

Poster C-2

Phylogenetic Analysis On Five STR- Loci Of Chromosome Y In Homo Sapiens Sapiens, Pan Troglodytes And Macaca Tonkeana



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Short Abstract: Phylogenetic analyses were conducted using five STR-loci of chromosome Y: DSY19, DSY385a-b, DSY391a-b. We used sequences from NCBI. Maximum likelihood approach was employed. In general, different species formed clades well supported except in the case of DSY391a in which human and chimpanzee were in the same clade.

Long Abstract:

In the last decade, a set of highly polymorphic chromosome Y specific microsatellites (STR – short tandem repeat) became available for forensic, population genetics and evolutionary studies. These markers show genetic Y-chromosomal heterogeneity within and between populations and seem to be very useful to trace back human evolutionary processes at a historical time-scale, i.e. delineating recently split, thus still closely related populations. In the present work, we analyzed five variable STR-loci of chromosome Y: DSY19, DSY385a and b, DSY391a and b. Our main objective is to compare specific mutations involving HTLV infected and non infected individuals. First, we used sequences from the NCBI. The analyses were conducted by the alignment by eye of the sequences employing the ClustalX and BioEdit softwares. PAUP* and Modeltest were used for the LRT (Likelihood Ratio Test) and the phylogenetic tree rebuilding. Our results showed, for each STR: DSY19 – five haplotypes (198 bp), all from *H. sapiens sapiens*, evolutionary model HKY85 and tree score of 254.12418; DSY385a – seven haplotypes (396 bp), all from *H. sapiens sapiens*, model F81+I, $-\ln L=502.8864$ and $I=0.9821$; DSY385b – six haplotypes (858 bp), two from *H. sapiens sapiens* and four from *Pan troglodytes*, model HKY85, $-\ln L=1248.1533$; DSY391a – 13 haplotypes (303 bp), two from *H. sapiens sapiens*, two from *Pan troglodytes*, nine from *Macaca tonkeana*, model HKY85, $-\ln L=3758.9863$; DSY391b – seven haplotypes (287 bp), five *H. sapiens sapiens*, two from *Pan troglodytes*, model F81, $-\ln L=473.2432$. DSY19, no resolution was found in the phylogenetic tree; For DSY 385a, we found a tree which showed high similarity between the haplotypes; DSY385b, two clades very consistent were found, one including all haplotypes from *Pan troglodytes* and other all haplotypes from *H. sapiens sapiens* results were the same with DSY391b; With DSY391a, sequences from *Macaca tonkeana* formed a clade very well supported and surprisingly two haplotypes, one from *H. sapiens sapiens* and one from *Pan troglodytes* composed another very well supported group. The next step of our work is to compare the STR haplotypes of chromosome Y from Brazilian HTLV infected individuals and the haplotypes studied here intending to examine the genetic and evolutionary relationships between them. GRANTS FROM FAPESB.