**Table S5.** **Summary of Bayesian estimates of population dynamics of WNV in humans in the US.**

|  |  |  |  |
| --- | --- | --- | --- |
| Molecular clock and demographic model  | Marginal Likelihood, mean | Mean substitution rate, (10-4 substitutions/site/year)  | Mean age of *tMRCA*, years  |
| S |  |  |  |
| BSP | -23507.39 | 4.84  | 15.82  |
| Constant | -23511.75 | 4.80  | 16.25  |
| Expansion | -23509.72 | 4.74  | 16.11  |
| Exponential | -23509.69 | 4.73  | 15.99  |
| Logistic  | -20509.47 | 4.72  | 16.06  |
|  |  |  |  |
| UCLN |  |  |  |
| **BSP** | **-23482.95** | **5.06**  | **15.57**  |
| Constant | -23485.52 | 5.09  | 16.27  |
| Expansion | -23485.12 | 4.97  | 15.96  |
| Exponential | -23485.50 | 4.97  | 15.72  |
| Logistic  | -23485.37 | 4.97  | 15.83  |

Dataset included strain IS-98, (n=62). Parameters calculated using BEAST 1.6.2. Best model is shown in bold.
BSP = Bayesian Skyline plot, S = strict clock, UCLN = uncorrelated lognormal clock, *tMRCA* = time to most recent common ancestor