

Supplementary material

Appendix 1.

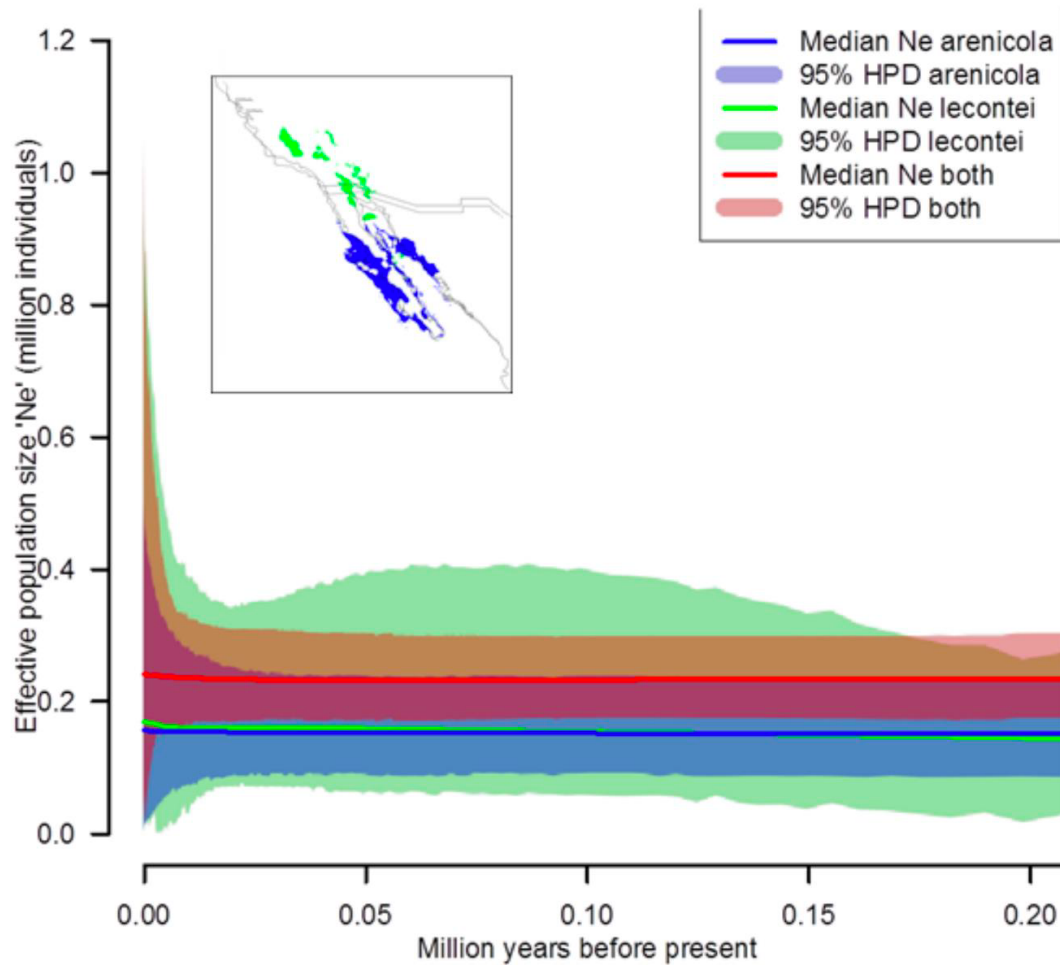


Figure A1. Historical demographics and effective population size (N_e) estimates from extended bayesian skyline plots (EBSs). Solid lines represent median N_e and their credibility intervals represent the 95% highest posterior density (HPD) for *Toxostoma lecontei lecontei* including 10 polymorphic loci and *T. l. arenicola* including 12 polymorphic loci in green and blue, respectively. Red lines and HPDs correspond to combined samples from both subspecies and 16 polymorphic loci (see main text for details). Dot-dashed map shows estimated distributions at the last glacial maximum computed separately for *T. l. arenicola* (blue) and *T. l. lecontei* (red) using ecological niche modeling.

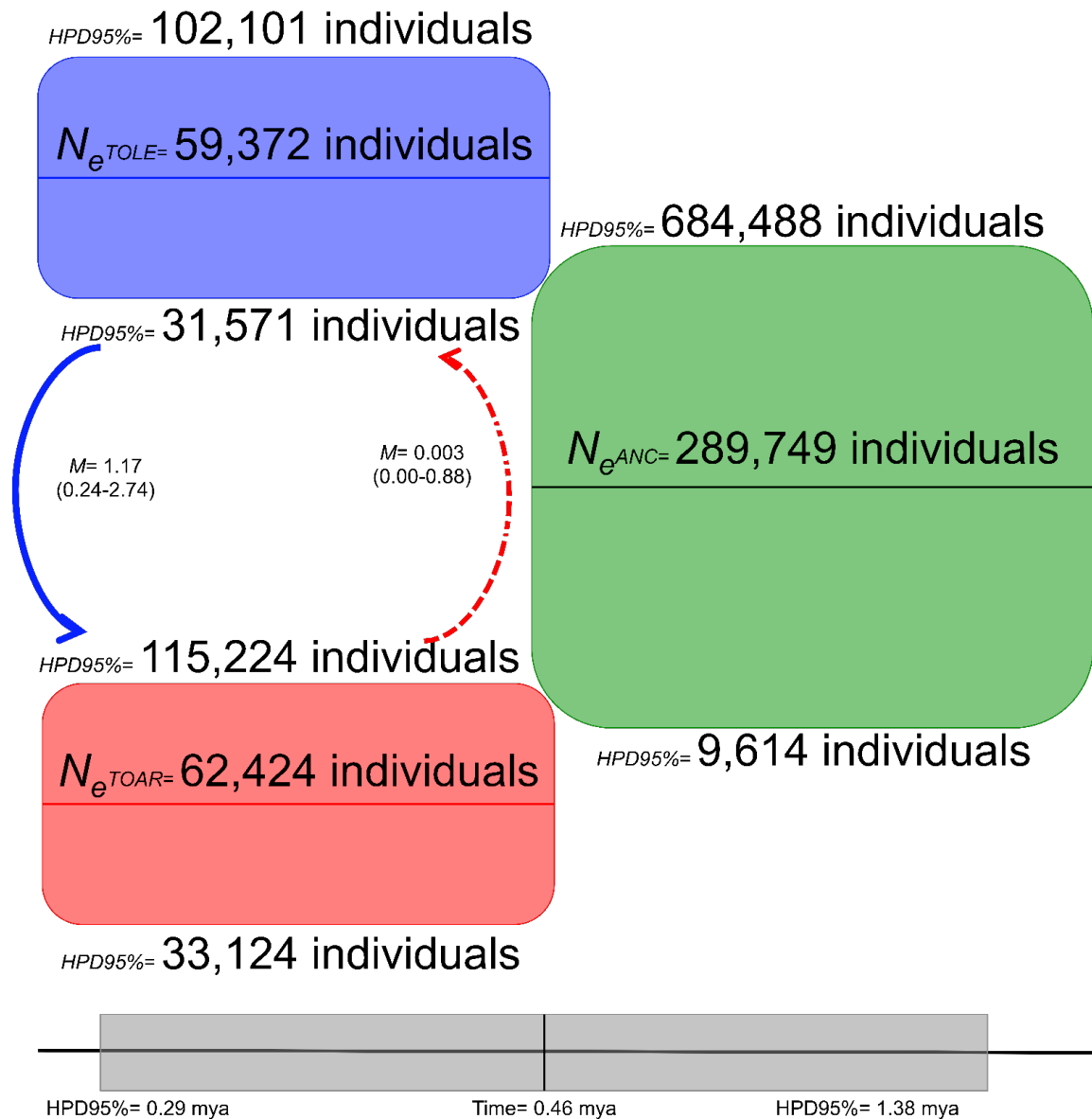


Figure A2. Effective population sizes (N_e) in number of individuals, splitting time (T) in millions of years ago (mya), and migration rates per generation (M) with their 95% highest posterior densities (HPD) estimated in IMa2p (Sethuraman et al. 2016). Colors represent ancestral population in green (N_{eANC}), *T. l. lecontei* in blue (N_{eTOLE}), and *T. l. arenicola* in red (N_{eTOAR}). A blue solid arrow represents a non-zero rate of individuals from *lecontei* migrating into *arenicola*. A red dashed arrow represents a rate of individuals from *arenicola* migrating into *lecontei* containing zero migrants (see text for transformed values).