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Association of Serum Magnesium Levels With Risk of Intracranial Aneurysm: A Mendelian Randomization Study

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Susanna C Larsson contributed to the conception and design of the study, conducted the statistical analyses, interpreted the results, and drafted the manuscript. Susanna C Larsson is the corresponding author and takes responsibility for the accuracy of the analysis and had authority over manuscript preparation and decision to submit the manuscript for publication. Dipender Gill contributed to the conception and design of the study, interpreted the results, and drafted the manuscript.

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Author Disclosures

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Abstract

Objective

Magnesium has been implicated in regulating blood pressure and vascular endothelial cell function, but its role in the pathophysiology of intracranial aneurysm is not known. Here we performed a Mendelian randomization analysis to investigate the association between serum magnesium concentration and risk of intracranial aneurysm.

Methods

Five single-nucleotide polymorphisms strongly associated with serum magnesium concentrations in a genome-wide association study in 23 829 individuals of European ancestry were used as genetic instruments. Genetic association estimates for intracranial aneurysm were obtained from a genome-wide association study in 79 429 individuals (7495 cases and 71 934 controls). The inverse-variance weighted method was used in the primary analyses to obtain the causal estimates.

Results

Higher genetically predicted serum magnesium concentrations were associated with lower risk of intracranial aneurysm. The odds ratios per 0.1 mmol/L increment in genetically predicted serum magnesium concentrations were 0.66 (95% confidence interval: 0.49-0.91) for intracranial aneurysm (unruptured and ruptured combined), 0.57 (95% confidence interval: 0.30-1.06) for unruptured intracranial aneurysm, and 0.67 (95% confidence interval: 0.48-0.92) for aneurysmal subarachnoid hemorrhage.

Conclusion

This study provides evidence to support that increased serum magnesium concentrations reduce the risk of intracranial aneurysm and associated hemorrhage.

Intracranial aneurysm rupture and resultant subarachnoid hemorrhage is associated with a high rate of morbidity and mortality.^{1, 2} Serum magnesium concentrations have been implicated in regulating blood pressure and function of the vascular endothelium.³⁻⁵ However, whether increased serum magnesium concentrations affect the risk of intracranial aneurysm and related subarachnoid hemorrhage is not known.

To investigate this, we leveraged randomly allocated genetic variants related to serum magnesium concentrations as instrumental variables in a two-sample Mendelian randomization (MR) study assessing whether higher genetically predicted serum magnesium concentrations are associated with a reduced risk of intracranial aneurysm. A multivariable MR analysis was further performed to investigate whether any potential association may be mediated through effects on blood pressure.

Methods

Genetic instruments and data sources

As instrumental variables for the primary analyses, we used single-nucleotide polymorphisms (SNPs) associated with serum magnesium concentrations at genome-wide significance $(p < 5 \times 10^{-8})$ in a genome-wide association study in 23 829 individuals of European ancestry. Six independent SNPs in different genetic loci and on different chromosomes were identified and proposed as instrumental variables for serum magnesium concentrations. In complementary analyses, we added two uncorrelated single-nucleotide polymorphisms in or near known magnesium transport genes and associated with serum magnesium concentrations after applying a Bonferroni-correction for the number of genetic variants examined in each region. Summary statistics data for intracranial aneurysm in individuals of European ancestry were obtained from a genome-wide association study of 23 cohorts comprising 79 429 individuals (7495 cases [69% with ruptured intracranial aneurysm, 28%

with unruptured intracranial aneurysm, and 3.8% with unknown rupture status] and 71 934 controls). Genetic association estimates for systolic blood pressure were taken from a genome-wide association study of 757 601 European ancestry individuals.

Standard protocol approvals, registrations, and patient consents

Only summary-level data were analyzed in this study, for which appropriate ethical approval and participant consent had previously been acquired in the original genome-wide association studies. The analyses were approved by the Swedish Ethical Review Authority (2019-03986).

Statistical analysis

In our main analyses, we applied the multiplicative random-effects inverse-variance weighted method to estimate the total association of serum magnesium concentrations with intracranial aneurysm. To assess the potential presence of directional pleiotropy, MR-Egger regression analysis was performed. Finally, to evaluate whether the results may be driven by potential outlier(s), we used the MR Pleiotropy RESidual Sum and Outlier method. To evaluate whether blood pressure may mediate any association, we implemented a multivariable MR model with adjustment for genetically predicted systolic blood pressure. The weighted median method was used as a complementary method. We scaled all odds ratios (ORs) per 0.1 mmol/L increase in serum magnesium concentrations, which corresponds to an approximate one standard deviation. Analyses were conducted using the mrobust package for Stata (StataCorp, College Station, TX) and the MendelianRandomization package for R.

Data availability

All data generated or analyzed during this study are included in Table 1.

Results

Of the six SNPs associated with serum magnesium at the genome-wide significance threshold, one SNP was unavailable in the intracranial aneurysm datasets and no proxy SNP was available at a linkage disequilibrium (LD) $R^2 > 0.6$. The other five SNPs (including one proxy SNP in strong LD with the original SNP) were used as instrumental variables for serum magnesium in the primary analyses. For the two SNPs in or near magnesium transport genes, we used proxy SNPs in strong or complete LD with the original SNPs (Table 1). Information on the SNPs used as instrumental variables and their associations with intracranial aneurysm is shown in Table 1.

Genetically predicted serum magnesium concentrations were inversely associated with risk of intracranial aneurysm. In the analyses based on the five genome-wide significant SNPs, the ORs per 0.1 mmol/L increase in genetically predicted magnesium concentrations were 0.66 (95% CI: 0.49-0.91) for intracranial aneurysm, 0.57 (95% CI: 0.30-1.06) for unruptured intracranial aneurysm, and 0.67 (95% CI 0.48-0.92) for aneurysmal subarachnoid hemorrhage. The sensitivity analysis based on the weighted median method provided similar results (corresponding ORs 0.64 [95% CI: 0.45-0.91], 0.62 [95% CI: 0.32-1.20], and 0.66 [95% CI: 0.44-0.98]). There was no evidence of directional pleiotropy (all *p*-values for the MR-Egger intercept >0.60), and no outlier was found in the MR Pleiotropy RESidual Sum and Outlier method. Adjustment for genetically predicted systolic blood pressure through a multivariable MR model attenuated the associations of genetically predicted serum magnesium with all three considered outcomes, consistent with a partial mediating effect (Figure 1).

The complementary analyses incorporating two SNPs in or near magnesium transport genes yielded similar results. In these analyses based on seven SNPs, the ORs per 0.1

mmol/L increase in genetically predicted magnesium concentrations were 0.55 (95% CI: 0.32-1.00) for intracranial aneurysm, 0.53 (95% CI: 0.25-1.10) for unruptured intracranial aneurysm, and 0.55 (95% CI: 0.32-0.97) for aneurysmal subarachnoid hemorrhage.

Discussion

This MR study provides evidence to support that higher serum magnesium concentrations reduces the risk of intracranial aneurysm and aneurysmal subarachnoid hemorrhage, with systolic blood pressure mediating part of this effect. While magnesium supplementation has been demonstrated to increase serum magnesium concentrations and reduce blood pressure in randomized clinical trials,³ to our knowledge this is the first MR study to identify a potential causal association between serum magnesium concentrations and risk of intracranial aneurysm and aneurysmal subarachnoid hemorrhage. The associations of genetically predicted serum magnesium with risk of intracranial aneurysm and aneurysmal subarachnoid hemorrhage did not fully attenuate after adjustment for genetically predicted systolic blood pressure, suggesting that magnesium may also affect the risk of these outcomes via other mechanisms. In addition to a blood pressure lowering effect, increased magnesium concentrations may reduce the risk of intracranial aneurysm rupture by improving endothelial function^{4,5} and reducing oxidative stress.¹²

A strength of this study is the MR design, which is less prone to confounding compared with conventional observational studies. Other major strengths are the relatively large number of cases of intracranial aneurysm and the robustness of the findings in different MR sensitivity analyses that are more robust to the inclusion of pleiotropic variants. Population stratification bias was minimized because all analyses were restricted to populations of European ancestry and adjustment was made for principal components for ancestry in the original genome-wide association studies from which summary data was used. In terms of

limitations, we cannot rule out that our genetic proxies for serum magnesium affect intracranial aneurysm risk through alternative pathways that may violate the requisite assumptions of MR. Another limitation is that we did not have access to appropriate data for a bidirectional MR analysis to investigate whether biological mechanisms predisposing to intracranial aneurysm influence circulating magnesium levels. Finally, the genetic variants used to proxy the effect of modifying serum magnesium concentration reflect small, lifelong effects in serum magnesium concentrations, while in contrast a clinical intervention would typically exert a greater change in serum magnesium concentrations later in life. Caution should be taken when extrapolating findings from MR to infer the effect of a clinical intervention, and clinical trials are warranted to guide optimal practice.

In conclusion, this MR study provides evidence to support that higher serum magnesium concentrations reduce the risk of intracranial aneurysm and aneurysmal subarachnoid hemorrhage. These finding add to the growing body of evidence highlighting a beneficial role of higher magnesium for preventing cerebrovascular and cardiovascular diseases. ¹³⁻¹⁵

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Appendix 1. Authors

Name	Location	Contribution				
Susanna C. Larsson	Uppsala University,	Design and conceptualized study;				
	Sweden	analyzed and interpreted the data; drafted				
		the manuscript for intellectual content				
Dipender Gill	Imperial College	Design and conceptualized study;				
	London, UK	interpreted the data; revised the				
		manuscript for intellectual content				



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Table 1. Characteristics of the single-nucleotide polymorphism used as instrumental variables for serum magnesium concentrations and their associations with intracranial aneurysm

				Serum magnesium concentrations		IA (unruptured and ruptured)		Unruptured IA		Ruptured IA (aSAH)	
rsID	Chr	Gene	EA	Beta (SE)*	p	Beta (SE)	p	Beta (SE)	p	Beta (SE)	p
rs4072037	1	MUC1	T	0.010 (0.001)	2.01E-36	-0.038 (0.021)	0.07	-0.048 (0.039)	0.22	-0.036 (0.024)	0.14
rs7965584†	12	ATP2B1	A	0.007 (0.001)	1.05E-16	-0.050 (0.022)	0.02	-0.098 (0.038)	0.01	-0.036 (0.027)	0.18
rs3925584	11	DCDC5	T	0.006 (0.001)	5.20E-16	0.016 (0.022)	0.48	0.029 (0.039)	0.46	0.008 (0.026)	0.75
rs13146355	4	SHROOM3	A	0.005 (0.001)	6.27E-13	-0.026 (0.019)	0.17	-0.010 (0.034)	0.77	-0.044 (0.023)	0.05
rs448378	3	MDS1	A	0.004 (0.001)	1.25E-8	-0.036 (0.021)	0.09	-0.062 (0.038)	0.11	-0.024 (0.024)	0.32
rs3740393‡	10	CNNM2	C	0.006 (0.001)	8.58E-7	-0.174 (0.030)	1.11E-8	-0.17 (0.056)	0.002	-0.018 (0.035)	3.98E-7
rs6746896‡	2	CNNM4	G	0.004 (0.001)	7.01E-5	-0.004 (0.023)	0.87	0.041 (0.041)	0.32	-0.023 (0.027)	0.41

aSAH, aneurysmal subarachnoid hemorrhage; Chr, chromosome; EA, effect allele (the allele that associates with higher serum magnesium concentrations); IA, intracranial aneurysm; SE, standard error.

*The beta coefficients represent the increase in serum magnesium concentrations in mmol/L per additional effect allele.

†The single-nucleotide polymorphism was unavailable in the intracranial aneurysm datasets but a proxy genetic variant (rs10858938, effect allele=G) in linkage disequilibrium (r²=0.96 in European populations) was identified and replaced this genetic variant.

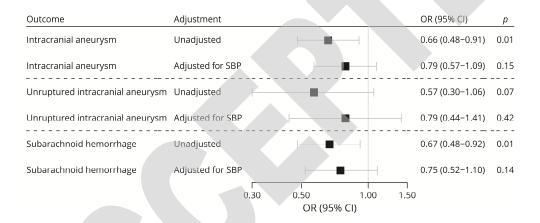
‡Used in complementary analyses that included genetic variants in or near known magnesium transport genes and associated with serum magnesium after applying a Bonferroni-correction for the number of genetic variants assessed in each region.⁶ The single-nucleotide polymorphisms described in the original study⁶ were unavailable in the intracranial aneurysm datasets, so proxy genetic variants in linkage disequilibrium (r²>0.9) were used: rs72841270 (effect allele=G) for rs3740393 and rs56351161 (effect allele=A) for rs6746896.

FIGURE TITLE

Figure 1. Association between genetically predicted serum magnesium concentrations and intracranial aneurysm.

FIGURE LEGEND

Estimates are scaled per genetically predicted 0.1 mmol/L (about one standard deviation) increase in serum magnesium concentrations. Adjustment for genetically predicted systolic blood pressure was made using a multivariable Mendelian randomization model. CI, confidence interval; OR, odds ratio; SBP, systolic blood pressure.





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