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Supplemental Information

***Plasmodium falciparum* Accompanied**

the Human Expansion out of Africa

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Table S1. Polymorphism of *P. falciparum* Genes in the Nine Populations Analyzed

Locus		Africa		Southeast Asia		Oceania			North America		Worldwide
		Tanzania	Ghana	Thailand	Philippines	Papua New Guinea	Solomon Is.	Vanuatu	Brazil	Venezuela	
Perca (3630 bp)	N	69	68	62	53	59	51	60	42	10	514
	S	30	13	10	4	5	4	3	9	3	49
	θ_{π}	0.00068 ± 0.00005	0.00042 ± 0.00006	0.00025 ± 0.00003	0.00024 ± 0.00003	0.00015 ± 0.00003	0.00010 ± 0.00004	0.00024 ± 0.00005	0.00073 ± 0.00006	0.00021 ± 0.00009	0.00041 ± 0.00002
	θ_{ξ}	0.00172 ± 0.00054	0.00085 ± 0.00033	0.00055 ± 0.00002	0.00024 ± 0.00013	0.00044 ± 0.00015	0.00024 ± 0.00014	0.00017 ± 0.00010	0.00058 ± 0.00025	0.00029 ± 0.00017	0.00198 ± 0.00029
	dS	0.00148 ± 0.00072	0.00103 ± 0.00071	0.00062 ± 0.00040	0.00049 ± 0.00036	0.00042 ± 0.00025	0.00030 ± 0.00023	0.00039 ± 0.00037	0.00111 ± 0.00072	0.00073 ± 0.00051	0.00088 ± 0.00042
	dN	0.00047 ± 0.00019	0.00026 ± 0.00011	0.00015 ± 0.00008	0.00018 ± 0.00018	0.00008 ± 0.00005	0.00005 ± 0.00004	0.00020 ± 0.00015	0.00063 ± 0.00028	0.00007 ± 0.00007	0.00029 ± 0.00009
		dS>dN: P= 0.090	dS>dN: P= 0.190	dS>dN: P= 0.133	dS>dN: P= 0.233	dS>dN: P= 0.095	dS>dN: P= 0.146	dS>dN: P= 0.332	dS>dN: P= 0.273	dS>dN: P= 0.102	dS>dN: P= 0.087
Act1 (1413bp)	N	72	67	63	53	64	51	77	42	10	519
	S	7	7	2	2	3	2	1	1	1	14
	θ_{π}	0.00047 ± 0.00007	0.00059 ± 0.00008	0.00037 ± 0.00006	0.00038 ± 0.00003	0.00032 ± 0.00004	0.00050 ± 0.00006	0.00015 ± 0.00004	0.00036 ± 0.00002	0.00025 ± 0.00011	0.00040 ± 0.00002
	θ_{ξ}	0.00102 ± 0.00039	0.00119 ± 0.00045	0.00028 ± 0.00020	0.00031 ± 0.00022	0.00042 ± 0.00024	0.00031 ± 0.00022	0.00014 ± 0.00014	0.00016 ± 0.00016	0.00025 ± 0.00025	0.00145 ± 0.00039
	dS	0.00211 ± 0.00148	0.00269 ± 0.00179	0.00174 ± 0.00173	0.00185 ± 0.00171	0.00151 ± 0.00130	0.00245 ± 0.00181	0.00073 ± 0.00072	0.00176 ± 0.00175	0.00123 ± 0.00123	0.00190 ± 0.00160
	dN	0.00005 ± 0.00003	0.00048 ± 0.00047	0.00002 ± 0.00002	0	0.00002 ± 0.00002	0	0	0	0	0.00002 ± 0.00001
		dS>dN: P= 0.074	dS>dN: P= 0.061	dS>dN: P= 0.144	dS>dN: P= 0.128	dS>dN: P= 0.114	dS>dN: P= 0.083	dS>dN: P= 0.156	dS>dN: P= 0.145	dS>dN: P= 0.145	dS>dN: P= 0.080
PercaHsd1 (5043 bp)	N										
	θ	0.00063 ± 0.00004	0.00048 ± 0.00006	0.00029 ± 0.00003	0.00028 ± 0.00003	0.00020 ± 0.00003	0.00022 ± 0.00004	0.00022 ± 0.00004	0.00062 ± 0.00005	0.00022 ± 0.00008	0.00043 ± 0.00002
		0.00153 ± 0.00025	0.00096 ± 0.00022	0.00048 ± 0.00014	0.00026 ± 0.00011	0.00043 ± 0.00013	0.00026 ± 0.00011	0.00016 ± 0.00008	0.00047 ± 0.00015	0.00028 ± 0.00014	0.00188 ± 0.00024

N: Number of sampled isolates

S: Number of segregating sites

θ_{π} : Average number of pairwise nucleotide differences

θ_{ξ} : Standardized number of polymorphic sites per site

dN: Mean number of synonymous substitutions

dS: Mean number of non-synonymous substitutions

Table S2. Entomological Infection Rates (EIR) Obtained from the Literature

Country	Malaria	Entomological Inoculation Rate	Reference *
	endemicity	(bites/year)	
Tanzania	Hyper to holo	285	1, 2
Ghana	Hyper	418	1, 3
Thailand	Hypo	0.4 **	4
Philippines	Hypo to meso	5 **	5
Papua New Guinea	Meso to hyper	26 **	6
Solomon Islands	Meso to hyper	509	7
Vanuatu	Hypo to hyper	4 (in Santo island) **	8
Brazil	Hypo	Not available	
Venezuela	Hypo	Not available	

*References:

1. Hay SI, et al. (2000) *Trans R Soc Trop Med Hyg* 94:113-127
2. Kelly-Hope LA and McKenzie FE *Malaria J* (2009) 8:19
3. Gemperli, A. et al., (2006) *Trop Med Int Health* 11:1032-1046
4. Lexemburger C, et al. (1996) *Trans R Soc Trop Med Hyg* 90:105-111
5. Oberst RB, et al., (1988) *Phil J Microbiol Infect Dis* 17:41-45
6. Benet A, et al. (2004) *Am J Trop Med Hyg* 71:277-84
7. Hii JL. et al. (1993) *Med Vet Entomol* 7:333-338
8. Williams RN, et al, (1995) *Ann Trop Med Parasitol* 89: 305-307.

**Values from the literature were halved in cases where numbers reported joint EIR for *P. falciparum* and *P. vivax*.

Table S3. Median Values and 90% Credibility Intervals of the Stepping Stone Parameters' Posterior Distributions, Given a Split between the *Plasmodium* Species Either at 2.5 or 6 Mya

Parameter	Split 2.5 Mya			Split 6 Mya		
	Median	90% CI		Median	90% CI	
t	41,000	19,000	77,000	78,000	33,000	96,000
m	0.0016	4×10^{-6}	0.1	0.0020	6×10^{-5}	0.05
r	0.063	0.004	0.6	0.10	0.005	0.8
c	2.0×10^{-4}	5×10^{-6}	0.10	1.3×10^{-4}	4×10^{-6}	0.04
K	50,000	5×10^2	6×10^5	100,000	2×10^3	8×10^5
c_0	0.0080	3×10^{-5}	0.5	0.0040	2×10^{-5}	0.4
K_0	32,000	2×10^2	3×10^5	100,000	8×10^3	5×10^5
cK	13	1	200	16	1	250
c_0K_0	130	3	2×10^4	320	3	5×10^4

The various parameters are defined in the methods.

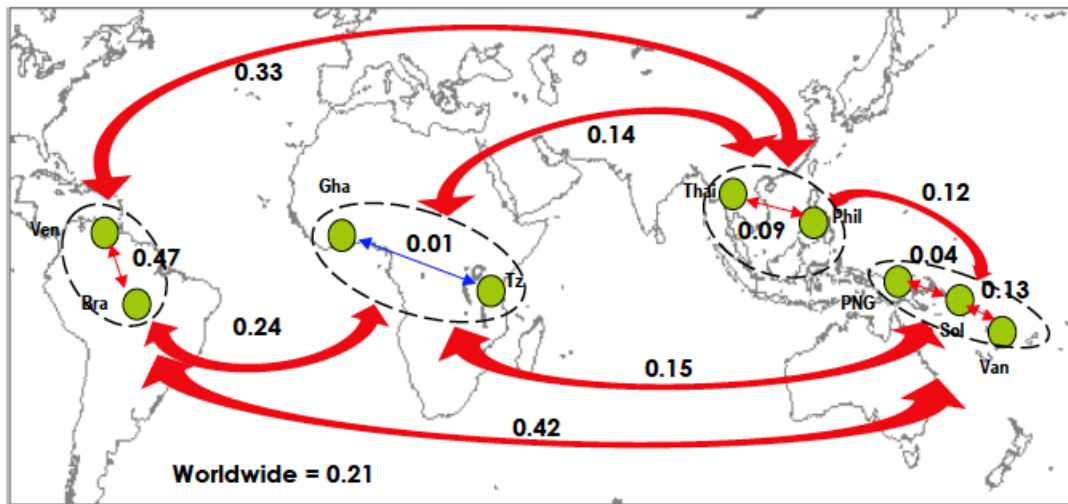


Figure S2. Genetic Differentiation between Populations of *P. falciparum*

Red arrows indicate significant differentiation (F_{ST} significantly greater than zero; $p < 0.05$) and blue arrows for non-significant differentiation.

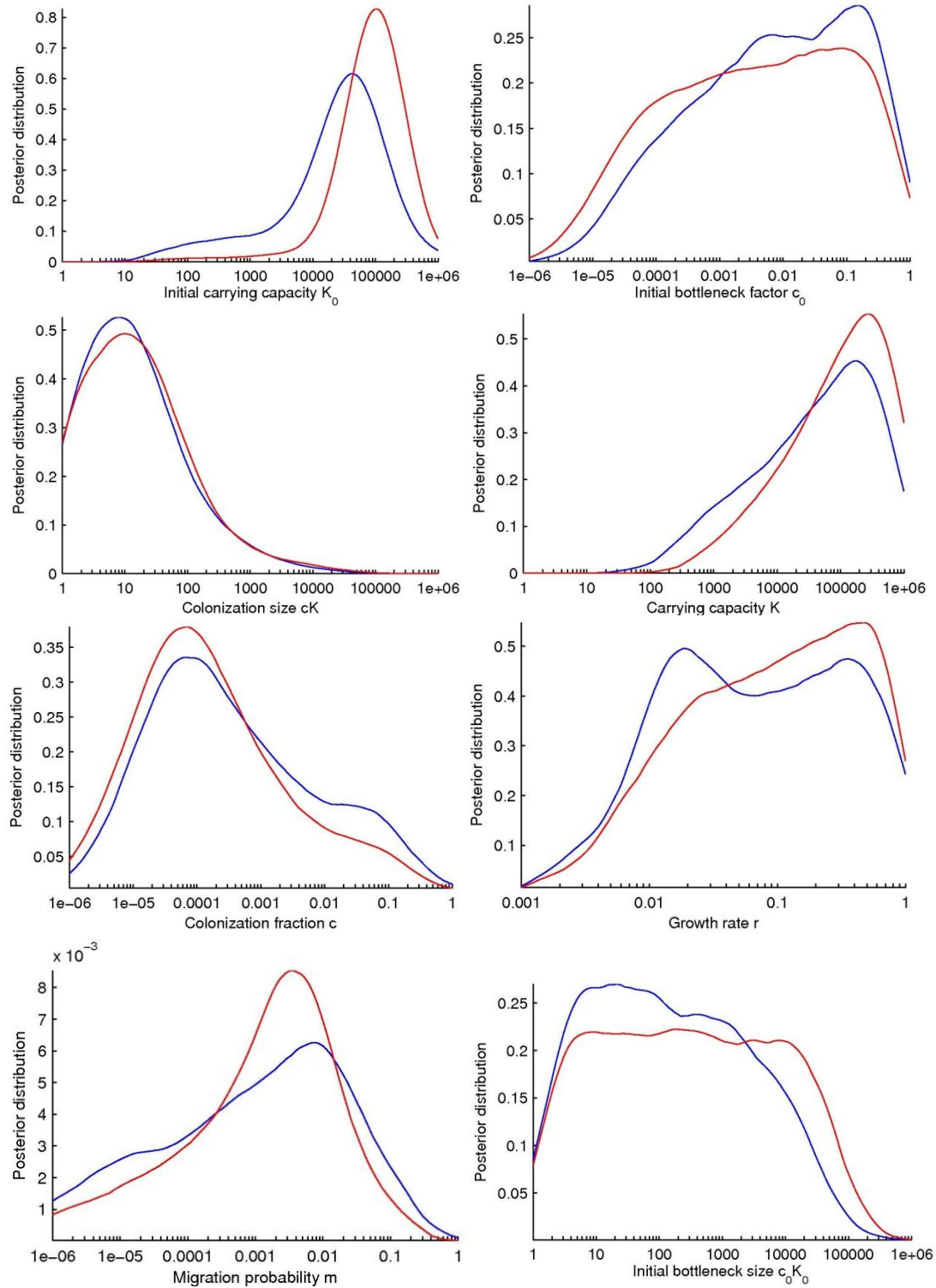


Figure S3. Posterior Distributions of the Stepping Stone Parameters, Given a Split between the *Plasmodium* Species at 2.5 (Blue) and 6 (Red) Mya