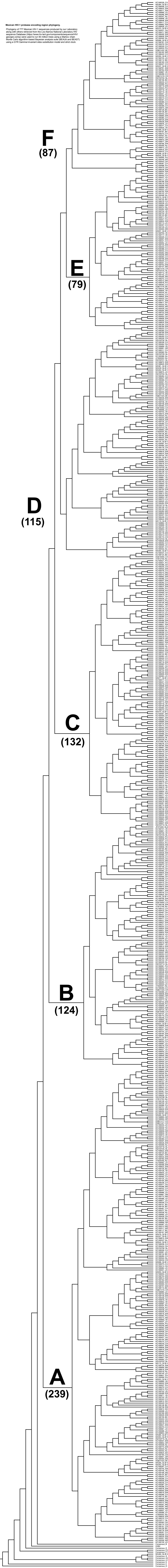


Mexican HIV-1 protease encoding region phylogeny.

Phylogeny of 777 Mexican HIV-1 sequences produced by our Laboratory along with others retrieved from the Los Alamos National Laboratory HIV sequence Database (<https://www.hiv.lanl.gov/components/sequence/HIV/geolgeo.comp>) were used to run 50 million trees using a Markov chain Monte Carlo algorithm-based Bayesian analysis suite (BEAUti and BEAST) using a GTR Gamma-invariant sites substitution model and strict clock.



F
(87)

E
(79)

D
(115)

C
(132)

B
(124)

A
(239)