TITLE: MOLECULAR CHARACTERIZATION OF HUMAN GAMMAHERPESVIRUS 8 FROM HIV-INFECTED PATIENTS WITH KAPOSI'S SARCOMA IN BRAZIL

AUTHORS: LOPES, A.O.¹, DIAS, N.S.T.¹, NETTO, J.S.B.²; TOZETTO-MENDOZA, T.R.³, DE PAULA, V.S.¹.

INSTITUTIONS:

¹Laboratory of Molecular Virology, Oswaldo Cruz Institute, FIOCRUZ (Av. Brasil, 4365 - Manguinhos, Rio de Janeiro, RJ - CEP: 21040-900, Brasil).

²National Institute of Infectology Evandro Chagas, FIOCRUZ (Av. Brasil, 4365 - Manguinhos, Rio de Janeiro, RJ - CEP: 21040-900, Brasil).

³Laboratory of Virology (LIM52), Tropical Medicine of São Paulo Institute, São Paulo University (Avenida Dr. Enéas Carvalho de Aguiar, 470 - CEP 05403-000 - SP/São Paulo – Brasil).

ABSTRACT:

Human gammaherpesvirus 8 (HHV-8) is the etiologic agent of the Kaposi's sarcoma (KS), that is most severe and resistant in HIV-infected patients. HHV-8 has highly variable open reading frame (ORF) of 870 bp called ORFK1. ORFK1 genetic variation yields six major molecular clades (A, B, C, D, E, and F) each comprising several sub-clades that were described in specimens obtained from all around the world, all exhibiting clear ethnic and geographic clustering. Although an association between genetic diversity of HHV-8 and pathogenic potential in HIV-infected patients has been demonstrated in some studies, other studies failed to do so. Such inconsistencies may be partially attributed to the lack of information about this HHV-8 diversity in these individuals. Brazil is a country with a wide spectrum of ethnicity derived from migratory flows from Africa, Europe, Asia, and indigenous communities, but there is scant information about HHV-8 genotype. The aim of this study was to characterize HHV-8 isolates from HIV-infected patients living with Kaposi's sarcoma from Brazil by analysis of complete ORFK1 region. DNA was extracted from 85 blood and saliva samples. Complete ORFK1 gene was amplified by Nested PCR and sequenced in 25 samples, and were then subjected to phylogenetic analysis. Complete ORF K1 gene reference sequences were downloaded from GenBank and used to determine the HHV-8 genotypes. Phylogenetic analyses showed that genotypes C (C1. C3 and C7), A (A, A1 and A4), and B (B1) were present in 48%, 28% and 24% of cases, respectively. This research reveals predominance of genotype C and a broad spectrum of HHV-8 genotypes in HIV/KS patients from Brazil. This study contribute to a better understanding of the genetic diversity of HHV-8 strains circulating Brazilian patients, and will be important to further studies about association between genetic diversity of HHV-8 and pathogenic potential in HIV patients.

Keywords: Human gammaherpesvirus 8, genetic diversity, Kaposi's sarcoma.

Development Agency: CAPES; CNPq; FIOCRUZ.