EPSTEIN-BARR VIRUS GENOME DELETIONS IN EBV+ T/NK CELL LYMPHOPROLIFERATIVE DISEASES

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ABSTRACT

The main target cells for Epstein-Barr virus (EBV) infection and persistence are B lymphocytes, although T and NK cells can also become infected. In this paper we characterise the EBV present in 21 pediatric and adult patients treated in France for a range of diseases that involve infection of T or NK cells. Of these 21 cases, 5 pediatric patients (21%) and 11 adult patients (52%) had a Caucasian origin. In about 30% of the cases, some of the EBV genomes contain a large deletion. The deletions are different in every patient but tend to cluster near the BART region of the viral genome. Detailed investigation of a family, in which several members have persistent T or NK cell infection by EBV, indicates that the virus genome deletions arise or are selected in each individual patient. Genome sequence polymorphisms in the EBV in T or NK cell diseases reflect the geographic origin of the patient, not a distinct type of EBV (the 21 cases studied included examples of both type 1 and type 2 EBV infection). Using virus produced from type 1 or type 2 EBV genomes cloned in bacterial artificial chromosome (BAC) vectors, we demonstrate infection of T cells in cord blood from healthy donors. Our results would be consistent with transient infection of some T cells being part of the normal asymptomatic infection by EBV, which usually occurs in infants or young children.

Oral presentation preferred, please