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MOLECULAR CHARACTERIZATION OF THE BRAZILIAN HTLV-1 SEQUENCES TO VACCINE DESIGN

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This study was developed to evaluate the molecular pattern of all Brazilian HTLV-1 *env* (n=15) and *pol* (n=37) nucleotide sequences through: physico-chemical analysis; protein potential sites determination and epitopes prediction, to the strategies development of vaccine. We could find twelve epitopes, in the *env* sequences, in twelve peptides, previously studied, as an MHC-I or MHC-II allelic specific binder. They have high similarity and a total variation of 9% and 18% for MHC-I and MHC-II epitopes respectively, comparing to the peptides. The physico-chemical analysis results demonstrated that the mutations present in the third, fifth, ninth, tenth and eleventh epitopes have changed the antigenicity profile. The potential domains showed that the D197N mutation in one epitope was responsible to the lost of a CK2- phosphorylation site, as the same time that one mutant epitope, characterized by both S246Y and V247I mutations, did not show the N-glycosilation site present in the savage epitope. The dn/ds ratio calculated was <1 and indicates that those sites are not been selected by escape pression. Similar epitopes prediction results were found to pol analysis because the bioinformatic tool used was able to predict epitopes in all (n=4) published peptides studied, with high similarity rates (Epitope Total Variation of 1,25%) as much for MHC-I how much for MHC-II. We could conclude that the *env* region, and these studied epitopes are very important to the virus fitness, they are very conservative and immune response target. So, it can be more analyzed, to create some vaccine strategies.

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