Phylogeny of Mexican HIV-1 protease-encoding nucleotide sequences (HxB2 positions 2253 to 2549).

Phylogenetic trees were reconstructed form nucleotide sequences using a Markov Chain Monte Carlo algorithm-based Bayesian analysis suite (BEAUti and BEAST) using a general time reversible (GTR) substitution model and log normal relaxed clock to produce 20 million sample trees which were simplified using a 10% burn-in to generate a single maximum clade credibility tree.