Table S14. Parameters’ prior distributions used in data simulations. For more details, see *ms* documentation (available at http://home.uchicago.edu/rhudson1/source/mksamples.html).

|  |  |  |
| --- | --- | --- |
| Parameter | Prior uniform distribution | Prior uniform distribution after parameter restriction step |
| Ne1 | 2,500,000 – 9,000,000 | 2,500,000 – 4,000,000 |
| 16S mutation rate2 | 2 x 10-9 – 5 x 10-9 | - |
| ND2 mutation rate | 5 x 10-9 – 5 x 10-8 | - |
| SiaH mutation rate | 3 x 10-10 – 1.5 x 10-9 | - |
| Rhodopsin mutation rate | 1 x 10-10 – 1 x 10-9 | - |
| T1 (Mya) – scenario 1 (Plio-Pleistocene)3 | 0.12 – 5.333 | 2 – 5.333 |
| T2 (Mya) – scenario 1 (more recent colonization) | 0 – T1 | - |
| T1 (Mya) – scenario 2 (present-LIG) | 0 – 0.12 | 0.01 – 0.12 |
| T2 (Mya) – scenario 2 (LGM-LIG) | 0.021 – 0.12 | - |
| T3 (Mya) – scenario 2 (present-LGM) | 0 – 0.021 | 0.005 – 0.021 |
| Population bottlenecks4 | 0.01 – 0.2 | - |
| Exponential growth (α)5 | 0.25 – 0.9 | - |

1Effective population size prior distribution was based on information from the mitochondrial loci [16S and ND2 substitution rates (0.28% and 0.957% per million years, respectively) and theta intervals calculated by dnasp (16S = 9–24; ND2 = 21–52)].

2Mutation rates based on the 95% HPD obtained in \*BEAST analysis for each region.

3Divergence times (in million years). For data simulations, values were converted in coalescent units (τ = divergence time (in years)/generation length\*4Ne)

4Bottleneck intensity measured as the ratio of the source population (1 to 20%).

5 α = [-(1/τ)\*log(Ne before/ Ne after expansion)]. The interval represents a 10 to 75% of population growth since the time of expansion.