**Table S3.** Molecular clock analysis of DENV-2 from all genotypes used in the study, showing the Effective Sample Size (ESS) for the studied parameters.

Best-fit model is shown in bold. GTR + Γ4 + I, General Time Reversible (GTR) substitution model with 4 categories of Γ plus invariable rates; 95% HPD, 95% highest probability density; TMRCA, time to the most recent common ancestor.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Model | Prior (mean) | Posterior (mean) | Marginal likelihood (mean ± stderr) | Substitution rate mean(10–4 substitutions/site/year [95%HPD]) | TMRCA (Root age)(mean no. of years [95%HPD]) |
| Bayesian coalescent prior: |  |  |  |  |  |
| **GTR + Γ + I, relaxed lognormal clock** | **-538.11** | **-8018.52** | **-7480.41 ± 0.34**  | **7.46** **(6.32–8.68)** | **120.61****(105.14–137.97)** |
| ESS | 340.02 | 427.164 | 961.58 | 1650.83 | 2177.96 |
|  |  |  |  |  |  |
| GTR + Γ + I, strict clock | -548.27 | -8030.81 | -7482.53 ± 0.35 |  7.58(6.43–8.79) | 118.88(103.93–135.03) |
| ESS | 1672.90 | 1002.79 | 922.43 | 2544.13 | 4535.78 |
| Constant size: |  |  |  |  |  |
| GTR + Γ + I, relaxed lognormal clock | -538.73 | -8022.66 | -7483.93 ± 0.33 | 7.49 (6.38–8.63) | 119.99(106.40–134.62) |
| ESS | 657.45 | 704.39 | 893.30 | 2447.27 | 3954.56 |
|  |  |  |  |  |  |
| GTR + Γ + I, strict clock | -549.27 | -8035.01 | -7485.73 ± 0.24 | 7.59(6.48–8.80) | 118.39(105.38–132.73) |
| ESS | 2768.95 | 1658.71 | 1814.31 | 4316.47 | 7202.24 |