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Letters to the Editor

Herpesvirus-like DNA in AIDS Kaposi's Sarcoma in Argentina

To the Editor: Recently, Chang et al. (1), using a new molecular biology technique termed *Representational Difference Analysis*, found herpesvirus-like DNA (KSHV) in AIDS patients with Kaposi's sarcoma (KS). The presence of KSHV DNA sequences suggests that a new human herpesvirus may be associated with KS. The 5′ end of the 1853-bp flanking region of KSHV (nucleotides 1 to 607) was found to have 66 and 67% homologies to the corresponding regions of the major capsid protein gene of Herpesvirus Saimiri (ORF25) and Epstein Barr virus (BcLF1), respectively, both members of the gammaherpesvirus family (1). This finding is an important breakthrough, because a sexually transmitted agent was suspected to cause KS. The putative virus was also detected in classical KS and in African endemic KS found in young black individuals from sub-Saharan regions (2). KSHV sequences have also been identified in KS tissues from Taiwanese (3) and French (4) patients.

Recently, Cesarman et al. (5) found KSHV DNA sequences in eight cases of body cavity-based lymphoma, a rare entity associated with AIDS, but not in other tumors, suggesting that this herpesvirus may be associated with tumors other than KS. Latin American countries have reported a large number of HIV-1-infected individuals, and since KS is the most common tumor found in patients with AIDS, a high prevalence of KS in these countries is expected. We sought to determine if KSHV sequences were also present in patients from Latin America and, if present, their degree of homology to the original published sequences. We PCR-amplified biopsy samples from four Argentinean AIDS patients. The patients were homosexual men with cutaneous KS. We used primers and PCR conditions, published by Chang et al. (1), which amplify a 233-bp from the KS-330 Bam fragment sequence of KSHV. All patients were strongly positive for the KSHV sequence. Two samples, directly sequenced by Sequenase peR Product Sequencing Kit (USB, Cleveland, Ohio, USA), were found to have a high degree of homology with the published sequence (94 and 95%, respectively). Our results from samples from Argentina, confirm the findings obtained in samples from the US, France, Africa, and Taiwan, suggesting that a distinct herpesvirus-like agent may be closely associated with KS. In addition, our DNA sequence analysis of these Argentinean samples indicates that the DNA sequence of this virus is very conserved, and similar strains can be found in AIDS-associated KS patients worldwide.

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