

**Poster C-3**  
**Phylogenetic Analysis Of The**  
**Mitochondrial DNA HVS2 Loci.**



**Authors:**

Thiago J Santana (*LASP/FIOCRUZ*)  
Flora M.C. Fernandes (*LASP/FIOCRUZ*)

**Short Abstract:** HVS2 is a D-loop hypervariable region of the mtDNA. We analyzed 346 sequences of HVS2 (297bp). Phylogeny was carried out using maximum likelihood, and 13 haplotypes lineages presented no resolution. The aim of the presente work is to analyze HVS2 polymorphism involving HTLV-1+ and - individuals for prevention programs.

**Long Abstract:**

The human mtDNA is a non recombinant haploid genome with maternal inheritance. Evolutionary relationships between mtDNA haplotypes might be subjected to phylogenetic analyses. HVS2 is a hypervariable region of the D-loop and specific mutations of HVS2 are used to identify haplotypes that belong to different haplogroups. These variations have been used in population genetic and evolutionary studies. Here we analyzed 346 sequences of HVS2 collected in the NCBI. After the alignment edition, 297 bp were selected and 55 haplotypes were identified. The alignment and its edition were carried out with ClustalX and BioEdit softwares. PAUP\* and Modeltest programs were employed in the phylogenetic analyses. After the Likelihood Ratio Test (LRT), we found the K2P plus I and Gamma nucleotide substitution model as the best one for our dataset ( $I=0.6363$  and  $\alpha$  parameter= $0.2285$ ). The likelihood value was  $-\ln L=778.8850$ . The algorithm "star decomposition" was used to the tree reconstruction. The unrooted tree showed that at least 13 haplotypes lineages presented no phylogenetic resolution, forming a single polytomy. On the other hand, the other presented a evolutionary dicotomic profile. The aim of the presente preliminary work is to analyze HVS2 polymorphism involving HTLV-1 infected and non infected individuals. Now we are sequencing HVS2 from HTLV+ individuals from Salvador, Bahia. According to Dourado and collaborators, in Brazil, a nationwide survey donors from 5 state capitals demonstrated that the highest rate of HTLV-1 prevalence is found in Salvador, Bahia. This way this work could be a contribution for prevention programs. Grants from FAPESB.