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Discussion Letter

A Commentary on 'Effect of the Antibody-Mediated Immune Responses on COPD, Asthma, and Lung Function: A Mendelian Randomization Study'

To the Director,

We carefully read the article by Xu et al. published in *Archivos de Bronconeumología*.¹ The authors used Mendelian randomization (MR) to explore the relationship between antibody-mediated immune responses and chronic obstructive pulmonary disease (COPD), asthma, and lung function. This MR study identified 20 antibody-mediated immune responses with significant causal relationships to COPD, asthma, and certain lung function indicators. These findings provide a new perspective on understanding the genetic association between antibody-mediated immune responses and respiratory disease risk, offering genetic evidence for the prevention and treatment of COPD and asthma. We sincerely appreciate this innovative study, but would like to share some different perspectives on the research.

We believe that the methodology of this study still requires further improvement. Specifically, regarding the sample source, there may be overlap between the exposure and outcome data, which could introduce bias in the causal inference of the study. First, for the exposure data, Xu et al. used the GWAS summary statistics of antibody-mediated immune responses provided by Butler-Laporte et al.² This data originates from the genetic analysis of 20 types of microbiome antibody levels in 9724 British adults from the UK Biobank (UKB) database. However, for the outcome data, Xu et al. also used GWAS data from the UKB database,³ including COPD, emphysema, bronchiectasis and asthma. Furthermore, for lung function-related indicators, including forced expiratory volume in 1-second (FEV₁), forced vital capacity (FVC) and FEV₁/FVC, Xu et al. referenced the largest global GWAS data from 49 cohorts. However, 320,656 individuals (67% of the total sample) in this GWAS data also come from the UKB. This suggests that the MR results may still be primarily driven by data from the UKB.

MR is a powerful research method used to distinguish causal relationships, particularly demonstrating unique advantages when causal relationships cannot be clearly identified due to potential confounding bias in observational studies. However, the reliability of its results depends on strict adherence to a series of methodological assumptions, including the statistical independence of exposure and outcome data. Since both the exposure and some of the outcome data come from the UK Biobank, and most of the samples for lung function analysis are also from this database. If there is sample overlap, it could lead to significant bias in the MR analysis and a high type I error rate, resulting in an overestimation of causal relationships.⁴ Previous studies have shown that when the sample overlap is low and the instrumental variable strength is high,

its impact on the study conclusion may be limited.⁵ Therefore, we recommend that the authors calculate the sample overlap between exposure and outcome to assess its potential impact on the study conclusions.

To enhance the robustness and reliability of the study results, we repeated the analysis in an independent external cohort. We used the recently released FinnGen R12 database (https://www.finnngen.fi/en/access_results), which provides high-quality, UKB-independent samples that can be used for validation analysis, thus avoiding potential bias from sample overlap. In this analysis, we used the same exposure data as Xu et al., which is the GWAS summary statistics of antibody-mediated immune responses. For the outcomes, we used the GWAS data for COPD (N=433,208) and asthma (N=301,060) from the FinnGen R12 database. Additionally, we used the GWAS data for FEV₁/FVC (N=51,396) and FEV₁ (N=44,671) from the Within Family GWAS Consortium. For the data analysis, we selected SNPs significantly associated with immune response levels ($P < 1E-05$) according to the standards of Xu et al. To remove linkage disequilibrium, we also used the standard of $r^2 = 0.001$, kb = 10,000. Additionally, SNPs related to outcome variables were excluded ($P < 1E-05$).

All results are detailed in Fig. 1. The results show that, after false discovery rate adjustment, only the level of anti-toxoplasma gondii IgG seropositivity remained significantly negatively associated with FEV₁/FVC. When false discovery rate adjustment was not applied to the P-values, we found that Epstein-Barr virus VCA p18 antibody levels, toxoplasma gondii p22 antibody levels, anti-chlamydia trachomatis IgG seropositivity, anti-helicobacter pylori IgG seropositivity, and helicobacter pylori catalase antibody levels were associated with COPD; Anti-Toxoplasma gondii IgG seropositivity, anti-human herpes virus 6 IE1A IgG seropositivity, anti-bk polyomavirus IgG seropositivity and toxoplasma gondii p22 antibody levels were associated with asthma; Helicobacter pylori cagA antibody levels were associated with FEV₁; and Toxoplasma gondii p22 antibody levels, anti-herpes simplex virus 2 IgG seropositivity, and helicobacter pylori UREA antibody levels were associated with FEV₁/FVC, indicating potential causal relationships.

Similar to the results of Xu et al., we also found potential causal relationships between Epstein-Barr virus VCA p18 antibody levels and toxoplasma gondii p22 antibody levels with COPD. However, we did not observe any significant statistical differences for the remaining results of Xu et al., and we additionally identified three new results: Anti-chlamydia trachomatis IgG seropositivity, anti-helicobacter pylori IgG seropositivity, and helicobacter pylori catalase antibody levels. For the MR analysis of asthma, FEV₁, and FEV₁/FVC, we did not obtain the same results as Xu et al., and most of the results did not pass the false discovery rate test.

In conclusion, we greatly admire the efforts of Xu et al. in exploring the causal relationship between immune responses and respiratory diseases. This provides new insights for further

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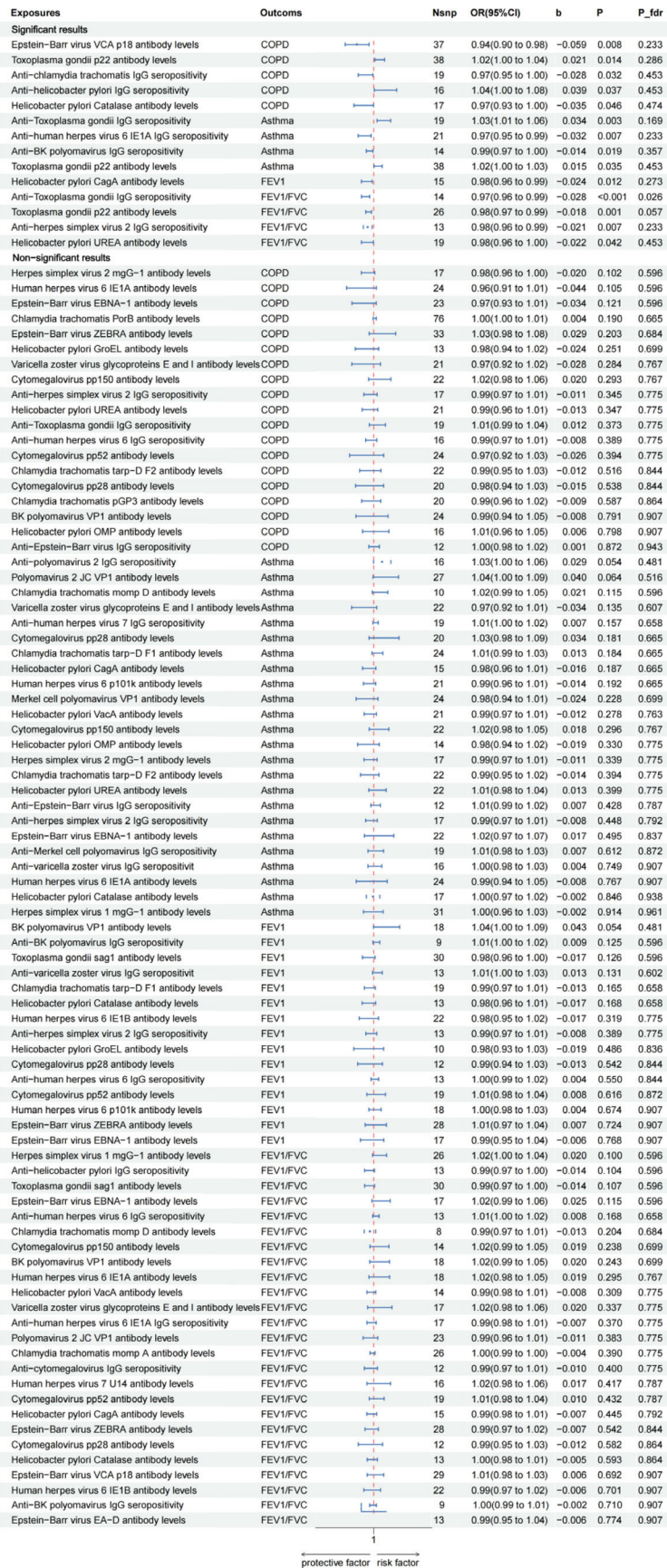


Fig. 1. Forest plot of the MR analysis results for antibody-mediated immune responses and respiratory diseases. All results were obtained using the inverse-variance weighted method. COPD, chronic obstructive pulmonary disease; FEV1, forced expiratory volume in 1-second; FVC, forced vital capacity; MR, Mendelian randomization; FDR, false discovery rate; CI, confidence interval; OR, odds ratio.

understanding the relationship between immune responses and respiratory diseases. However, we hope that adjusting the sample data sources can further strengthen the conclusions of this study and potentially yield new results to advance the field.

Ethics Approval and Consent to Participate

Not applicable.

Consent for Publication

Not applicable.

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Conflict of Interests

The authors declare that they have no competing interests.

Availability of Data and Materials

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

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