

SUPPLEMENTAL TABLE 1
Marker diversity and genotyping success rate in *Plasmodium falciparum* and *Plasmodium vivax*

Species	Markers	CS H_E	ESS H_E	TES H_E	Failure, N (%)
<i>P. vivax</i> ⁷⁵ (N = 477)	MS12	0.736	0.754	0.840	99 (20.8)
	pv3.27	0.868	0.897	0.845	88 (18.4)
	msp1f3	0.822	0.784	0.841	90 (18.9)
	MS10	0.897	0.900	0.896	97 (20.3)
	MS5	0.847	0.854	0.833	90 (18.9)
	MS1	0.779	0.747	0.843	102 (21.4)
	MS16	0.951	0.926	0.952	93 (19.5)
<i>P. falciparum</i> ²² (N = 470)	MS20	0.892	0.893	0.917	125 (26.2)
	Poly-alpha	0.748	0.596	0.627	57 (12.1)
	TA42	0.410	0.062	0.170	122 (26.0)
	TA81	0.827	0.783	0.703	88 (18.7)
	TA87	0.698	0.585	0.680	44 (9.4)
	ARAI	0.810	0.755	0.746	57 (12.1)
	PfPK2	0.733	0.693	0.319	52 (11.1)
	TA60	0.744	0.662	0.635	26 (5.5)
	TA1	0.706	0.601	0.418	118 (25.1)
	TA109	0.230	0	0.044	41 (8.7)

CS = community survey; ESS = ex vivo susceptibility study; H_E = expected heterozygosity; TES = treatment efficacy study; # Indicates the number of samples that failed all loci.

SUPPLEMENTAL TABLE 2
Temporal analysis of genetic diversity and within-host diversity

Sampling method	Year	Species	All cases	MOI,* Mean SD† (range)	Polyclonality, N (%)	H_E ‡ Mean ±SD (range)	R_s § Mean (SD)	
Passively detected	2011	<i>P. falciparum</i>	11	1.1, 0.3 (1–2)	1 (9)	0.511 ± 0.3 (0–0.782)	2.571 (1.11)	
		<i>P. vivax</i>	35	1.3, 0.5 (1–3)	8 (23)	0.841 ± 0.082 (0.716–0.959)	5.075 (1.20)	
	2012	<i>P. falciparum</i>	36	1.1, 0.2 (1–2)	2 (6)	0.530 ± 0.307 (0–0.794)	2.831 (1.11)	
		<i>P. vivax</i>	30	1.6, 0.8 (1–4)	13 (43)	0.846 ± 0.079 (0.720–0.929)	5.285 (0.91)	
	2013	<i>P. falciparum</i>	13	1.3, 0.5 (1–2)	4 (31)	0.608 ± 0.278 (0–0.808)	3.328 (1.19)	
		<i>P. vivax</i>	25	1.3, 0.5 (1–2)	7 (28)	0.840 ± 0.073 (0.747–0.913)	4.927 (0.90)	
	2014	<i>P. falciparum</i>	34	1.2, 0.4 (1–2)	7 (21)	0.502 ± 0.283 (0–0.763)	2.672 (1.02)	
		<i>P. vivax</i>	14	1.6, 0.6 (1–3)	7 (50)	0.861 ± 0.084 (0.714–0.967)	5.336 (1.23)	
	2015	<i>P. falciparum</i>	37	1.1, 0.3 (1–2)	3 (8)	0.469 ± 0.246 (0.054–0.766)	2.690 (1.00)	
		<i>P. vivax</i>	39	1.3, 0.5 (1–2)	12 (32)	0.870 ± 0.047 (0.820–0.956)	5.481 (0.70)	
	2016	<i>P. falciparum</i>	8	1, NA	0	0.448 ± 0.311 (0–0.786)	2.778 (1.48)	
		<i>P. vivax</i>	9	2, 1.0 (2–4)	6 (67)	0.881 ± 0.047 (0.806–0.944)	5.306 (0.88)	
	Actively detected	2013	<i>P. falciparum</i>	331	1.2 (1–3)	51 (19)	0.656 ± 0.2 (0.230–0.827)	7.112 (2.38)
			<i>P. vivax</i>	324	1.7 (1–4)	125 (52)	0.848 ± 0.069 (0.734–0.951)	13.00 (3.94)

* Multiplicity of infection.
† Standard deviation.
‡ Expected heterozygosity.
§ Allelic richness.
NA = not applicable.

SUPPLEMENTAL TABLE 3
Temporal analysis of linkage disequilibrium

Subgroup	All infections N	I_A^S	Low complexity N	I_A^S	Unique haplotypes N	I_A^S	
<i>P. falciparum</i>	2011	11	–0.0201 ^{NS}	11	–0.0201 ^{NS}	11	–0.0201 ^{NS}
	2012	36	0.0833 ^{NS}	35	0.0901 ^{**}	28	0.0346 ^{**}
	2013	13	0.0338 ^{NS}	10	0.0606 [*]	13	0.0338 [*]
	2014	34	0.0314 ^{**}	30	0.0243 [*]	28	0.0147 [*]
	2015	37	0.1642 ^{**}	35	0.1582 ^{**}	25	0.0624 ^{**}
<i>P. vivax</i>	2011	35	0.0334 [*]	29	0.0232 ^{NS}	25	0.0334 [*]
	2012	30	0.0015 ^{NS}	25	0.0092 ^{NS}	21	0.0015 ^{NS}
	2013	28	–0.0046 ^{NS}	22	0.007 ^{NS}	23	–0.0046 ^{NS}
	2014	14	0.0092 ^{NS}	9	–0.0323 ^{NS}	14	0.0092 ^{NS}
	2015	37	0.0123 ^{NS}	30	0.0222 [*]	30	–0.0038 ^{NS}

Only samples with no missing data were included in the analyses. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; NS = not significant.

SUPPLEMENTAL TABLE 4

Within-host and population diversity between adults and children with asymptomatic *Plasmodium falciparum* and *Plasmodium vivax* infections

	N	MOI Mean* (SD)	P†	Polyclonality N (%)	Chi	R _S ‡ Mean (SD)	P†	H _E § mean (SD)	P†	F _{ST}	P ± SD	F'_{ST}¶
<i>P. falciparum</i>												
All adults#	92	1.2 (0.4)	0.868	19 (20)	0.796	5.44 (1.92)	0.635	0.701 (0.169)	0.536	0.009	0.987 ± 0.0004	-0.031
All children**	90	1.2 (0.4)		21 (22)		5.66 (1.71)		0.675 (0.187)				
<i>P. vivax</i>												
All adults	57	1.6 (0.8)	0.242	25 (44)	0.157	10.83 (4.44)	0.52	0.829 (0.088)	0.429	-0.003	0.710 ± 0.0015	-0.020
All children	112	1.7 (0.8)		62 (55)		10.56 (3.77)		0.855 (0.066)				

MOI = multiplicity of infection.

* Standard deviation.

† Mann-Whitney *U* test.

‡ Allelic richness.

§ Expected heterozygosity.

|| Fixation index.

¶ Standardized fixation index.

Adults ≥ 15 years old.

** Children < 15 years old.

SUPPLEMENTAL TABLE 5

Within-host and population diversity between capillary and venous samples from asymptomatic *P. falciparum* and *P. vivax* infections

Subgroups	N	MOI Mean* (SD)	P†	Polyclonality N (%)	Chi	R _S ‡ Mean (SD)	P†	H _E § Mean (SD)	P†	F _{ST}	P ± SD	F'_{ST}¶
<i>P. falciparum</i>												
All capillary	182	1.1 (0.343)	0.122	39 (21)	0.124	6.00 (1.83)	0.081	0.687 (0.171)	0.113	0.026	0.002 ± 0.0001	0.073
All venous	82	1.2 (0.428)		11 (13)		4.81 (1.90)		0.563 (0.283)				
<i>P. vivax</i>												
All capillary	169	1.7 (0.791)	0.346	87 (51)	0.837	12.85 (5.37)	0.809	0.846 (0.071)	0.959	0.008	0.017 ± 0.0004	0.048
All venous	68	1.6 (0.608)		34 (50)		12.88 (5.65)		0.848 (0.079)				

MOI = multiplicity of infection.

* Standard deviation.

† Mann-Whitney *U* test.

‡ Allelic richness.

§ Expected heterozygosity.

|| Fixation index.

¶ Standardized fixation index.

SUPPLEMENTAL TABLE 6

Within-host diversity and stage synchronicity between *Plasmodium falciparum* and *Plasmodium vivax* sample sets

Sample sets	Synchronous*	Synchronous N (%)	MOI Mean† (SD)	Polyclonality N (%)	Total
<i>P. falciparum</i>					
CS	Yes	84 (89)	1.23 (0.42)	19 (23)	94
	No	10 (11)	1.27 (0.48)	3 (30)	
TES	Yes	44 (98)	1.07 (0.25)	3 (7)	45
	No	1 (2)	1.00 (0)	0 (0)	
ESS	Yes	94 (100)	1.15 (0.36)	14 (15)	94
	No	0 (0)	0 (0)	0 (0)	
All	Yes	222 (95)	1.16 (0.37)	36 (16)	233
	No	11 (5)	1.27 (0.47)	3 (27)	
<i>P. vivax</i>					
CS	Yes	9 (11)	1.80 (1.03)	4 (44)	81
	No	72 (89)	1.75 (0.82)	39 (54)	
TES	Yes	19 (44)	1.07 (0.25)	7 (37)	46
	No	27 (56)	1.52 (0.75)	11 (41)	
ESS	Yes	104 (100)	1.39 (0.61)	35 (34)	104
	No	0 (0)	0 (0)	0 (0)	
All	Yes	132 (57)	1.55 (0.73)	46 (35)	231
	No	99 (43)	1.69 (0.80)	50 (51)	

CS = community survey; ESS = ex vivo susceptibility study; MOI = multiplicity of infection; TES = treatment efficacy study.

* Ring stage > 70%.

† Standard deviation.