre JA, et al. suggested that serum GDF-15 level was undifferentiated with AF or not in folks with HF from BIOSTAT-CHF trial[25] and people with chronic kidney disease(CKD) from CRIC study[26] respectively. Dissimilitude could have been explained for specific reasons. GDF-15, belonging to transforming growth factor β (TGF- β) cytokine superfamily, may be a sensitive but not specific biomarker. It involved in the progress of inflammatory and oxidative stress [27], which consist in the process of diverse conditions, such as HF, CAD and CDK[28–30] and may lead the course of disease to a varying degree. Besides, GDF-15 might be an early warning, a composite sign of disease and a reflection determined by various but general elements[31]. Nevertheless, in our research, MR could avoid confounding factors to clarify causality between exposure (GDF-15 level) and outcome (AF). Mechanisms association of increased GDF-15 levels with enhance incidence of AF are unknown and need to be dug deeper. We assumed that GDF-15 expression, just similar to TGF- β , may promote ionic and structural remodeling of the atria leading vulnerability to AF by PI3K/Akt signaling and SMAD2/ 3 signaling[32, 33]. Besides, GDF-15 was demonstrated strongly related to p53[34] which induced fibrotic signaling, endothelial dysfunction and cardiac inflammation[35–37], linking to AF. Nevertheless, though our result suggested the causal relation between GDF-15 and AF, it needs more genetic instruments for GDF-15 to identify the relationship.

Cardioembolic strokes were tripled in the past few decades and could triple by 2050 worldwide which AF is the most common risk [38]. Our study developed a new perspective that GDF-15 could positively correlate to cardioembolic strokes. Similar states that the incidence of any stroke could be predicted by GDF-15 in individuals with AF[39] and CVD[7, 8]. Mechanistically, on the one hand, systemic inflammation especially IL-1 β , IL-6 and TNF- α was a potential mechanism promoting the formation of cerebral cardioembolism[40] and GDF-15 was proved related to them [41] [42]. On the other hand, AF, HF, CAD were one of the precondition of cardioembolic strokes which were affiliated to augment of serum GDF-15 [43]. Admittedly, analyzing for CAD may provide useful insight into the mechanism or reason of GDF-15 is a causally contributing to cardioembolic stroke. Whereas, according previous works, GDF-15 may unlikely have a causal association with CVD [14].

However, our result did not support that incremental GDF-15 had a causality with HF. Arguments were prevailing that GDF-15 concentration not only had a promising value of diagnosis but was a superior prognostic biomarker [44]. Presumably, it is HF that promoted the concentration of GDF-15. Furthermore, the severer state of HF, the more comorbidities existed liking hypertension diabetes, aging, renal dysfunction, which may affect the expression of GDF-15 and needed to be eliminated.

There are certain strengths in the study. Our work provided an alternative perspective to clarify the role of GDF-15 in CVD unprecedentedly and supported an intrinsically positive relationship between GDF-15 and AF, CES. Further investigations in therapies of GDF-15 control is demanded for it may be rewarding for patients with AF or CES. Besides, these selected SNPs were not associated with the other CVDs, indicating that the relationship between the SNPs of GDF15 and some related phenotypes could not confound the null association. Furthermore, it needs to remain aware of metformin employing in individuals with high risks of AF or CES since metformin could facilitate the expression of GDF-15, possibly leading to sick and exacerbate.

Limitations were inevitable. Many of those shared common problems of Mendelian randomization[45]. Firstly, the SNPs we selected could not satisfy the demand of independence principle. However, our work did bring a fresh vision to the relationship between GDF-15 and CVD. Besides, The MR is not sensitive to confounders from environmental exposures and might violate exclusion restriction unless we took into consideration all influence of GDF-15. Also, our statistics based on European populations, limiting the generalizability of our work. Furthermore, our work did not focus on coronary CAD since recent Mendelian randomization studies had already provide there was not strong evidence for the role of GDF-15 in it[11, 14].

Conclusion

In summary, a genetic approach we utilized to represent an option to determine causality besides randomized controlled trials and suggested that GDF-15 is causally associated with risk of AF and CES, providing conceivable strategies to alleviate the burden of CVD.

Abbreviations

GDF-15, Growth differentiation factor 15

CVD, cardiovascular disease

HFrEF, heart failure with reduced ejection fraction

ACS, acute coronary syndrome

CAD, stable coronary artery disease

GWAS, genome-wide association study

SNP, single-nucleotide polymorphism

AIS, any ischemic stroke

CES, cardioembolic stroke

LAS, large artery stroke

SVA, small vessel stroke

AF, atrial fibrillation

HF, heart failure

NICM, nonischemic cardiomyopathy

Declarations

Availability of data and materials:

All data are freely available for scientific purpose.

Consent for publication:

Not applicable.

Competing interests:

The authors declare that they have no competing interests.

Funding:

No funding sources for research.

Authors' contributions

All authors had made contributions in the manuscript .

Acknowledgements:

Not applicable.

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Figures

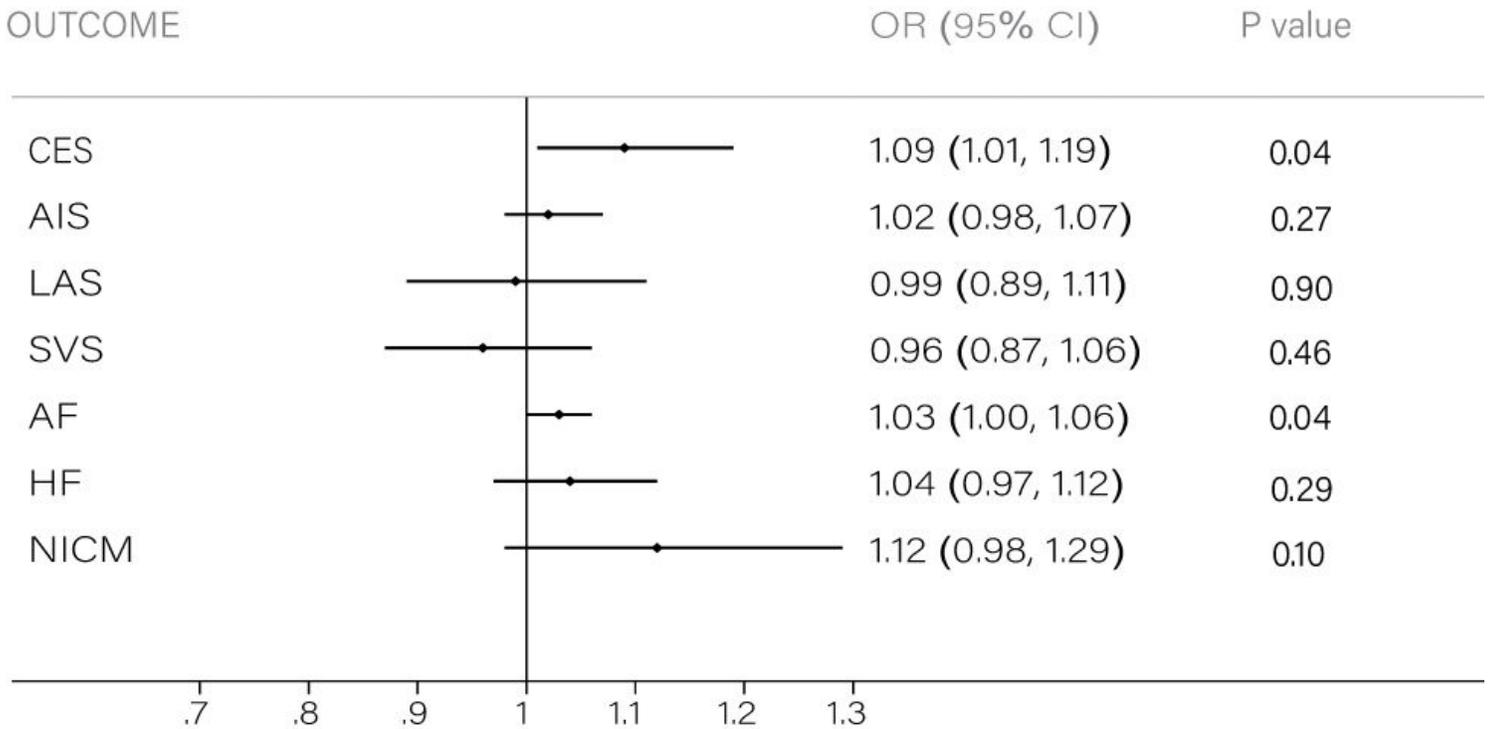


Figure 1

the relationship of GDF-15 and outcomes. Data are reported as OR(odd ratio) and 95% CI(confidence interval). AIS (any ischemic stroke), CES (cardioembolic stroke), LAS (large artery stroke), SVS (small vessel stroke), AF (atrial fibrillation), HF (heart failure), NICM (nonischemic cardiomyopathy).

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