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634.MYELOPROLIFERATIVE SYNDROMES: CLINICAL AND EPIDEMIOLOGICAL

Association between Inflammatory Factors and Myeloproliferative Neoplasm: A Bidirectional Mendelian Randomization StudyYang Li¹, Chen Jia², Ting Sun², Renchi Yang², Lei Zhang, MD³¹ Chinese Academy of Medical Sciences & Peking Union Medical College, Tianjin, China² Institute of Hematology & Blood Diseases Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College, Tianjin, China³ State Key Laboratory of Experimental Hematology, National Clinical Research Center for Blood Diseases, Haihe Laboratory of Cell Ecosystem, Tianjin Key Laboratory of Gene Therapy for Blood Diseases, CAMS Key Laboratory of Gene Therapy for Blood Diseases, Tianjin, China

Introduction: Mounting epidemiological and observational evidence supports the association between chronic inflammation and the development of myeloproliferative neoplasm (MPN). Despite ongoing research, the causal or biased nature of genetic associations with specific inflammatory biomarkers remains unclear. The objective of this study is to evaluate the impact of C-reactive protein (CRP) and systemic regulators of inflammation on MPN using a bidirectional Mendelian randomization approach.

Methods: Genetic associations with MPN were derived from a publicly available genome-wide association study (GWAS) comprising 1,086 cases and 407,155 controls of European ancestry. Additionally, data on inflammation were extracted from two GWASs focusing on CRP and cytokines. The primary analysis employed inverse-variance weighted Mendelian randomization (MR) as the statistical method. To validate the findings, various sensitivity analyses, such as MR-Egger, weighted median, and MR-pleiotropy residual sum and outlier (MR-PRESSO), were conducted simultaneously.

Results: The findings of our study indicate that decreased levels of macrophage-migration inhibitory factor (MIF, IVW estimate odds ratio [OR] per SD genetic cytokines change: 0.641; 95% CI: 0.427-0.964; P=0.032) and elevated levels of interleukin-2 receptor α (IL2R α , 1.377, 1.006-1.883; P=0.046) are associated with an elevated risk of MPN. Moreover, genetically predicted MPN is correlated with heightened levels of RANTES (IVW estimate β : 0.043, 95% CI: 0.002-0.084; P=0.039) and interleukin-10 (IL-10, 0.030, 0.001-0.060; P=0.041).

Conclusion: Our study provides evidence supporting the significant association between MIF and IL2R α with the etiology of MPN, while RANTES and interleukin-10 are more likely to be involved in MPN development. These findings offer valuable insights into the causal relationship between systemic inflammatory regulators and MPN, contributing to a better understanding of the etiology, prevention, and prognosis of MPN.

Disclosures No relevant conflicts of interest to declare.

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