

## PHYLOGENETIC ANALYSIS OF THE LMP1 REGION OF EPSTEIN-BARR VIRUS IN CANCER PATIENTS FROM THE STATE OF PARÁ

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**Introduction:** Epstein-Barr virus (EBV) is a ubiquitous human herpesvirus that infects over 90% of the global population and is etiologically associated with a variety of human neoplasms, including nasopharyngeal carcinoma (NPC) and gastric cancer (GC). Among the most studied regions of the EBV genome is latent membrane protein 1 (LMP1), recognized for its crucial role in cell transformation, immune modulation, and oncogenesis. Investigating the genetic variability of this region may provide insights into the pathogenic mechanisms of the virus and contribute to the molecular surveillance of circulating strains, especially in high-incidence areas such as northern Brazil.

**Objectives:** To analyze the genetic diversity and evolutionary relationships of complete LMP1 region sequences of EBV isolated from oncology patients. **Methodology:** This is an analytical study involving 26 adult patients diagnosed with NPC and GC between July 2023 and August 2024. Clinical care was provided at João de Barros Barreto University Hospital and Ophir Loyola Hospital, both located in Belém, Pará. Clinical samples were collected using oropharyngeal swabs, and DNA was extracted using the Extracta 96 system. EBV detection was performed using real-time polymerase chain reaction (qPCR). The LMP1 region was sequenced using the Sanger method. Phylogenetic analysis was conducted using IQ-TREE software version 2.2.0, applying the maximum likelihood method. The study was approved by the Research Ethics Committee (CAAE: 68356923.4.0000.5634). **Results:** Phylogenetic analysis revealed substantial genetic diversity in the EBV LMP1 region among the analyzed samples. The resulting tree identified five main clades: Ia, Ib, Ic, IIa, and IIc. Clades Ia and Ib showed greater genetic proximity, while Ic, IIa, and IIc formed more divergent clusters. Notably, sample 55 BF presented an isolated branch, suggesting distinct ancestry. The observed diversity may be associated with differences in viral tropism, immune escape, or oncogenic potential among strains. **Conclusions:** High genetic variability was identified in the EBV LMP1 region in cancer patients from the state of Pará. The clustering into distinct clades indicates the co-circulation of multiple viral lineages, which may influence clinical outcomes and host-pathogen interactions. These findings reinforce the

Importance of regional molecular surveillance and highlight the utility of phylogenetic tools for mapping EBV evolution.

**Keywords:** Neoplasms; Molecular Diagnostic Techniques; Epstein-Barr Virus Infections.