Unmasking viral sequences in human blood samples during graft-versus-host disease

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Video Byte

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Abstract

Primary viral infections and reactivations are common complications after allogeneic hematopoietic stem cell transplantation (allo-HSCT). Some allo-HSCT recipients develop graft-versus-host disease (GvHD) and must be highly immunosuppressed, making them more vulnerable to infection. In particular, weakly pathogenic or commensal viruses may cause illnesses in these patients yet remain undetected in the clinic. A new study sought to identify the viruses acquired by patients following allo-HSCT. Using metagenomics next-generation sequencing, they evaluated 25 adult allo-HSCT recipients from 2016 to 2019 with acute or chronic GvHD. During a period of immunosuppression with a median duration of 5.1 months, the GvHD mortality rate for these patients was 36%. Sequence analysis detected viral nucleotide sequences in 24 out of 25 patients, with ≥ 3 distinct viruses detected in 16 patients. The most prevalent viruses were Anelloviridae and human pegivirus-1, and clinically unrecognized viral infections were found in 28% of the patients evaluated. Although further research is needed to understand the significance of these infections, the results suggest that some patients with GvHD experience unrecognized viral infections following allo-HSCT.