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Opinion Article

The Role of Gut Microbiota in the Growth of Seven Common Hematological Tumors

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DESCRIPTION

Hematological malignancies are a diverse group of tumors that can arise from uncontrolled growth of hematopoietic and lymphoid cells at different stages of their maturation and differentiation. These tumors can affect the bone marrow, lymph nodes, and blood. Hematologic malignancies make up 6.5% of all cancers and roughly 7% of all newly diagnosed cancers worldwide, and their incidence is rising. Hematological malignancies with highly variable prognoses, persistent relapse after treatment, and long-term complications cause significant stress for patients and the healthcare system. The underlying causes and mechanisms of these diseases are still unknown, despite prior research showing the importance of immunosuppression, radiation, viruses, and carcinogenic chemicals in the development of hematologic malignancies. Thus, further research into the etiology of hematological malignancies and the development of novel treatment approaches are imperative. It has been demonstrated that the Gut Microbiome (GM) regulates many aspects of host homeostasis, such as inflammation, immunity, metabolism, and cardiovascular function. A growing body of research has revealed that the GM is essential to hematological malignancies. *Helicobacter pylori* infection was found in 92% of 110 patients with gastric Mucosa-Associated Lymphoid Tissue (MALT) lymphoma in a retrospective study. The majority of early-stage gastric MALT lymphomas can be cured with antibiotic management of *H. pylori* infection, according to more clinical research. Simultaneously, a number of clinical investigations discovered that, in contrast to healthy people, the GM of patients with hematologic malignancies exhibits dysbiosis. GM-derived metabolites, which function as signaling molecules and substrates for immune and metabolic responses, may change as a result of the dysbiosis of GM. This could then contribute to the development of hematologic malignancies. In all leukemia types studied, recent studies have shown a significant reduction in GM diversity that continues even after five years of survival. Reduced genetic diversity has also been noted in a leukemia mouse model where anticancer and antimicrobial prophylaxis was not used, despite the fact that these interventions are most likely to blame for the decline. Additionally, the microbiota-based approach is regarded as a therapeutic modality with promise. Nonetheless, more research is necessary to determine the precise role that various GM taxa play in hematologic malignancy. Mendelian Randomization (MR) is a statistical method for epidemiological research that assesses the causality of relationships between exposure and outcome by employing a set of genetic variants as an instrumental variable for the exposure. Since genetic variants are randomly assigned at fertilization and are therefore unaffected by environmental factors and self-selected lifestyle, one advantage of MR is that residual confounding can be minimized. The current study sought to investigate the possible causal relationship between GM taxa and seven prevalent hematological malignancies, including MM and related plasma cell neoplasms, ML, LL, FL, HL, DLBCL, and MPN. It did this by using MR analysis. Remarkably, the findings demonstrated a strong causative relationship between an increased risk of ML and a genetic propensity to the Oxalobacteraceae family. 22 GM taxa were also found to be potential risk factors for hematological malignancies in the study. The metabolome analysis of SCFAs revealed a decrease in butyrate levels in the intestinal contents of patients with Acute Myeloid Leukemia (AML), which consequently resulted in a compromised intestinal barrier and increased bloodstream absorption of Lipopolysaccharide (LPS). Furthermore, the addition of intestinal butyrate preserved the integrity of the intestinal mucosa and lessened the severity of AML, whereas the elevated levels of LPS accelerated the development of AML.

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