

S5 Table. Parameter estimation for the most likely demo-genomic model (2M).

Parameter	Point estimate	Confidence Interval (95%)	Definition
NeNorth	10,136	4,051 – 38,040	Current haploid effective size of the North population
NeSouth	9,834	3,684 – 38,560	Current haploid effective size of the South population
TBottle	3,197	1,625 – 9,760	Age (generations BP) of the expansion onset
NeBottle_North	10,101	2,173 – 29,986	Haploid effective size of the North ancestral population
NeBottle_South	1,548	52 – 9,676	Haploid effective size of the South ancestral population
TSplit	5,844	3,425 – 21,943	Age (generations BP) of the divergence between the North and South ancestral populations
NeAncestral	10,464	146 – 40,450	Haploid effective size of the earliest population
M[N→S]	1.06E-4	1.17E-5 – 1.43E-4	Per-generation migration rate from North to South present populations
M[S→N]	3.48E-5	2.83E-5 – 2.48E-4	Per-generation migration rate from South to North present populations
MutationRate	4.15E-8	9.14E-9 – 8.35E-8	Number of neutral substitutions per site per generation