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CARACTERIZAÇÃO MOLECULAR DO EPSTEIN-BARR
VIRUS (EBV) EM PACIENTES PORTADORES DE HIV,
EM TRATAMENTO, ATENDIDOS NO SISTEMA
HOSPITALAR DO SISTEMA PENITENCIÁRIO
DO ESTADO DE SÃO PAULO

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RESUMO

RODRIGUES, J. N. M. Epidemiologia e Caracterização Molecular do Epstein-Barr Virus (EBV) em Pacientes Portadores de HIV, em Tratamento, Atendidos pelo Sistema Hospitalar do Sistema Penitenciário do Estado de São Paulo. 2008. 71 f. Dissertação (Doutorado em Ciências) - Instituto de Ciências Biomédicas, Universidade de São Paulo, São Paulo, 2008.

O Epstein-Barr vírus (EBV) é a única espécie humana pertencente ao gênero *Lymphocryptovirus*. A transmissão ocorre através da saliva contaminada e geralmente ainda na infância. Nossa pesquisa analisou 165 amostras clínicas de pacientes, portadores de HIV, em tratamento com antiretrovirais, atendidos no Sistema Hospitalar do Sistema Penitenciário do Estado de São Paulo. Nossa abordagem foi pesquisar o EBV nas células mononucleares do sangue periférico, através das técnicas de PCR, *Nested-PCR* e seqüenciamento de nucleotídeos. Os resultados obtidos, indicaram que 11,51% (19) das amostras analisadas, apresentaram-se positivas para o EBV. Essas 19 amostras, foram seqüenciadas com *primers* específicos para a região da EBNA-1 (Epstein Barr Nuclear Antigen 1). As amostras foram alinhadas com o auxílio do DNASTAR. Ao alinharmos as amostras, encontramos uma troca de base (de G para A) em 7 amostras e essa troca não alterou a conformação da proteína EBNA-1. Na análise filogenética de nossas sequências com as depositadas no GenBank, foi possível observar dois grupos, que representam tipo 1 e o tipo 2 do EBV. 100% das amostras estudadas por nós foram identificadas como pertencentes ao grupo que caracteriza o tipo 2. Sendo assim, as 7 amostras que apresentaram a troca sugerem a origem um novo subtipo.

Palavras-chaves: Epstein-Barr vírus. EBNA-1. Seqüenciamento de nucleotídeos.

ABSTRACT

RODRIGUES, J. N. M. Molecular Characterization of Epstein-Barr Virus (EBV) in HIV-1 Patients in Treatment from the Hospitalar System in the Penitentiary System from São Paulo State. 2008. 71 p. Ph. D. Thesis (Microbiology) - Instituto de Ciências Biomédicas, Universidade de São Paulo, São Paulo, 2008.

The Epstein-Barr Virus (EBV) is the only species to the genus *Lymphocryptovirus* that infects humans. One of the possible route for its transmission thought by contaminated saliva and usually occurs in the childhood. This study analysed 165 clinical samples from HIV infected patients, treated by HARRT, attended in the Hospitalar System in the Penitentiary System from São Paulo State. The aim of this study was to search EBV in peripheral blood mononuclear cells by PCR, Nested-PCR and sequencing analysis. The results showed 11,51% of the analysed samples, positive for EBV. This samples, was sequenced with specifics primers from the EBNA-1 (Epstein Barr Nuclear Antigen 1) region. The samples were aligned by DNASTAR program. The aligned sequences showed the base conversion G to A in seven samples. This conversion caused no alteration in the EBNA-1 protein conformation. In the phylogenetic analysis the studied sequences with the sequences from GenBank was possible to observe two groups represented with type 1 and type 2 from EBV. 100% the samples studied was identified with the group characterized by the type 2 to EBV. So the seven samples showed the conversion, suggesting the origin of the one new subtype.

Key words: Epstein-Barr Virus. EBNA-1. Nucleotide Sequency.

1 INTRODUÇÃO

O Epstein-Barr vírus (EBV), também conhecido com Herpesvírus Humano tipo 4 (HHV-4), é um membro da família *Herpesviridae*, subfamília *Gammaherpesvirinae* e infecta segundo dados sorológicos, aproximadamente 90% da população mundial. A transmissão ocorre através da saliva contaminada e geralmente ocorre ainda na infância. Após a infecção primária o vírus permanece no indivíduo por toda a vida. O EBV possui tropismo para linfócitos B e células epiteliais, podendo coexistir na forma latente e replicativa (ou lítica) (SIXBEY et al., 1983; RAAB-TRAUB e WEBSTER-CYRIAQUE, 1997; MURRAY e YOUNG, 2000).

O EBV foi o primeiro vírus humano a ser associado à carcinogênese (THOMPSON e KURZROCK, 2004). Desde a sua descoberta, vem sendo associado a várias doenças e atualmente tem sido muito estudado devido ao seu potencial oncogênico (FARRELL et al., 1997; PAGANO et al., 2004; AMON e FARRELL, 2005). Investiga-se a sua associação a doença de Hodgkin, doença proliferativa ligada ao cromossomo X, linfoma não-Hodgkin, linfoma de células T periféricas, carcinoma nasofaríngeo, carcinoma gástrico, adenocarcinoma de estômago e carcinoma de células escamosas (HIGA et al., 2002; LOPES et al., 2003; BUSSON et al., 2004; WILLIAMS e CRAWFORD, 2005). Além destas, o EBV está fortemente associado ao linfoma de Burkitt endêmico e é comprovadamente o agente etiológico da mononucleose infecciosa e da leucopenia pilosa oral (EPSTEIN et al., 1964; GREENSPAN et al., 1984). O ciclo viral no interior do hospedeiro, inclui um período de latência, cujo estado pode permanecer anos, e outro de replicação, no qual pode emergir em quantidade suficiente para causar estimulação do sistema imune (MCCLAIN et al., 2003).

São conhecidos dois tipos de EBV: o tipo 1 (EBV-1 ou EBV-A) e o tipo 2 (EBV-2 ou EBV-B). Sua identificação é possível devido às diferenças existentes nas seqüências de DNA que codificam os抗ígenos nucleares do EBV (EBNA). Os dois genótipos de EBV exibem variantes epidemiológicas. Estudos sorológicos descrevem que o EBV tipo 1 é predominante nas regiões ocidentais e o tipo 2 em regiões endêmicas da África e em pacientes soropositivos para HIV-1. Sabe-se que *in vitro*, o EBV-1 tem melhor capacidade de se estabelecer e induzir a proliferação celular em cultura de linfócitos B (JILG et al., 1990; GRATAMA e ERNBERG, 1995; KAHNIN et al., 1996, COHEN et al., 2000).

Sabe-se que infecções causadas por genótipos diferentes de um mesmo vírus podem resultar em respostas diferentes a um determinado tratamento (DE COCK et al., 1993; ALTER et al., 1999; LAL et al., 2005). Alguns estudos avaliam a prevalência, as diferenças genômicas e a comparação do tipo de infecção que os EBV tipo 1 e 2 desenvolvem nas diferentes lesões a ele associadas, por meio de técnicas de biologia molecular, como a reação em cadeia pela polimerase (polymerase chain reaction – PCR) e sequenciamento genômico. Estas técnicas permitem a identificação do genoma viral em qualquer tipo de tecido estando o vírus em fase latente ou lítica (OSHIMA et al., 1999, WALLING et al., 2004, CORVALAN et al., 2005).

O papel da infecção do EBV, seus mecanismos de ação de patogêneses e a interação com o hospedeiro ainda não são bem conhecidos. Além disso, estudos de genotipagem do EBV associados á lesões orais ou dérmicas em pacientes imunocomprometidos ou portadores de HIV são raros e ainda não se tem de forma estabelecida a existência da prevalência de um dos tipos de EBV nessas patogêneses.

9 CONCLUSÕES

1. Nossos dados mostram que o EBV está presente em pacientes portadores de HIV, em tratamento com a Terapia Antiretroviral de Alta Atividade.
2. Nosso estudo demonstrou a importância da análise genotípica do EBV, dando o incentivo inicial para estudos futuros que possam esclarecer o desenvolvimento de patogêneses que ainda não estão bem esclarecidas em relação á biologia do vírus.
3. Pelo sequenciamento parcial do gene da proteína EBNA1, foi possível diferenciar os dois tipos (1 e 2) do EBV, mostrando que nessa população está em circulação o tipo 2. Além disso, conseguimos encontrar uma variação em nossos isolados que sugerem o aparecimento de um novo subtipo.

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