

Appendix. Bayesian skyline plots based on Beast analysis of the three populations included in the coalescent simulations: (A) Grenada, (B) St. Vincent, and (C) Trinidad. The analysis used the GTR+I+ Γ model of nucleotide substitution and the dataset was partitioned between genes via duplication of model parameters and MCMC operators. Tree prior selected was a coalescent Bayesian skyline assuming a constant model with three size groups. The posterior distribution of trees was estimated with a MCMC with 20 million steps, sampled every 1,000 steps, and a burn-in of 2 million steps.

