Objectives: We implement a two-sample Mendelian Randomization (MR) analysis to investigate the potential association.

Methods: The summary statistics of blood leukocyte counts were available from public databases (n=172435)[4]. The SNPs related to SLE risk were extracted from a large SLE GWAS with 5201 cases and 9066 controls of European ancestry[5]. All genetic variants significantly associated with blood leukocyte counts (p<5x10^-8) were used as instrumental variables (IVs). Then, the linkage disequilibrium (LD) was excluded (distance threshold = 10,000 kb, r² = 0.001). In this study, the inverse variance weighted (IVW) method, the MR-Egger method, and the weighted median (WM) were used to estimate the causal effect of the blood leukocyte counts and SLE. In addition, Cochran’s Q test, MR pleiotropy residual sum and outlier (MR-PRESSO), and leave-one-out analysis were implemented as sensitivity tests.

Results: We selected 119 independent SNPs as IVs in the MR analysis of total WBC. Higher blood leukocyte counts were associated with a lower risk of SLE (OR: 0.629, 95% CI: 0.436-0.907, P: 0.013) by IVW method (Figure 1). However, the results of Cochrane Q statistics showed heterogeneity (p<0.05). Therefore, we used the random-effects model[6].

Conclusion: Our study predicted genetically that individuals with lower blood leukocyte counts face a higher risk of SLE, which was consistent with the previous observational studies.

REFERENCES:

Figure 1: (A) Forest plot for MR estimates for causal effect of blood leukocyte counts on SLE from different methods. (B) Scatter plots for MR analyses. (C) Funnel plot for MR analyses. SLE, systemic lupus erythematosus.

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