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Impact of atopy on risk of glioma: a Mendelian randomisation study

Linden Disney-Hogg1†, Alex J. Cornish1†, Amit Sud1, Philip J. Law1, Ben Kinnersley1, Daniel I. Jacobs2, Quinn T. Ostrom3, Karim Labreche1, Jeanette E. Eckel-Passow4, Georgina N. Armstrong2, Elizabeth B. Claus5,6, Dora Il’yasova7,8,9, Joellen Schildkraut8,9, Jill S. Bamholtz-Sloan3, Sara H. Olson10, Jonine L. Bernstein10, Rose K. Lai11, Minouk J. Schoemaker1, Matthias Simon12, Per Hoffmann13,14, Markus M. Nöthen14,15, Karl-Heinz Jöckel16, Stephen Chanock17, Preetha Rajaraman17, Christoffer Johansen18,19, Robert B. Jenkins20, Beatrice S. Melin21, Margaret R. Wrensch22,23, Marc Sanson24,25, Melissa L. Bondy2 and Richard S. Houlston1,26*

Abstract

Background: An inverse relationship between allergies with glioma risk has been reported in several but not all epidemiological observational studies. We performed an analysis of genetic variants associated with atopy to assess the relationship with glioma risk using Mendelian randomisation (MR), an approach unaffected by biases from temporal variability and reverse causation that might have affected earlier investigations.

Methods: Two-sample MR was undertaken using genome-wide association study data. We used single nucleotide polymorphisms (SNPs) associated with atopic dermatitis, asthma and hay fever, IgE levels, and self-reported allergy as instrumental variables. We calculated MR estimates for the odds ratio (OR) for each risk factor with glioma using SNP-glioma estimates from 12,488 cases and 18,169 controls, using inverse-variance weighting (IVW), maximum likelihood estimation (MLE), weighted median estimate (WME) and mode-based estimate (MBE) methods. Violation of MR assumptions due to directional pleiotropy were sought using MR-Egger regression and HEIDI-outlier analysis.

Results: Under IVW, MLE, WME and MBE methods, associations between glioma risk with asthma and hay fever, self-reported allergy and IgE levels were non-significant. An inverse relationship between atopic dermatitis and glioma risk was found by IVW (OR 0.96, 95% confidence interval (CI) 0.93–1.00, \( P = 0.041 \)) and MLE (OR 0.96, 95% CI 0.94–0.99, \( P = 0.003 \)), but not by WME (OR 0.96, 95% CI 0.91–1.01, \( P = 0.114 \)) or MBE (OR 0.97, 95% CI 0.92–1.02, \( P = 0.194 \)).

Conclusions: Our investigation does not provide strong evidence for relationship between atopy and the risk of developing glioma, but findings do not preclude a small effect in relation to atopic dermatitis. Our analysis also serves to illustrate the value of using several MR methods to derive robust conclusions.

Keywords: Mendelian randomisation, Allergy, Cancer, Glioma, Risk

* Correspondence: richard.houlston@icr.ac.uk
† Equal contributors
1 Division of Genetics and Epidemiology, The Institute of Cancer Research, 15 Cotswold Road, London SM2 5NG, UK
2 6 Division of Molecular Pathology, The Institute of Cancer Research, London, UK
Full list of author information is available at the end of the article

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**Background**

Although glioma accounts for approximately 80% of malignant primary brain tumours [1], to date, few aetiological risk factors are well established for the disease [2]. Over the past three decades the search for an immune-mediated risk factor that might influence risk has led to studies of a possible relationship between multiple allergic conditions and autoimmune disorders with glioma [3].

Several case-control studies have shown that self-reported allergic conditions may protect against glioma [4]. For example, in the International Adult Brain Tumour Study, based on 1178 glioma patients, an odds ratio (OR) of 0.59 was found for any self-reported allergy [5]. Other case-control studies have reported similar ORs, however, most have been reliant on substantial numbers of proxy informants (up to 44%) [4, 6] and have potential bias as a consequence of how controls were ascertained, thereby casting doubt on findings. In contrast to case-control studies, evidence for an association between glioma and allergy from cohort-based analyses has been less forthcoming [7], although such studies have been poorly powered to demonstrate a relationship.

Assaying IgE potentially reduces bias stemming from self-reporting despite levels not necessarily corresponding to specific allergies or equating to a single allergic response. Nevertheless, measurement of IgE has been explored by a number of researchers seeking to identify risk factors for glioma [8–10]. In a case-control study of 228 cases and 289 controls performed in 2004 [8], self-reported allergies and IgE levels were both inversely associated with glioma, but concordance between the two outcomes was poor. In a larger study of 535 cases and 532 controls [11], both self-reported allergies and IgE levels were inversely related to glioma risk; however, IgE levels in patients were affected by temozolomide treatment. A case-control study nested within the European Prospective Investigation into Cancer and Nutrition cohort based on prospectively collected serum IgE levels reported a non-significant OR of 0.73 [9]. A similar nested case-control study performed in the USA based on 181 cases reported a non-significant OR of 0.72 for high serum IgE [10].

Several mechanisms have been proposed to explain a possible association between atopic disease and glioma [12]. The findings could reflect a true causal effect of the heightened immune function reported for atopy on tumour development. Alternatively, the associations observed might be non-causal, arising as a consequence of methodological biases inherent in the study design. Imprecisely defined exposures, such as allergic disease, are likely to have affected the validity of the findings of both case-control and cohort studies. The heterogeneous description of allergy in studies and different levels of detail in self-reporting on individual allergies complicate the interpretation of results. Additional biases include possible selection bias in controls, recall bias from self-reported allergy assessment and reverse causation or confounding from unmeasured effects. Finally, the high frequency of exposure ascertainment by proxy for cases is also likely to have systematically biased findings.

Mendelian randomisation (MR) analysis can be used to minimise potential biases in conventional observational studies and to determine the causal association of an exposure with an outcome such as disease risk [13]. The causal association can also be manifested by common genetic and biological pathways that determine two sequentially developed phenotypes such as an atopic trait and glioma risk. Atopy has a strong heritable basis [14, 15] and, thus far, genome-wide association studies (GWAS) have identified over 50 loci associated with different atopy-related traits [16]. The alleles associated with atopy should be randomly assigned to offspring from parents during mitosis, a process analogous to the random assignment of subjects to an exposure of interest in randomised clinical trials. Thus, genetic scores summarising the effects of single nucleotide polymorphisms (SNPs) associated with atopy-related traits can serve as instrumental variables (IVs) in a MR analysis of atopy and glioma risk.

To examine the nature of the association between atopy and glioma, we implemented two-sample MR [17] to estimate associations between atopy-associated SNPs and glioma risk using summary data from the recent GWAS meta-analysis performed by the Glioma International Case-Control Consortium study [18].

**Methods**

Two-sample MR was undertaken using GWAS data. Ethical approval was not sought for this specific project because all data came from the summary statistics of published GWAS, and no individual-level data were used.

**Glioma genotyping data**

Glioma genotyping data were derived from the most recent meta-analysis of GWAS in glioma, which related > 10 million genetic variants (after imputation) to glioma, in 12,488 glioma patients and 18,169 controls from eight independent GWAS datasets of individuals of European descent [18] (Additional file 1: Table S1). Comprehensive details of the genotyping and quality control of the seven GWAS have been previously reported [18].

**Genetic variant instruments for atopic traits**

SNPs associated with each of the atopy-related traits investigated, namely atopic dermatitis (eczema), asthma and hay fever, IgE level, and self-reported allergy, by the
NHGRI-EBI GWAS Catalog [19–26] at genome-wide significance (*i.e.*, *P* ≤ 5.0 × 10−8) in individuals with European ancestry were used as IVs. To avoid co-linearity between SNPs for each trait, we excluded SNPs that were correlated (*i.e.*, *r*2 value of ≥ 0.001) within each trait, and only considered the SNPs with the strongest effect on the trait for use as IVs (Additional file 2: Table S2). For each SNP, we recovered the chromosome position, risk allele, association estimates (per-allele log-OR) and standard errors (Table 1). The allele that was associated with increased risk of the exposure was considered the effect allele. For IgE level, the allele associated with an increase in serum IgE was considered the effect allele. Allele frequencies for these SNPs were compared between the groups. The effect estimates were recorded with respect to the same allele. Gliomas are heterogeneous and different tumors with the effect estimates were recorded with respect to the same allele.

Atopic dermatitis, asthma and hay fever, and self-reported allergy as well as all of the disease outcomes (all glioma, GBM and non-GBM glioma) are binary. The causal effect estimates therefore represent the odds for outcome disease per unit increase in the log OR of the exposure disease [32]. These ORs were converted to represent the OR for the outcome disease per doubling in odds of the exposure disease to aid interpretation [32].

For each statistical test we considered a global significance level of *P* < 0.05 as being satisfactory to derive conclusions. To assess the robustness of our conclusions, we initially imposed a conservative Bonferroni-corrected significance threshold of 0.0125 (*i.e.*, 0.05/4 atopy-related traits). We considered a *P* value ≥ 0.05 as non-significant (i.e. no association), a *P* < 0.05 as evidence for a potential causal association, and a *P* < 0.0125 as significant evidence for an association. All statistical analyses were undertaken using R software (Version 3.1.2). The meta and gsmr packages were used to generate forest plots and perform HEIDI-outlier analysis [29].

The power of a MR investigation depends greatly on the proportion of variance in the risk factor that is explained by the IV. We estimated study power *a priori* using the methodology of Burgess et al. [33], making use of published estimates of the heritability of trait associated IV SNPs [34–36], as well as estimates found by direct calculation (Additional file 3: Table S3), and the reported effect of each trait on glioma risk reported in a meta-analysis of epidemiological studies [18]. Additional file 4: Table S4 shows the range of ORs for which we had less than 80% power to detect for each of the four atopy-related traits.

### Simulation model

Through simulation we evaluated the suitability of using each employed MR method in a two-sample setting with binary-exposure and binary-outcome data. Let *i* index genetic variants, *N* be the total number of genetic variants, and *j* index individuals. Genetic variants *g*ij were generated independently by sampling from a Binomial(2, *p*ij) distribution with probability *p*ij drawn from a Uniform(0.1,0.9) distribution, to mimic bi-allelic SNPs in Hardy–Weinberg
### Table 1

Variant and effect allele with frequencies and magnitude of effect on each atopy-related trait and strength of association with glioma

| Region | SNP      | Position (bp) | Alleles | MAF  | Hay fever and asthma | Glioma          |
|--------|----------|---------------|---------|------|----------------------|-----------------|
|        |          |               |         |      | OR (95% CI)          | OR (95% CI)     |
| 2q12.1 | rs10197862 | 102,966,549   | G/A     | G = 0.161 | 1.24 (1.16–1.32) | 0.98 (0.93–1.03) |
| 4p14   | rs4833095  | 38,799,710    | C/T     | T = 0.425 | 1.20 (1.14–1.26) | 1.03 (0.99–1.08) |
| 5q22.1 | rs1837253  | 110,401,872   | T/C     | T = 0.382 | 1.17 (1.11–1.23) | 0.96 (0.93–1.00) |
| 8q21.13| rs7009110  | 81,291,879    | C/T     | C = 0.467 | 1.14 (1.09–1.19) | 0.98 (0.94–1.01) |
| 9p24.1 | rs72699186 | 6,175,855     | A/T     | T = 0.110 | 1.26 (1.17–1.36) | 0.97 (0.93–1.02) |
| 11q13.5| rs2155219  | 76,299,194    | G/T     | G = 0.468 | 1.17 (1.13–1.21) | 1.01 (0.97–1.05) |
| 15q22.33| rs17294280 | 67,468,285    | A/G     | A = 0.120 | 1.18 (1.12–1.25) | 0.98 (0.94–1.03) |
| 16p13.13| rs62026376 | 11,228,712    | T/C     | T = 0.144 | 1.17 (1.11–1.23) | 0.97 (0.93–1.01) |
| 17q21.1| rs7212938  | 38,122,680    | T/G     | G = 0.473 | 1.16 (1.11–1.22) | 1.00 (0.97–1.04) |

**Region** | **SNP** | **Position** | **Alleles** | **MAF** | **IgE level** | **Glioma** |
|------------|---------|--------------|-------------|---------|--------------|-----------|
|            |         |              |             |         | OR (95% CI)  | OR (95% CI) |
| 1q21.3     | rs11205006 | 152,440,176  | T/A         | A = 0.265 | 1.62 (1.48–1.77) | 0.96 (0.91–1.02) |
| 1q21.3     | rs2228145  | 154,426,970  | A/C         | C = 0.293 | 1.15 (1.10–1.20) | 0.99 (0.96–1.03) |
| 2p25.1     | rs10199605 | 8,495,097    | A/G         | A = 0.244 | 1.04 (1.03–1.06) | 1.01 (0.97–1.05) |
| 2p13.3     | rs11211145 | 71,100,105   | G/A         | G = 0.224 | 1.08 (1.05–1.10) | 0.98 (0.92–1.03) |
| 2q24.3     | rs6720763  | 167,992,286  | T/C         | C = 0.320 | 1.29 (1.18–1.41) | 1.02 (0.97–1.06) |
| 5p13.2     | rs10214237 | 35,883,734   | C/T         | C = 0.176 | 1.06 (1.05–1.08) | 0.98 (0.94–1.02) |
| 5q31.1     | rs1295686  | 131,995,843  | C/T         | T = 0.422 | 1.35 (1.22–1.49) | 0.99 (0.95–1.03) |
| 6p21.32    | rs12153855 | 32,074,804   | T/C         | C = 0.125 | 1.58 (1.40–1.78) | 0.97 (0.92–1.03) |
| 8q21.13    | rs6473227  | 81,285,892   | A/C         | A = 0.473 | 1.06 (1.05–1.08) | 0.98 (0.94–1.02) |
| 9p21.3     | rs10738626 | 22,373,457   | C/T         | C = 0.397 | 1.23 (1.15–1.32) | 0.96 (0.93–1.00) |
| 10p15.1    | rs6602364  | 6,038,853    | G/C         | G = 0.492 | 1.05 (1.03–1.07) | 1.03 (0.99–1.07) |
| 11q13.1    | rs10791824 | 65,559,266   | A/G         | G = 0.490 | 1.15 (1.12–1.19) | 0.99 (0.95–1.02) |
| 11q24.3    | rs7127307  | 128,187,383  | C/T         | C = 0.488 | 1.09 (1.07–1.11) | 0.99 (0.95–1.03) |
| 11q13.5    | rs7130588  | 76,270,683   | G/A         | G = 0.216 | 1.29 (1.20–1.38) | 1.02 (0.98–1.06) |
| 14q13.2    | rs2143950  | 35,572,357   | C/T         | T = 0.215 | 1.08 (1.06–1.10) | 1.01 (0.97–1.06) |
| 16p13.13   | rs2041733  | 11,229,589   | C/T         | T = 0.496 | 1.09 (1.06–1.11) | 0.97 (0.94–1.01) |
| 19p13.2    | rs2164983  | 8,789,381    | C/A         | A = 0.169 | 1.16 (1.10–1.22) | 0.95 (0.90–1.00) |
| 20q13.33   | rs909341   | 62,328,742   | T/C         | T = 0.262 | 1.32 (1.21–1.44) | 1.32 (1.26–1.37) |

**Region** | **SNP** | **Position** | **Alleles** | **MAF** | **Self-reported allergy** | **Glioma** |
|------------|---------|--------------|-------------|---------|--------------------------|-----------|
|            |         |              |             |         | OR (95% CI)               | OR (95% CI) |
| 2q12.1     | rs10189699 | 102,879,464  | A/C         | A = 0.143 | 1.16 (1.12–1.20) | 0.99 (0.94–1.04) |
| 2q33.1     | rs10497813 | 198,040,072  | T/G         | T = 0.401 | 1.08 (1.05–1.11) | 0.99 (0.96–1.03) |
| 3q28       | rs9860547  | 188,128,979  | G/A         | A = 0.272 | 1.08 (1.05–1.11) | 1.02 (0.98–1.06) |
| 4p14       | rs2101521  | 38,811,551   | A/G         | A = 0.475 | 1.15 (1.12–1.18) | 1.02 (0.98–1.07) |
equilibrium. Let $w_j$ correspond to the per-allele OR for the exposure disease, sampled from ORs reported for genome-wide significant SNPs reported in the GWAS Catalog [37], and $v$ be the OR for the outcome disease per doubling in odds of the exposure disease. For each individual, exposure disease odds $x_j$, outcome disease odds $y_j$, exposure disease status $a_j$, and outcome disease status $b_j$ were determined as follows:

$$x_j = x_0 \prod_{i=1}^{N} w_i^x$$

$$y_j = y_0 \times 2^{\log(x_j) \times \log(v)}$$

$$a_j \sim \text{Binomial}\left(1, \frac{x_j}{1+x_j}\right)$$

$$b_j \sim \text{Binomial}\left(1, \frac{y_j}{1+y_j}\right)$$

Data for 1,000,000 individuals were simulated and partitioned at random to reflect the two-sample setting. Cases and controls for the exposure and outcome GWAS were sampled from each half of the dataset using the exposure and outcome disease statuses of each individual, and association statistics computed under an additive logistic regression model. To ensure the simulated data closely resembled the atopy-related trait and glioma data, the simulation analysis was repeated for each binary atopy-related trait using the same number of genetic variants as IVs and the same numbers of case and control individuals as used to estimate the atopy-related trait and glioma association statistics (Additional file 5: Table S5). Parameters $x_0 = 0.0005$ and $y_0 = 0.01$ were chosen to ensure the prevalence of the simulated exposure and outcome diseases were similar to that of the atopy-related traits and glioma, respectively (Additional file 5: Table S5). To determine the suitability of each MR method we considered two scenarios: (1) no causal relationship between exposure and outcome ($v = 1.00$) and (2) a causal relationship between exposure and outcome ($v = 1.33$). We performed 100 simulations for each scenario for each binary atopy-related trait.

**Results**

The atopic dermatitis risk SNP rs909341, which is highly correlated with the chromosome 20q13.33 glioma risk SNP rs2297440 ($D' = 0.89$, $r^2 = 0.77$), was strongly associated with risk of glioma ($P = 2.10 \times 10^{-34}$). Testing for pleiotropy using HEIDI-outlier analysis formally identified rs909341 as violating the assumption of the instrument on the outcome. Henceforth, we confined our analysis of the relationship between atopic dermatitis and glioma to a dataset excluding this SNP.

Figure 1 shows forest plots of ORs for glioma generated from the SNPs. There was minimal evidence of heterogeneity between variants for asthma and hay fever, atopic dermatitis, IgE levels and self-reported allergy (respective $I^2$ and $P_{het}$ values being 28% and 0.192, 8% and 0.377, 0% and 0.444, and 0% and 0.707). Including rs909341 in the analysis for atopic dermatitis, the $I^2$ value was 90% and $P_{het} < 10^{-4}$ (Additional file 6: Figure S1), providing further evidence that inclusion of this SNP would invalidate the MR analysis.

The results of the IVW, MLE, WME, MBE and MR-Egger methods are summarised in Table 2. Using the IVW method to pool results from individual SNPs, no associations (i.e. $P \geq 0.05$) were identified between genetically conferred risk of raised IgE level (OR 0.88, 95% CI 0.69–1.13, $P = 0.319$), asthma and hay fever (OR 0.96, 95% CI 0.90–1.03, $P = 0.248$), or self-reported allergy (OR 1.03, 95% CI 0.95–1.11, $P = 0.534$) with risk of all glioma. There was some support for an inverse relationship
between atopic dermatitis and glioma risk (OR 0.96, 95% CI 0.93–1.00, \( P = 0.041 \)), albeit not significant after adjustment for multiple testing.

Using MLE, no associations were identified between asthma and hay fever (OR 0.96, 95% CI 0.93–1.00, \( P = 0.066 \)), IgE levels (OR 0.88, 95% CI 0.74–1.05, \( P = 0.157 \)) or self-reported allergy (OR 1.02, 95% CI 0.97–1.08, \( P = 0.429 \)) with risk of all glioma. For atopic dermatitis, an OR of 0.96 (95% CI 0.94–0.99, \( P = 0.003 \)) was shown, which remained significant after adjusting for multiple testing. Figure 2 shows relaxation of the assumption that the correlation between the errors in \( X_k \) and \( Y_k \) is zero for each of the atopy-related traits demonstrating the consistency of findings. Specifically, for a correlation in the range −0.15 to 0.15, the association between atopic dermatitis and glioma risk remained significant.

In contrast to findings from IVW and MLE, no significant support was provided by either the WME or MBE for an association between any of the atopy-related traits and glioma risk, including atopic dermatitis (WME: OR 0.96, 95% CI 0.91–1.01, \( P = 0.114 \); MBE: OR 0.97, 95% CI 0.92–1.02, \( P = 0.194 \); Table 2).

The respective effect estimated from MR-Egger regression (Fig. 3) were 0.97 for atopic dermatitis (95% CI 0.92–1.03; \( P = 0.375 \)), 0.63 for IgE levels (95% CI 0.32–1.25; \( P = 0.184 \)), 0.99 for asthma and hay fever (95% CI 0.72–1.36, \( P = 0.951 \)) and 0.92 for self-reported allergy (95% CI 0.69–1.22; \( P = 0.540 \)), with intercepts of −0.004 (95% CI −0.014 to 0.006, \( P = 0.396 \)), 0.027 (95% CI 0.001 to 0.053, \( P = 0.042 \)), −0.007 (95% CI −0.030 to 0.016, \( P = 0.542 \)) and 0.017 (95% CI 0.003–0.031, \( P = 0.018 \)). Collectively, these findings provide possible evidence of systematic bias in the IVW estimate for IgE level and self-reported allergy, which might have arisen through overall unbalanced horizontal pleiotropy. There was no such evidence for such pleiotropy in respect of atopic dermatitis.

We explored the possibility that a relationship between atopy and glioma might be subtype specific, considering GBM and non-GBM separately. Imposing a stronger significance threshold of \( P = 0.00625 \) (0.05/8, to correct for testing four traits over two outcomes), no histology-specific associations were shown by the IVW method between asthma and hay fever, IgE levels and self-reported allergy (95% CI 0.69–1.22; \( P = 0.540 \)), with intercepts of −0.004 (95% CI −0.014 to 0.006, \( P = 0.396 \)), 0.027 (95% CI 0.001 to 0.053, \( P = 0.042 \)), −0.007 (95% CI −0.030 to 0.016, \( P = 0.542 \)) and 0.017 (95% CI 0.003–0.031, \( P = 0.018 \)). Collectively, these findings provide possible evidence of systematic bias in the IVW estimate for IgE level and self-reported allergy, which might have arisen through overall unbalanced horizontal pleiotropy. There was no such evidence for such pleiotropy in respect of atopic dermatitis.
Table 2. Inverse-variance weighting, maximum likelihood estimation, weighted median estimate, mode-based estimate and Mendelian randomisation-Egger test results for combined atopy-related instrumental variables.

| Trait                | IVW OR (95% CI) | P   | MLE OR (95% CI) | P   | WME OR (95% CI) | P   | MBE OR (95% CI) | P   | MR-Egger slope OR (95% CI) | P   | MR-Egger intercept Estimate (95% CI) | P   |
|----------------------|----------------|------|----------------|------|----------------|------|----------------|------|---------------------------|------|--------------------------------------|------|
| Asthma and hay fever | 0.96 (0.90–1.03)| 0.248| 0.96 (0.93–1.00)| 0.066| 0.93 (0.86–1.01)| 0.087| 0.91 (0.82–1.04)| 0.191| 0.99 (0.72–1.36)          | 0.951| -0.007 (~0.03 to 0.016)          | 0.542|
| Atopic dermatitis    | 0.96 (0.93–1.00)| 0.041| 0.96 (0.94–0.99)| 0.003| 0.96 (0.91–1.01)| 0.114| 0.97 (0.92–1.02)| 0.194| 0.97 (0.92–1.03)          | 0.375| 0.004 (~0.01 to 0.03)          | 0.396|
| IgE level            | 0.88 (0.69–1.13)| 0.319| 0.88 (0.74–1.05)| 0.157| 0.83 (0.61–1.12)| 0.218| 0.82 (0.57–1.19)| 0.355| 0.63 (0.32–1.25)          | 0.184| 0.027 (~0.01 to 0.03)          | 0.042|
| Self-reported allergy| 1.03 (0.95–1.11)| 0.534| 1.02 (0.97–1.08)| 0.429| 1.08 (0.97–1.20)| 0.184| 1.12 (0.92–1.36)| 0.275| 0.92 (0.69–1.22)          | 0.540| 0.017 (~0.03 to 0.031)          | 0.018|

CI: confidence interval, IVW: inverse-variance weighting, MBE: mode-based estimate, MLE: maximum likelihood estimation, MR: Mendelian randomisation, OR: odds ratio, WME: weighted median estimate.
GBM tumours, and 0.96, 0.97 and 1.04 for non-GBM tumours (Additional file 7: Table S6). For atopic dermatitis, a significant OR of 0.94 (95% CI 0.90–0.98, \( P = 0.004 \)) was shown for GBM but not for non-GBM (OR 0.98, 95% CI 0.93–1.03, \( P = 0.421 \)). The association between atopic dermatitis and risk of GBM was also apparent in the MLE analysis, which provided an OR of 0.94 (95% CI 0.91–0.97, \( P = 2.17 \times 10^{-4} \)). MR-Egger regression provided for an intercept of \(-0.007\) (95% CI \(-0.019\) to 0.005, \( P = 0.247 \)). As with the analysis of all glioma, the association between atopic dermatitis and GBM was weaker under the WME (OR 0.96, 95% CI 0.91–1.02, \( P = 0.172 \)) and MBE (OR 0.95, 95% CI 0.90–1.01, \( P = 0.096 \)) frameworks.

Although previously implemented in other studies \([32, 38]\), ratio estimators may not fully recapitulate an estimate of the causal OR in the case of binary exposures, such as atopic dermatitis, and binary outcomes such as glioma \([39]\). We therefore evaluated, through simulation, whether the IVW, MLE, WME, MBE and MR-Egger methods provide reliable estimates of causal ORs. When no causal relationship between exposure and outcome was simulated, each MR method provided accurate estimates of the null relationship (Additional file 5: Table S5). Conversely, when a causal relationship was simulated, the magnitudes of the relationship estimates were weakly inflated in some instances (Additional file 5: Table S5), indicating the importance of considering additional evidence when evaluating causal relationships between binary exposures and binary outcomes.

**Discussion**

To our knowledge, this is the first MR study evaluating a range of atopy-related traits with glioma risk. Overall, our results provide evidence for a causal protective effect of atopic dermatitis with GBM tumours, but do not provide evidence that asthma and hay fever, raised IgE
levels, or self-reported allergy is protective against the risk of developing glioma.

Possible mechanisms explaining an observed inverse relation between the risk of atopic dermatitis and the risk of glioma have been suggested in previous papers [12], postulated to be the consequence of immune system hyperactivity. The question thus arises as to how such divergent findings for other atopic traits can be explained or reconciled, when they have been previously reported in high numbers.

A key assumption in MR is that the instrument affects glioma risk through its effect on a specific phenotype/exposure (i.e. atopic traits), and does not have a direct effect on glioma risk. We tested this assumption using MR-Egger regression and HEIDI-outlier analysis and found possible evidence of violation of this assumption for IgE and self-reported allergy. It is notable that self-reported allergy does not show an approximately quadratic response to correlation, in contrast to asthma and hay fever, atopic dermatitis and IgE level. This is likely to be a consequence of imprecise estimates of the association between SNPs and allergy, illustrating the inherent issue in attempting to make use of self-reported allergy data as an atopy-related trait.

The meta-analyses of published epidemiological observational studies has indeed provided strong evidence for an inverse relationship between atopy and glioma risk [40]. However, most of the support for such a relationship came from case-control studies [4]. A common limitation in retrospective studies of glioma has been the use of proxy respondents for patients with cognitive impairment, who may not remember past exposures accurately due to cognitive deficits [4]. Such issues are compounded by the fact that, across studies, multiple atopic traits have been assessed. The strength of support for a relationship seen across case-control studies contrasts markedly with the limited evidence for a relationship from prospective cohort-based analyses [7].

![Fig. 3](image-url) Scatter plots of genetic associations with glioma against genetic associations with the exposure. a Asthma and hay fever, b atopic dermatitis, c IgE level, d self-reported allergy
By inference, a relationship between long-term antihistamine use could theoretically provide supporting evidence, albeit indirect, that atopic-mediated mechanisms influence glioma risk. However, the impact of antihistamine use is difficult to disentangle from that of allergies, as these factors are highly correlated and few individuals without allergies use antihistamines regularly. Paradoxically, an increased risk for glioma associated with antihistamines, particularly among individuals with allergic conditions, has been found in some studies [41, 42].

Raised IgE levels and self-reported allergy suffer limitations as traits used to assess the effect of atopy on glioma risk as they are both variable over short time scales in their level of expression (in contrast to clinical diagnosis of atopic dermatitis). Further, allergies may develop later in life, and patients may not necessarily exhibit symptoms. This introduces the possibility of bias and error due to the time varying association of SNPs with the exposure. However, it has been suggested that seasonality does not have a significant effect [11].

An additional possible explanation for the lack of causal association between IgE levels and glioma risk seen in this study is that the causality is in fact reversed, which could result in epidemiological observational studies reporting inverse relationships [8, 9], but would not affect an MR analysis. Immunosuppression caused by glioblastoma is well documented [43, 44] and may lead to reduced expression of atopy. Furthermore, in addition to steroids, temozolomide therapy, routinely used to treat GBM nowadays, leads to reduced blood IgE levels [11].

Using data from large genetic consortia for multiple atopy-related traits and glioma risk has enabled us to more precisely test our study hypotheses than if we had used individual-level data from a smaller study. Through simulation scenarios, the IVW, MLE, WME, MBE and MR-Egger methods have been demonstrated to accurately estimate causal effects using summary-level data [28, 30, 31, 45]. However, using summary-level data instead of individual-level data limits the approaches that can be used to test the validity of genetic variants as IVs, as adjusting for measured covariates and assessing gene-environment interactions is generally not possible using summary-level data [46]. The first-stage F statistic was large (> 25 for all traits), and therefore weak instrument bias is unlikely.

Epidemiological observational studies have reported inverse relationships between atopy-related traits and glioma risk, with ORs in the range 0.43–0.96 for asthma [6, 47], 0.42–0.90 for atopic dermatitis [6, 47], 0.37–0.73 for IgE levels [8–10] and 0.47–0.69 for self-reported allergies [4, 5, 8]. Odds ratios for binary exposures estimated in this MR study represent the OR for the outcome disease per doubling in odds of the exposure disease, and the magnitudes of these causal effect estimates are therefore not directly comparable to those reported in observational studies.

Our MR analysis has several strengths. Firstly, by utilising the random allocation of genetic variants, we were able to overcome potential confounding and reverse causation that may bias estimates from observational studies. Secondly, given that a poor outcome from glioma is almost universal, it is unlikely that survival bias will have influenced study findings. Lastly, the findings from this study represent the association of a lifelong atopy with glioma in the general European population.

Nevertheless, our study does have limitations. Firstly, while it is entirely appropriate to implement different MR methods to assess the robustness of findings, they have a differing power to demonstrate associations, with the WME, MBE and MR-Egger methods having less power than IVW and MLE. Irrespective of such factors, our study only had 80% power to detect ORs of 1.16, 1.09, 1.16 and 1.22 for asthma and hay fever, atopic dermatitis, IgE level and self-reported allergy, respectively (Additional file 4: Table S4), due to the very low proportion of variability in the atopy-related traits explained by the SNPs used. Hence, we cannot exclude the possibility that these traits influence glioma risk, albeit modestly. To explore this possibility, will require additional IVs and larger sample sizes affording increased power. Furthermore, it is possible that an effect of atopy on glioma risk might be mediated through mechanisms associated with a trait that we have not captured by using MR to assess asthma and hay fever and self-reported allergy. Secondly, a weakness of the two-sample MR strategy is that it does not allow examination of non-linear relationships between exposures and outcomes. Finally, we have sought to examine whether bias could be introduced when considering a binary exposure for a binary outcome. Although in our simulation study we found no evidence of bias when estimating non-causal relationships, we did not extend our analysis to consider the potential impact of invalid SNPs.

Conclusions
In conclusion, our investigation does not provide strong evidence for a relationship between atopy-related diseases and risk of developing glioma, but findings do not preclude a small effect for atopic dermatitis. Our analysis also serves to illustrate the value of using several MR methods to derive robust conclusions.

Additional files

Additional file 1: Figure S1. Forest plot of Wald odds ratios (ORs) and 95% confidence intervals generated from single nucleotide polymorphisms (SNPs) associated with atopic dermatitis, including...
Genotype data from the Glioma International Case-Control Consortium Study are available from the database of Genotypes and Phenotypes (dbGaP) under accession phs001319.v1.p1. Additionally, genotypes from the GliomaScan GWAS can be accessed through dbGaP accession phs000652.v1.p1.

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Availability of data and materials
Genotype data from the Glioma International Case-Control Consortium Study GWAS are available from the database of Genotypes and Phenotypes (dbGaP) under accession phs001319.v1.p1. Additionally, genotypes from the GliomaScan GWAS can be accessed through dbGaP accession phs000652.v1.p1.

Authors' contributions
RSH and AJC managed the project. LD-H, AJC, AS, PJL and RSH drafted the manuscript. LD-H and AJC performed statistical analyses. BK, KL, MIS and RSH acquired and analysed the data. MU, PH, MMN and K-HJ acquired and analysed the German data. DU, QTO, JEE-P, GNA, EBC, DI, JS, ISB-S, SHO, JLB, RKL, CI, RBJ, BSM, MRW, MB, JLC, LRB, LL, RKL, CI, RJ, BSK, LMB, MLB and RSH acquired and analysed the glioma International Case-Control Consortium Study data. SC and PR acquired and analysed the National Cancer Institute data. MSa acquired and analysed the International Case-Control Consortium Study data. SC and PR acquired and analysed the Glioma Scan GWAS data. AJC and LD-H acquired and analysed the UK data. DIJ, QTO, JEE-P, GNA, EBC, DI, JS, JSB-S, SHO, JLB, RKL, CJ, RBJ, BSM, MRW, MLB and RSH acquired and analysed the Glioma Scan GWAS data. AJC and LD-H acquired and analysed the Swedish data. DIJ and QTO acquired and analysed the Swedish data. EBC acquired and analysed the Swedish data. DI acquired and analysed the Swedish data. JS acquired and analysed the Swedish data. JSB-S acquired and analysed the Swedish data. SHO acquired and analysed the Swedish data. JLB acquired and analysed the Swedish data. RKL acquired and analysed the Swedish data. AJC and LD-H acquired and analysed the German data. MU acquired and analysed the German data. MU acquired and analysed the German data.

Ethics approval and consent to participate
Two-sample Mendelian randomisation was undertaken using GWAS data. Ethical approval was not sought for this specific project because all data came from the summary statistics of published GWAS, and no individual-level data were used.

Consent for publication
Not applicable.

Competing interests
The authors declare that they have no competing interests.

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Author details
1 Division of Genetics and Epidemiology, The Institute of Cancer Research, 15 Cotswold Road, London SM2 5NG, UK. 2 Department of Medicine, Section of Epidemiology and Population Sciences, Dan L. Duncan Comprehensive Cancer Center, Baylor College of Medicine, Houston, TX, USA. 3 Case Comprehensive Cancer Center, School of Medicine, Case Western Reserve University, Cleveland, OH, USA. 4 Department of Biomedical Statistics and Informatics, Mayo Clinic College of Medicine, Rochester, MN, USA. 5 School of Medicine, Yale University, New Haven, CT, USA. 6 Department of Neurosurgery, Brigham and Women’s Hospital, Boston, MA, USA. 7 Department of Epidemiology and Biostatistics, School of Public Health, Georgia State University, Atlanta, GA, USA. 8 Duke Cancer Institute, Duke University Medical Center, Durham, NC, USA. 9 Cancer Control and Prevention Program, Department of Community and Family Medicine, Duke University Medical Center, Durham, NC, USA. 10 Department of Epidemiology and Biostatistics, Memorial Sloan Kettering Cancer Center, New York, NY, USA. 11 Departments of Neurology and Preventive Medicine, Keck School of Medicine, University of Southern California, Los Angeles, CA, USA. 12 Department of Neurosurgery, University of Bonn Medical Center, Sigmund-Freud Str. 25, 53105 Bonn, Germany. 13 Human Genomics Research Group, Department of Biomedicine, University of Basel, Basel, Switzerland. 14 Department of Genomics, Life & Brain Center, University of Bonn, Bonn, Germany. 15 Institute of Human Genetics, University of Bonn School of Medicine & University Hospital Bonn, Bonn, Germany. 16 Institute for Medical Informatics, Biometry and Epidemiology, University Hospital Essen, University of Duisburg-Essen, Essen, Germany. 17 Division of Cancer Epidemiology and Genetics, National Cancer Institute, Bethesda, USA. 18 Institute of Cancer Epidemiology, Danish Cancer Society, Copenhagen, Denmark. 19 Righospitalet, University of Copenhagen, Copenhagen, Denmark. 20 Department of Laboratory Medicine and Pathology, Mayo Clinic Comprehensive Cancer Center, Mayo Clinic, Rochester, MN, USA. 21 Department of Radiation Sciences, Umeå University, Umeå, Sweden. 22 Department of Neurological Surgery, School of Medicine, University of California, San Francisco, San Francisco, CA, USA. 23 Institute of Human Genetics, University of California, San Francisco, CA, USA. 24 Sorbonne Universités UPMC Univ Paris 06, INSERM CNRS, U11217, UMR 7225, ICM, F-75013 Paris, France. 25 AP-HP, Groupe Hospitalier Pitié-Salpêtrière, Service de neurologie 2-Mazarin, Paris, France. 26 Division of Molecular Pathology, The Institute of Cancer Research, London, UK.

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