Mendelian randomization study shows no causal effects of serum urate levels on the risk of MS

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Abstract

Objective
To examine whether lifelong genetically increased serum urate levels, a potent antioxidant, contribute to MS susceptibility using Mendelian randomization (MR).

Methods
This 2-sample MR study included 25 independent genetic variants strongly associated with serum urate levels in a genome-wide association study meta-analysis of 140,949 individuals. Effects on the risk of MS were assessed with summary statistics from 3 large-scale MS genetic data sets totaling 61,667 MS cases and 86,806 controls from the International MS Genetic Consortium. Multiple sensitivity analyses were performed to evaluate the assumptions of MR and remove potentially pleiotropic variants.

Results
Using inverse-variance weighted MR, we found no evidence for a causal effect of serum urate level on the risk of MS in any of the cohorts (MS1: OR 0.99 per each mg/dL unit increase in urate, 95% CI 0.89–1.08, p = 0.76; MS2: OR = 0.99, 95% CI 0.89–1.11, p = 0.90; MS3: OR = 1.00, 95% CI 0.98–1.2, p = 0.91). Pleiotropy robust MR methods yielded consistent estimates.

Conclusion
This MR study does not support a clinically relevant causal effect of serum urate levels on the risk of MS.
Urate, the anionic form of uric acid, is the final metabolite of purine metabolism in humans. Urate acts as a potent free radical scavenger and accounts for 60% of the antioxidant capacity in plasma. Evidence involving oxidative stress in the pathogenesis of MS and proposed neuroprotective effects of urate have motivated the investigation into the role of urate in MS. Indeed, an early population study revealed lower than predicted co-occurrence of MS and gout, a condition characterized by hyperuricemia. In addition, several case-control studies and 2 meta-analyses have reported lower serum urate levels in individuals with MS compared with healthy controls and other neurologic disorders. These data have led to the hypothesis that elevated serum urate may be protective against the development of MS. However, other case-controls studies have demonstrated discordant findings, with 1 prospective study suggesting that the association between lower serum urate and higher risk of MS could be due to bias from reverse causality. In addition, observational studies are also susceptible to residual confounding, which further limits causal inference.

Although randomized clinical trials would be ideal to provide evidence for or against a causal role for urate in MS, the few that have been performed have focused on disease outcomes among patients with MS rather than testing the proposed preventive effects. The latter question has population-wide implications, but such a trial would require prohibitively large sample sizes followed for an extended period of time and is probably not feasible. Therefore, the role of urate in the risk of developing MS remains unclear.

In the absence of such experimental evidence, Mendelian randomization (MR) can provide an alternative approach for causal inference. MR uses genetic associations to investigate the causal effect of a risk factor on an outcome. This approach greatly reduces the likelihood of residual confounding because these genetic variants are randomly assigned at conception and relatively independent of socioeconomic and lifestyle characteristics that could bias observational studies. The fact that genotypes are not modifiable by disease onset also limits reverse causality. Serum urate levels show a large heritable component estimated at 40%–60%. As such, several genetic loci have been robustly associated with serum levels, including variants in urate transporters. This makes MR ideally suited to resolve questions of causality involving serum urate levels, as recently shown in Parkinson disease.

In this article, we aimed to assess whether genetic predisposition toward lifelong higher serum urate levels alters the risk of developing MS. For this analysis, we undertook a 2-sample MR approach in 3 large genetic studies of MS susceptibility with up to 61,667 MS cases and 86,806 controls.

**Methods**

**Genetic variants associated with serum urate**

We identified genetic variants reliably associated with serum urate levels in a large genome-wide association study meta-analysis of up to 140,949 individuals from 48 cohorts. Details of serum urate measurement for each of the cohorts have been described previously by the Global Urate Genetic Consortium (GUGC). Summary statistics were retrieved for 29 single nucleotide polymorphisms (SNPs), which were genome-wide significant in the meta-analysis. The effect of each allele on serum urate levels is presented in mg/dL and adjusted for age, sex, and study-specific covariates. To mitigate bias from population stratification, all effect estimates were derived from individuals of European ancestry. We calculated linkage disequilibrium (LD) between each pair of variants to ensure that they are not correlated (r² < 0.01) as this can lead to biased MR estimates. We also excluded from analysis variants within the extended major histocompatibility complex (MHC) region, defined as base positions 24,000,000 to 35,000,000 on chromosome 6 (GRCh37). This is because the strength of the association of this region with MS and its complex LD structure renders it susceptible to horizontal pleiotropy and violation of the MR assumptions.

**MS genetic data**

For each genetic variant associated with serum urate levels, we obtained corresponding effect estimates on MS susceptibility using summary statistics from 3 MS genetic studies by the International MS Genetics Consortium (IMSGC) and totaling 148,473 individuals (61,667 MS cases and 86,806 controls). Participants for each data set are presented in the table. The first data set (MS1) corresponds to the discovery cohort of the latest IMSGC meta-analysis and contains more than 8 million genotyped and imputed variants. The 2 remaining data sets are identified by the genotyping array used for the majority of participants, namely the Immunochip (MS2) and Exome Chip (MS3). The former corresponds to the discovery cohort of IMSGC et al. 2013 and lists 161,312 markers. The latter is the combined cohort from IMSGC et al. 2018, which focused on low frequency and rare variants (173,746 markers).
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All participants were of European ancestry. For each SNP, the effect size on MS susceptibility was aligned with respect to the urate increasing allele. All genetic data sets reported alleles on the forward strand, except the Immunochip data for which strand mismatches were reconciled. No palindromic variants were present. Participant overlap between the GUGC and IMSGC data sets was negligible and limited to controls (1.0% for MS1) or absent (MS2 and MS3), meaning that no bias should have been introduced.33 When urate-associated variants were not present in either of the MS genetic data sets, we identified a proxy SNP in LD ($r^2 > 0.6$) using PLINK v1.934 and samples of European ancestry from 1000 Genomes phase 3.35

**MR analysis**

For each of the MS data sets separately, we performed an inverse-variance weighted (IVW) 2-sample MR to estimate the effect of a genetically related unit increase in plasma urate levels (in mg/dL) on the odds of MS, using previously described methods.36,37 In brief, we weighted the effect of each variant on MS susceptibility by its effect on serum urate using the Wald ratio method.37 These individual MR estimates were then combined into a summary measure using random effect meta-analysis with inverse-variance weighting. There is no participant overlap between the MS1 and MS2 cohorts, but there is at least partial overlap between the MS2 and MS3 study samples.38 Therefore, we combined the IVW MR results from the MS1 and MS2 data sets (but not MS3) in a fixed effect meta-analysis. To ensure that the overall MR results were not driven by any particular variant, we iteratively removed each SNP and recalculated the IVW MR estimate in each of the data sets.

A fundamental assumption of MR is that the genetic variants associated with the exposure phenotype (serum urate) must not affect the risk of the outcome phenotype (MS) through independent pathways. Presence of such pathways is known as horizontal pleiotropy and can bias the MR estimates. For each of the MS data sets, we investigated the robustness of our main results to pleiotropy by applying 3 established MR sensitivity methods with complementary attributes.39 First, we formally examined for overall horizontal pleiotropy using the MR pleiotropy residual sum and outlier (MR-PRESSO) Global test.38 This method compares the observed distance of all variants to the regression line of the SNP-outcome effects on SNP-exposure effects with the expected distance under the null hypothesis of no horizontal pleiotropy. We also applied the MR-PRESSO outlier test using the imputed MS1 data set to identify and exclude from all analyses outlier and thus potentially pleiotropic variants.38 Second, we applied MR-Egger regression, a weighted linear regression of the SNP-outcome effects on the SNP-exposure effects allowing for the intercept to be estimated.40 This intercept provides a measure of average pleiotropic bias. The slope coefficient gives an unbiased estimate even in the presence of pleiotropic effects, as long as the size of these pleiotropic effects is independent of the effect of the SNP on the exposure. Third, we performed a
weighted median analysis, which provides consistent estimates robust to the presence of pleiotropy in a subset (<50%) of the variants.41 In addition, we inspected funnel plots of the individual MR estimates against their precision.42 Asymmetry on this plot is indicative of directional horizontal pleiotropy.40

All statistical analyses were performed in R (version 3.6.0). The alpha level for statistical significance was set to 0.05.

**Standard protocol approvals, registrations, and patient consents**

The data sources used in this study (GUGC and IMSGC) obtained informed consent from all participants.26,30–32 Separate institutional review board approval was not required for this study.

**Data availability**

Summary level genetic data for serum urate levels and MS susceptibility are publicly available through their respective consortia. In addition, the data used to generate the main results are available in the table.

**Results**

**Selection of genetic variants**

Of the 29 genome-wide significant variants for serum urate in the GUGC meta-analysis, none were in LD. We excluded a single SNP in the extended MHC region (rs1165151 in SLC17A1), leaving 28 variants. Next, we applied the MR-PRESSO outlier test using the MS1 data set and identified 3 potentially pleiotropic variants (rs642803 near OVOL1, rs653178 near ATXN2, and rs675209 near RREB1). These were excluded from all subsequent analyses. We estimated the remaining 25 variants to explain approximately 6.7% of the variance in serum urate levels, with 3.4% explained by SLC2A9 and ABCG2 alone.26 All 25 urate-associated variants were available in the MS1 data set for assessing the genetic association with MS susceptibility. Both MS2 (using Immunochip) and MS3 (using Exome Chip) studies have lower genome coverage and no imputed variants. Therefore, we were able to identify 11/25 variants in MS2, 4 directly present and 7 via proxies (median $r^2 = 0.96$), as well as 15/25 variants in MS3, 4 directly present and 11 via proxies (median $r^2 = 0.94$). The list of variants and proxies for each data set can be found in the table.

**MR analysis**

The main IVW MR analysis did not provide evidence for a causal effect of serum urate levels on odds of MS in either of the MS data sets (MS1: OR per each mg/dL unit increase in serum urate was 0.99, 95% CI 0.89–1.08; MS2: OR = 0.99, 95% CI 0.89–1.11; MS3 OR = 1.00, 95% CI 0.98–1.13). Similarly, meta-analysis of the MS2 and MS3 results in a null effect with narrow CI (OR = 0.99, 95% CI 0.92–1.06) and no heterogeneity (Q = 0.01, $p = 0.91$; $I^2 = 0$%). These results remained consistent after iteratively removing each individual SNP from the IVW MR analysis (figures e-1 to e-3, links.lww.com/NXI/A349), including the strongest variants near SLC2A9 and ABCG2.

There was weak evidence of horizontal pleiotropy on the MR-PRESSO Global test ($p = 0.051$) using the more complete MS1 data set. Similarly, the MR-Egger intercept was centered around the null and showed no evidence of directional pleiotropy across all MS case-control studies (MS1: intercept $−0.01$, $p = 0.41$; MS2: intercept $−0.003$, $p = 0.73$; MS3: intercept $−0.001$, $p = 0.73$). The pleiotropy robust methods (weighted median and MR-Egger) yielded effect estimates consistent with the main finding across all samples (figure 1). In addition, the funnel plots for each variant were symmetric and provided no evidence of directional horizontal pleiotropy (figure 2).

**Discussion**

In this study, we investigated the causal relationship between serum urate levels and MS susceptibility, using a 2-sample MR design in 3 MS case-control studies with a cumulative sample size of 148,473 individuals (61,667 MS cases and 86,806 controls). The main results consistently found no effect of lifelong genetically related differences in urate levels on the risk of developing MS. The narrow CIs around this null effect afforded by our large sample size provide strong evidence against any clinically relevant influence. In addition, we applied several sensitivity analyses, each with different underlying assumptions, which found no evidence of pleiotropy and further reinforce the validity of the results. This suggests that the previously reported association between serum urate and MS risk could be attributed to residual confounding, reverse causality, or both.

Our findings conflict with the results of most case-control studies conducted on serum urate and MS. A previous study reported lower serum urate levels in MS when compared to noninflammatory neurologic disease controls. The same study also found that the rate of MS and gout co-occurrence was lower than expected by chance. A more recent meta-analysis of 1308 MS cases and 908 controls similarly reported lower serum urate levels in MS.14 However, there was considerable between-study heterogeneity,14 and a recent umbrella review classified the evidence for an association between serum urate levels and MS as Class IV (weak).22 Importantly, those studies used urate measurements in prevalent MS cases. Therefore, they cannot determine whether the decrease in serum levels precedes MS onset or is a consequence thereof, rendering them susceptible to bias from reverse causality. In contrast, a small prospective case-control study, which measured serum urate levels years before MS symptom onset, found no association with the risk of MS.18 The same study also observed lower urate levels as the interval between sample collection and MS symptom onset decreased.18 In combination, these findings are consistent with the interpretation that higher serum urate levels are not
protective against MS, but rather a consequence of the MS disease process. This is in line with the results from our MR approach, which is robust to reverse causality. In addition, using genetic proxies of urate levels lowers the risk of confounding from diet and body weight, which were not routinely accounted for in previous observational studies.43

Indeed, serum urate levels are modulated in part by dietary purine consumption, particularly the intake of purine-rich food groups such as meat, seafood, and alcohol.43 In addition, obesity is a risk factor for the development of hyperuricemia, whereas weight loss in that group results in serum urate level reduction.43 That said, a recent study combining food frequency questionnaire and genetic data from 5 US cohorts found that dietary patterns explained only 4.3% of variation in serum urate levels, whereas common genetic variants explained 23.9% (of which 7.9% was captured by the genome-wide significant SNPs included in the present study).44

Our study did not address the separate question of whether serum urate levels influence MS disease course. This has been explored in 3 small randomized clinical trials in relapsing-remitting MS cohorts. However, the results from these trials were inconsistent, with 2 showing no significant effect and one showing a significant but modest effect.45

Figure 1 Forest plot of the main MR estimates and sensitivity analyses for each of the MS data sets

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<td>0.98 (0.90–1.08)</td>
<td>1.00 (0.92–1.10)</td>
<td>1.02 (0.90–1.17)</td>
</tr>
<tr>
<td>MS2 (n = 38,589)</td>
<td>0.99 (0.89–1.10)</td>
<td>1.00 (0.91–1.10)</td>
<td>1.01 (0.87–1.18)</td>
</tr>
<tr>
<td>MS1 + MS2 IVW</td>
<td>0.99 (0.92–1.06)</td>
<td>0.99 (0.92–1.06)</td>
<td>0.99 (0.92–1.06)</td>
</tr>
<tr>
<td>MS3 (n = 68,379)</td>
<td>1.00 (0.98–1.02)</td>
<td>1.00 (0.99–1.02)</td>
<td>1.00 (0.97–1.04)</td>
</tr>
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The combined MS1 and MS2 data set IVW MR results were obtained after fixed-effects meta-analysis. IVW = inverse-variance weighted; MR = Mendelian randomization.

Figure 2 Funnel plots of the individual MR estimates against their precision in each of the MS cohorts
remitting MS using inosine, an oral precursor of urate, which increases its serum levels. A first small study in 16 patients reported an improvement in EDSS scores at 1 year with inosine treatment compared with placebo. However, 2 subsequent clinical trials in 36 and 159 patients with relapsing-remitting MS, of 1- and 2-year duration, respectively, compared the combination of interferon β and inosine vs interferon β with placebo and did not find any effect on disability or other clinical and MRI metrics. These results are not directly comparable to our research findings.

Our study has some limitations. First, while the use of summary statistics in a 2-sample MR design maximized statistical power, it precluded sex-stratified analyses. However, despite women having generally lower serum urate levels, the association with MS in case-control studies was similar between sexes. Second, this study did not differentiate between MS subtypes. Although a small study reported higher serum urate levels in 11 primary progressive MS cases compared with other subtypes, others have found no difference. Third, the estimates reported in our study assume a linear effect between the risk factor and outcome. Last, the possibility of horizontal pleiotropy cannot be entirely excluded. Nevertheless, we undertook several sensitivity analyses, which found no evidence of pleiotropy. In addition, we excluded variants in the MHC region and those showing outlier effects using an established method.

In conclusion, we provide strong evidence against a causal effect of serum urate levels on the risk of MS. This helps inform the role of this metabolite in MS pathogenesis and indicates that approaches to increase urate levels would not be effective in preventing disease while potentially leading to adverse events.

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Disclosure
The authors report no disclosures. Go to Neurology.org/NN for full disclosures.

Publication history

Appendix Authors

<table>
<thead>
<tr>
<th>Name</th>
<th>Location</th>
<th>Contribution</th>
</tr>
</thead>
<tbody>
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<td>Designed and conceptualized the study; interpreted the data; and drafted the manuscript for intellectual content</td>
</tr>
</tbody>
</table>

References
Mendelian randomization study shows no causal effects of serum urate levels on the risk of MS
Adil Harroud, J. Brent Richards and Sergio E. Baranzini
Neurol Neuroimmunol Neuroinflamm 2021;8; DOI 10.1212/NXI.0000000000000920

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