Supplemental Note S1

Plagnol and Wall (2006) considered a two-population model where there was migration between the populations, and then at some time in the past, the two populations merged into the same ancestral population. In ms (cf. Hudson 2002), two populations are joined (going backwards in time) using the “-ej” flag. This flag moves lineages from one population into the other population. In the version of ms used in Plagnol and Wall (2006) the “-ej” flag did not set the migration rate (going backwards in time) equal to zero at the time the two populations merged. Instead, the migration rate was left unchanged. The “-eM” flag would have to be used to explicitly set the migration matrix equal to zero at the time the two populations merged. Thus, in Plagnol and Wall (2006), it was assumed that all lineages were in the same ancestral population, when in reality, some of those lineages could migrate back to the other population. The net effect of this is to model population structure in the ancestral population without intending to do so. We point out that if there was no migration between the two populations at all, then the “-ej” flag would correctly move the lineages from one population to the other without allowing any migration into the second population—simply because there is no migration being allowed.

The effect that this error had on demographic parameter estimates is substantial (Table S1). In particular, the unaccounted for population structure tends to produce a skew in the frequency spectrum towards more common alleles. To counteract this, the Plagnol and Wall (2006) model estimated longer population growth (in both populations) in order for the simulated data to fit the observed frequency spectrum.

Table S1. Comparison of parameter estimates between Plagnol and Wall (2006) and this study.

Parameter	Plagnol and Wall (2006) estimate	Estimate from this study
g_1	80 Kya	25 Kya
g_2	10 Kya	0 Kya
t_b	60 Kya	30 Kya
b	130	160
T	130 Kya	120 Kya
m	$4 * 10^{-5}$	$7 * 10^{-5}$

Supplemental Table S2. Summary statistics for the actual data and for data simulated under the best-fit model. Total refers to summaries from the total sample. The middle 95% of simulated averages (based on 100 replicates of 222 loci) is given in parentheses.

	West Africans + Europeans		West Africans + East Asians	
	Data	Simulations	Data	Simulations
θ_W, African [1]	0.88	0.85 (0.82 – 0.88)	0.88	0.88 (0.85 – 0.90)
θ_W, non-African [1]	0.58	0.57 (0.55 – 0.60)	0.54	0.56 (0.54 – 0.59)
θ_W, total [1]	0.89	0.86 (0.84 – 0.89)	0.88	0.88 (0.86 – 0.91)
π, African [2]	0.79	0.76 (0.73 – 0.79)	0.79	0.77 (0.73 – 0.81)
π, non-African [2]	0.59	0.57 (0.54 – 0.61)	0.55	0.57 (0.54 – 0.61)
D, African [3]	-0.47	-0.47 (-0.41 – -0.54)	-0.47	-0.51 (-0.43 – -0.60)
D, non-African [3]	-0.08	-0.06 (-0.17 – 0.08)	-0.09	0.02 (-0.10 – 0.13)
D, total [3]	-0.73	-0.66 (-0.75 – -0.57)	-0.81	-0.72 (-0.81 – -0.64)
ρ, African [4]	0.41	0.44 (0.38 – 0.49)	0.41	0.46 (0.40 – 0.52)
ρ, non-African [4]	0.14	0.14 (0.12 – 0.15)	0.11	0.13 (0.11 – 0.15)
F_{ST} [5]	0.15	0.17 (0.16 – 0.18)	0.16	0.16 (0.15 – 0.18)

[1] cf. Watterson (1975). Average value per Kb.

[2] cf. Tajima (1983). Average value per Kb.

[3] cf. Tajima (1989). Average value per locus.

[4] cf. Hudson (2001). Median estimated value (across loci) per Kb.

[5] Average value across loci.

Supplemental Table S3. List of loci with significant S* values

European Locus name	Yoruba (w/Europe) Locus name	East Asia Locus name	Yoruba (w/E. Asia) Locus name
abl2 *	abcb1 **	abl2 *	abcb1 **
adh1c *	anapc10 **	adh1b *	anapc10 **
adh5 *	angpt17 *	atrx *	apex2 *
atrx *	apex2 *	blm *	atrx **
birc2 **	atrx *	ccl5 *	birc2 *
chrna4 *	capn3 *	cdk5r2 **	casp5 *
fdxr *	casp5 *	cyp1a2 *	cyp1a1 *
fgf5 *	ctnna1 **	ddit3 *	dut **
fmo5 *	cyp1a1 *	esrra *	fancd2 *
gsta4 *	dut **	fancf *	fmo4 *
hspa2 *	fancd2 *	fdxr *	gab1 *
ncoa3 *	fmo4 *	hspa2 *	hspa9b *
oxr1 ***	oxsr1 *	map2k4 *	mapk1 *
rpa3 *	prdx2 *	mapk1 *	msh5 *
rrm2b **	prdx3 *	mmp11 *	oxsr1 *
scara3 *	prkd1 *	mmp8 *	prdx2 *
sepp1 *	rad51l1 *	ncoa3 **	recql4 *
tp53bp1 ***	tdp1 *	oxr1 **	rrm2b *
tp53i3 *	tert *	oxsr1 *	spo11 *
tuba2 **	tjp1 *	rad1 **	tdp1 **

vnn2 *	tpo *	rpa3 **	tert *
	trex2 *	scara3 *	tjp1 **
	xrcc4 ***	sepp1 *	trex2 *
		sirt1 *	ucp2 *
		smarcb1 *	xrcc4 **
		tbx1 *	
		tp53bp1 ***	
		tp53i3 *	
		ube2v2 *	
		vnn2 *	

* $p < 0.05$

** $p < 0.01$

*** $p < 0.002$

Supplemental Table S4a. Estimated parameter values for the profile likelihood curve for *a* for the Yoruba-European simulations. g_1, g_2, t_b and T are given in units of 1,000 years ago. Likelihoods were estimated using 5 * 10^6 replicates.

								Non-Afr	Afr.
a	g_1	g_2	t_b	b	T	m	Lik	S* p-value	S* p-value
0	25	0	30	160	120	7e-05	-860.054	$4.81 * 10^{-3}$	$2.12 * 10^{-8}$
0.02	25	0	30	160	100	7e-05	-858.255	$4.29 * 10^{-2}$	$5.95 * 10^{-9}$
0.04	25	0	30	160	100	7e-05	-857.136	> 0.1	$2.85 * 10^{-9}$
0.06	30	0	30	180	80	7e-05	-856.295	> 0.1	$1.61 * 10^{-9}$
0.08	30	0	30	160	80	7e-05	-855.456	> 0.1	$2.38 * 10^{-11}$
0.1	35	0	35	200	60	7e-05	-854.834	> 0.1	$9.93 * 10^{-11}$
0.12	35	0	35	200	60	7e-05	-854.053	> 0.1	$8.63 * 10^{-11}$
0.14	35	0	35	200	60	7e-05	-853.687	> 0.1	$2.18 * 10^{-11}$
0.16	35	0	35	200	60	7e-05	-854.163	> 0.1	$2.25 * 10^{-11}$
0.18	35	0	35	200	60	7e-05	-854.765	> 0.1	$7.23 * 10^{-12}$
0.2	35	0	35	200	60	7e-05	-855.571	> 0.1	$9.69 * 10^{-12}$
0.22	40	0	40	220	60	7e-05	-857.094	> 0.1	

Supplemental Table S4b. Estimated parameter values for the profile likelihood curve for *a* for the Yoruba-East Asian simulations. g_1, g_2, t_b and T are given in units of 1,000 years ago. Likelihoods were estimated using 5 * 10^6 replicates.

								Non-Afr	Afr.
a	g_1	g_2	t_b	b	T	m	Lik	S* p-value	S* p-value
0	35	0	30	160	80	5e-05	-827.279	$4.21 * 10^{-4}$	$1.62 * 10^{-12}$
0.005	35	0	30	180	60	5e-05	-823.459	$3.46 * 10^{-4}$	$1.14 * 10^{-10}$
0.01	35	0	30	180	60	5e-05	-821.946	$6.57 * 10^{-3}$	$2.54 * 10^{-11}$
0.015	40	0	30	180	60	5e-05	-821.875	$2.27 * 10^{-2}$	$1.18 * 10^{-11}$
0.02	40	0	30	180	60	5e-05	-822.522	> 0.1	$2.03 * 10^{-11}$
0.025	40	0	30	180	60	5e-05	-824.133	> 0.1	$1.12 * 10^{-11}$
0.03	40	0	30	180	60	5e-05	-826.424	> 0.1	$4.71 * 10^{-12}$

Supplemental Note S5

We present ms command lines used for producing simulated 25 Kb regions under our best-fit models. Briefly, the –t flag specifies θ, -r specifies ρ, -I specifies the migration rate, -g and –eg specify growth parameters, -en specifies bottleneck parameters, and –ej and –eM specify the population split time. Time is scaled in units of $4N_0$ generations, which corresponds to 10^8 years. For further details, please see Hudson (2002).

The ms command line for simulating a 25 Kb region under the best-fit model without ancient admixture (*a* = 0) for the West African – European data is

```
ms 68 1 –t 1744.1 –r 627.9 25000 –I 2 24 44 280 –g 1 18420.7 –n 2 0.01 –eg 0.00025 1
0. –en 0.0003 2 6.25e-05 –en 0.00031 2 0.01 –ej 0.0012 2 1 –eM 0.0012 0
```

The ms command line for simulating a 25 Kb region under the best-fit model with ancient admixture (a = 0.14) for the West African – European data is

```
ms 68 1 –t 1719.5 –r 619. 25000 –I 2 24 44 280 –g 1 13157.6 –n 2 0.01 –eg 0.00035 1
0. –en 0.00035 2 5e-05 –en 0.00036 2 0.01 –es 0.0005 2 0.86 –en 0.0005 3 0.01 –ej
0.0006 2 1 –eM 0.0006 0 –ej 0.004 3 1
```

The ms command line for simulating a 25 Kb region under the best-fit model without ancient admixture (*a* = 0) for the West African – East Asian data is

```
ms 72 1 –t 1802.8 –r 649.0 25000 –I 2 24 48 200 –g 1 13157.6 –n 2 0.01 –eg 0.00035 1
0. –en 0.0003 2 6.25e-05 –en 0.00031 2 0.01 –ej 0.0008 2 1 –eM 0.0008 0
```

The ms command line for simulating a 25 Kb region under the best-fit model with ancient admixture (a = 0.015) for the West African – East Asian data is

```
ms 72 1 –t 1750.1 –r 630.0 25000 –I 2 24 48 200 –g 1 11512.9 –n 2 0.01 –eg 0.0004 1
0. –en 0.0003 2 5.556e-05 –en 0.00031 2 0.01 –es 0.0005 2 0.985 –en 0.0005 3 0.01 –
ej 0.0006 2 1 –eM 0.0006 0 –ej 0.016 3 1
```