Supplementary Table S1: Demographic model parameter ranges, sampling density and rejection statistics

Parameter	Range[a] (units)	Growth		Bottleneck		Migration	
		M	S	M	S	M	S
Fold population expansion (N_{anc}/N_{curr})	0 – 10,000	42	33	22	19	11	11
Generations since growth (T_1)	0.05 – 1.2 ($4N_{curr}$ generations)	64	55	29	29	17	13
Fold population reduction during bottleneck ($N_{pre\text{-}bottle}/N_{anc}$)	1.25 – 10,000	---	---	4	4	---	---
Duration of bottleneck (T_{bot})	0.01 – 0.5 ($4N_{curr}$ generations)	---	---	4	5	---	---
Subpopulation size ($N_{unsampled}/N_{sampled}$)	0.1 – 1.0	---	---	---	---	9	8
Rate of migration ($4Nm$)	10^{-4} – 10 (migrants per generation)	---	---	---	---	10	10
Total number parameter combinations[b]		2,688	1,815	7,888	7,556	16,830	11,440
Percentage of simulations accepted[c]		9.74	10.66	9.42	10.17	8.28	9.47
Total number parameter combinations accepted[d]		432	267	1,269	1,062	88	149
Percentage of simulations accepted within accepted models[e]		10.39	11.64	10.40	11.66	11.29	13.63

[a] For each demographic model and molecular form, we searched the parameter space uniformly over coarse intervals. We then adjusted the parameter space to include a higher density of grid points (parameter combinations) in the region with the highest likelihood values in the first search and evaluated the grid a second time.

[b] Total number of parameter combinations searched in grid after increasing density of parameter values sampled in the second grid search.

[c] Percentage of all simulations that was not rejected within likelihood framework. Each locus was simulated 20,000 times for each parameter combination.

[d] Total number of parameter combinations that received likelihood value within 1.92 likelihood units of the maximum.

[e] Percentage of simulations within accepted models (see [d]) that were not rejected within the likelihood framework.

Supplementary Table S2: Population genetic re-analysis of Obbard et al. (2009) data under SNE and MLE migration models

		Tajima's *D*		
Locus	Population[a]	*D*	*SNE*[b]	*MLE*[c]
Control 4	Burkina Faso	0.16	0.3715	0.1894
	Kenya	0.34	0.3066	0.0622
Serpin 4C	Burkina Faso	-0.11	0.5093	0.6333
	Kenya	0.90	0.1575	**0.0372**
Control 5	Burkina Faso	-1.74	**0.0235**	**0.0160**
	Kenya	0.36	0.3123	0.1784
Serpin 5	Burkina Faso	-1.33	0.0737	0.0609
	Kenya	0.07	0.4158	0.2077
Control 6	Burkina Faso	-1.85	**0.0113**	**0.0076**
	Kenya	---	---	---
Serpin 6	Burkina Faso	-0.63	0.2943	0.3361
	Kenya	1.25	0.0836	**0.0069**
Control 16	Burkina Faso	-0.75	0.2569	0.2850
	Kenya	---	---	---
Serpin 16	Burkina Faso	-0.29	0.4284	0.5539
	Kenya	-0.77	0.2507	0.3504

[a] location where *An. gambiae* were sampled

[b] *P* values indicating probability of statistic when compared to null distribution simulated under standard-neutral equilibrium

[c] *P* values indicating probability of statistic when compared to null distribution simulated under MLE migration model

- Values in bold font were significantly inconsistent with the simulated null model at the nominal 5% threshold (no correction for multiple testing)