**Table S4. Bayesian Coalescent Estimates inferred from the SNPs of the toxigenic Haiti *V. cholerae* O1 strains collected from 2010 - 2012**

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| --- | --- | --- | --- | --- | --- | --- |
| **Clock model a** | **Demographic model b** | **LmLik c** | **LmLik d** | **LogBF**  **SC vs. RC e** | **TMRCA f** | **Evolutionary rate g** |
| SC | Constant | -459.7 | -459.6 | 0 | Mar 2010  (Jul 2009, Aug 2010) | 9.32 10-2  (2.59 10-2, 0.190) |
| RC | Constant | -459.7 | -459.6 | Feb 2010  (May 2009, Jul 2010) | 9.29 10-2  (2.51 10-2, 0.188) |
| SC | Exponential | -456.9 | -456.9 | 0.9 | Apr 2010  (Sep 2009, Aug 2010) | 9.47 10-2  (2.87 10-2, 0.193) |
| RC | Exponential | -457.8 | -457.7 | Apr 2010  (May 2009, Sep 2010) | 9.77 10-2  (2.69 10-2, 0.207) |
| SC | BSP | -450.0 | -450.0 | 0.6 | Aug 2010  (Apr 2010, Oct 2010) | 9.58 10-2  (2.93 10-2, 0.195) |
| RC | BSP | -449.4 | -449.4 | Sep 2010  (Apr 2010, Oct 2010) | 9.69 10-2  (2.87 10-2, 0.200) |
| SC | Skyride | -455.9 | -455.8 | 1.0 | May 2010  (Feb 2010, Aug 2010) | 8.77 10-3  (2.81 10-2, 0.189) |
| RC | Skyride | -456.9 | -456.8 | May 2010  (Jan 2010, Aug 2010) | 8.85 10-2  (2.4 10-2, 0.180) |
| SC | Skygrid | -450.9 | -450.7 | 1.3 | Jul 2010  (Mar 2010, Oct 2010) | 0.1  (3.0 10-2, 0.200) |
| RC | Skygrid | -449.6 | -448.9 | Aug 2010  (Mar 2010, Oct 2010) | 0.1  (2.7 10-2, 0.200) |

1. Two molecular clock models were compared for each demographic model: strict (SC) versus relaxed uncorrelated lognormal clock (RC);
2. Five demographic models were compared: constant population size, exponential population size, and the non-parametric models Bayesian Skyline Plot (BSP), Bayesian Skyride, and Gaussian Markov randomfield (GMRF) Skygrid;
3. The log marginal likelihood (LmLik) obtained from stepping-stone implemented in BEAUti/BEAST 1.8.0;
4. The log marginal likelihood (LmLik) obtained from path-sampling implemented in BEAUti/BEAST 1.8.0;
5. The LogBF is the Bayes factor (in logarithmic scale) comparing the SC (null hypothesis) and RC (alternative hypothesis) models for each demographic model. LogBF<6 indicates strong evidence in favor of the null hypothesis;
6. TMRCA represents the time of the most common recent ancestor of the sampled toxigenic O1 *V. cholerae* strains estimated from the posterior distribution of trees inferred from the genome-wide SNP alignment. 95% high posterior density intervals (95%HPD) are given in parenthesis;
7. Median evolutionary rate estimate expressed in nucleotide substitutions/hqSNP site/year with 95% HPD given in parenthesis.