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Mapping epitope candidates from HIV-1 Brazilian sequences for vaccine Development

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Short Abstract: Epitope mapping presented on HIV proteins provide information for vaccine development. All Brazilian HIV sequences were collected from GenBank for epitope mapping. The HIVbase epitope mapping showed 30 CD8 and eight CD4 epitopes with high frequency. The objective of this work is perform molecular characterization of Brazilian HIV env sequences

Long Abstract:

The mapping of the epitopes presented on diverse virus proteins can provide information for vaccine development. The use of bioinformatics softwares to data analyze is an easier way to search epitopes for HIV epidemic study, and it will provide important information about the HIV epidemic characteristics in our country and to develop an effective vaccine. The objective of this study is perform the molecular characterization of the Brazilian HIV-1 env sequences, mapping into this region the possible previously related epitopes from Los Alamos Database. All sequences of Brazilian HIV-1 (3,813 sequences) were collected from GenBank and added in HIVbase Database for the epitope mapping analysis as described in the HIV Immunology and HIV/SIV Vaccine Databases 2003 from Los Alamos. We selected and analyzed only the env region, comprehending 2,644 sequences. The multiple alignment of these sequences was done using ClustalX software. Genedoc software was used to edit and translate the alignment, and the potential sites analyses were performed using Prosite tool. Besides, we have calculated the dN/dS ratio to suggest the positive selection pressure. The HIVbase epitope mapping showed 30 CD8 and eigth CD4 epitopes with a high frequency. The subtype B was the most conserved of the subtypes on C1 and C3 epitope regions, followed by subtype F. On V3loop region the most conserved was the subtype F, however none of the most frequent mutations had been associated with the loss of the N-glican site at this domain. This epitope conservation suggests that these regions have great importance for viral fitness and also suggest that these conserved regions are not exposed to the immune system pressure, in these Brazilian sequences. The epitope VPVWKEATTTL, associated with rapid progression allele, B35 , presented 100% of variation in the subtype C isolates and had low variation in non-C subtypes (18%), suggesting that this allele may be imposing selective pressure in this subtype. In this study, the functional regions responsible for N-glycosylation sites mapped in HIV-1 proteins were highly conserved. These sites are potentially important for these proteins function and their

exclusion could reduce the viral fitness. An ideal vaccine must contain epitopes to create immune pressure on virus functional regions that cannot escape. In addition, it is very important to continue mapping the genetic information of the circulating HIV-1 strains from Brazil