

Table 7. Prior distributions for the parameters of the tested evolutionary models

Parameter	Model								Values		Distribution
	A F R I G	A F R E G	A S I G	A S E G	M R E 1 S	M R E 2 S	M R E B I G	M R E B E	Min.	Max.	
Effective population sizes											
Current size in Africa N_{AF}	X		X			X	X		5,000	10^6	Log-uniform
Current size in Asia N_{AS}	X		X			X	X		1,000	10^5	Log-uniform
Current size in America N_{AM}	X		X			X	X		1,000	10^5	Log-uniform
Current size in Africa N_{AF}^*		X		X				X	5,000	5×10^6	Log-uniform
Current size in Asia N_{AS}^*		X		X				X	1,000	10^6	Log-uniform
Current size in America N_{AM}^*		X		X				X	1,000	10^6	Log-uniform
Current size in Africa N_{AF}^{**}					X				100	10^6	Log-uniform
Current size in Asia N_{AS}^{**}					X				100	10^5	Log-uniform
Current size in America N_{AM}^{**}					X				100	10^5	Log-uniform
Archaic size in Africa N_{A-AF}	X	X	X	X					1,000	10^5	Log-uniform

Archaic size in Africa N_{A-AF}^*						X	X	X	100	10^4	Log-uniform
Archaic size in Asia N_{A-AS}	X	X	X	X		X	X	X	100	10^4	Log-uniform
Size during the peopling of the Americas N_{bAM}	X	X	X	X	X	X	X	X	2	5,000	Uniform
Size during modern out-of-Africa N_{bAS}	X	X	X	X					2	5,000	Uniform
Size during modern human speciation N_{bMH}	X	X	X	X			X	X	2	5,000	Uniform
Size during <i>H. erectus</i> out-of-Africa N_{bA-AS}			X	X	X	X	X	X	2	5,000	Uniform
Forward in time migration rates											
Current migration rate from Africa to Asia M_1					X	X	X	X	10^{-7}	10^{-3}	Log-uniform
Current migration rate from Asia to Africa M_2					X	X	X	X	10^{-7}	10^{-3}	Log-uniform
Ancient migration rate from Africa to Asia M_3						X	X	X	10^{-7}	10^{-3}	Log-uniform
Ancient migration rate from Asia to Africa M_4						X	X	X	10^{-7}	10^{-3}	Log-uniform
Timing											
Time for the peopling of the Americas T_{AM}	X	X	X	X	X	X	X	X	300	1,600	Uniform
Time for modern out-of-Africa T_{AS}	X	X	X	X					1,600	4,000	Uniform
Time for population increase in Asia T_{AS}^*						X	X	X	1,600	4,000	Uniform

Time for modern speciation T_{MH}	X	X	X	X					4,000	8,000	Uniform
Time for modern speciation T_{MH}^*						X	X	X	1,600	8,000	Uniform
Time for <i>H. erectus</i> out-of-Africa T_{A-AS}			X	X	X	X	X	X	3.2×10^4	4×10^4	Uniform
Duration of the peopling of the Americas bottleneck Δb_{AM}	X	X	X	X	X	X	X	X	1	50	Uniform
Duration of the modern out-of-Africa bottleneck Δb_{AS}	X	X	X	X					1	50	Uniform
Duration of the modern speciation bottleneck Δb_{MH}	X	X	X	X					1	500	Uniform
Duration of the modern speciation bottleneck Δb_{MH}^*							X	X	1	50	Uniform
Duration of the <i>H. erectus</i> out-of-Africa bottleneck Δb_{HE}			X	X	X	X	X	X	1	50	Uniform
Admixture level											
Proportion of archaic genes in current Asian population ADM			X	X					0.00	1.00	Uniform

Population sizes are in number of chromosomes, Times are in number of generations.

We used uniform priors for parameters with a search space made up of discrete values or of continuous values with one order-of-magnitude between the smallest and largest values, or for parameters where no prior information is available (e.g. the timing of all events, bottleneck population sizes, duration of the bottlenecks, and the fraction of the archaic chromosomes to invade the “modern” Asian population). We used a log-uniform distribution for parameters with a larger search space, such as the current population size, migration rates, and the “archaic” population sizes in Africa and Asia. This strategy implies that the sampling for these parameters is denser for smaller values, which seems reasonable since most studies suggest population sizes of a few thousand individuals

[Takahata N, Lee SH, Satta Y (2001) *Mol Biol Evol* 18:172-183], or low recurrent migration between continents [Rosenberg NA, Mahajan S, Ramachandran S, Zhao C, Pritchard JK, Feldman MW (2005) *PLoS Genet* 1:e70]. Relevant parameters for a given model are indicated with “X.”