

A molecular study on the evolution of a subtype B variant frequently found in Brazil

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ABSTRACT. In spite of the remarkable diversity of HIV-1 *env* genes, several amino acids are extremely conserved, probably due to functional constraints. One example is the proline found at the second position of the GPGR motif. Several viruses, however, bear substitutions at this site, for instance, GWGR subtype B variant. GWGR viruses are described in Brazil since the beginning of the epidemics, but the extent of their dispersion or the geographical origin of the variant remains unknown. In the present study, phylogenetic trees were constructed in order to study the origin and spread of this variant. All GWGR sequences as well as a subset of subtype B sequences available were included in the analyses. Analyses of differential selection were also performed on GWGR and non-GWGR sequences in order to unveil evolutionary novelties due to the action of positive selection. Although the GWGR variant was found at least in 23 countries, its expansion probably has a single origin, and Brazil is the epicenter.

Key words: HIV-1; Subtype B; GWGR variant; Molecular evolution; Origin; Selective pressure