SUPPLEMENTAL INFORMATION

Over a 2-week period in June 2012 at the end of the dry season, blood samples (thick/thin blood films and dried blood spot) and malaria related questionnaires were collected after obtaining informed consent from 698 participants between the ages of 1–85 years during this cross-sectional survey (Supplemental Table 1). From this survey, 267 (38.3%) participants were microscopy positive for any *Plasmodium* spp. with most being infected with *P. falciparum* (97.4%, $N = 260$), a few infected with mixed *P. falciparum*/*P. malariae* infections (1.9%, $N = 5$), and 0.7% ($N = 2$) with *P. malariae* infections (Supplemental Table 1). All the participants with *P. malariae* infections ($N = 2$) by microscopy were confirmed to be harboring *P. falciparum* infections by *msp2* PCR and are included in the analyses as mixed *P. falciparum*/*P. malariae* infections. Supplemental Table 1 summarizes the parasitological characteristics of the total cross-sectional study population by participants' age group, gender and catchment area. *P. falciparum* infections occurred across all age groups in both catchment areas with the highest prevalence of *P. falciparum* infection occurring among children between 6-10 years of age, with 58.1% (95% CI: 54.1-62.1%) of 6-10 year olds across both catchment areas having a *P. falciparum* infection (Supplemental Table 1). When male participants were compared with females there were no differences in the prevalence *P. falciparum* infection for the total study population and within/between the catchment areas. From this cross-sectional survey on the reservoir of *P. falciparum* infections in BD, 200 participants with confirmed *P. falciparum* infections (including mixed *P. falciparum*/*P. malariae* infections) were selected for the microsatellite analyses.

SUPPLEMENTAL TABLE 1

Demographics and parasitological characteristics of the study population collected at the end of the dry season in June 2012

Characteristic	Total	Vea/Gowrie	Soe
Age groups*			
All	698	354 (50.7)	344 (49.3)
1–5 years	133 (19.1)	76 (21.5)	57 (16.6)
6–10 years	155 (22.2)	79 (22.3)	76 (22.1)
11–20 years	140 (20.1)	73 (20.6)	67 (19.5)
21–39 years	112 (16.0)	49 (13.8)	63 (18.3)
≥ 40 years	158 (22.6)	77 (21.8)	81 (23.5)
Gender*			
Female	355 (50.9)	182 (51.4)	173 (50.3)
Male	343 (49.1)	172 (48.6)	171 (49.7)
Microscopic *Plasmodium* spp. prevalence ($N = 267$)			
P. falciparum	260 (97.4)	140 (96.6)	120 (98.4)
P. falciparum/*P. malariae*	5 (1.9)	4 (2.7)	1 (0.8)
P. malariae	2 (0.7)	1 (0.7)	1 (0.8)
Plasmodium spp. median density ($N = 267$)†			
All	280 [120–880]	280 [120–800]	280 [150–1,000]
1–5 years	960 [480–2,200]	900 [640–1,860]	960 [440–2,760]
6–10 years	240 [120–940]	200 [120–700]	400 [140–1,240]
11–20 years	240 [120–520]	240 [120–490]	240 [120–660]
21–39 years	180 [110–500]	240 [120–470]	160 [80–730]
≥ 40 years	120 [80–230]	100 [80–280]	160 [80–200]
Female	290 [120–890]	240 [120–800]	280 [120–880]
Male	320 [160–880]	280 [120–880]	360 [160–960]
P. falciparum prevalence ($N = 267$)‡			
All	267 (38.3)	145 (41.0)	122 (35.5)
1–5 years	51 (38.3)	28 (36.8)	23 (40.4)
6–10 years	90 (58.1)	45 (57.0)	45 (59.2)
11–20 years	72 (51.4)	42 (57.5)	30 (44.8)
21–39 years	22 (19.6)	10 (20.4)	12 (19.0)
≥ 40 years	32 (20.3)	20 (26.0)	12 (14.8)
Female	134 (37.7)	71 (39.0)	63 (36.4)
Male	133 (38.8)	74 (43.0)	59 (34.5)
P. falciparum median MOI ($N = 267$)§			
All	2 [1–3]	2 [1–3]	2 [1–3]
1–5 years	2 [1–3]	2 [1–3]	1.5 [1–3.25]
6–10 years	2 [1–3]	2 [1–3]	3 [2–4]
11–20 years	2 [1–3]	2 [2–3]	2 [1–3]
21–39 years	1 [1–2]	1 [1–3]	1 [1–2]
≥ 40 years	1 [1–2]	1 [1–2]	1 [1–2]

IQR = inter quartile range; MOI = multiplicity of infection; PCR = polymerase chain reaction.

* Data reflect No. (% (*n*/*N*)) of subjects.

† Median parasite density for microscopically positive *P. falciparum* (including mixed *P. falciparum*/*P. malariae* infections) (value/μL, IQR) samples.

‡ Data reflect No. (% (*n*/*N*)) of participants sampled that were positive for *P. falciparum* (including mixed *P. falciparum*/*P. malariae* infections) by microscopy and *msp2* PCR.

§ Data reflect the median MOI for the participants sampled that were positive for *P. falciparum* (including mixed *P. falciparum*/*P. malariae* infections) by microscopy and *msp2* PCR (median, [IQR]).

SUPPLEMENTAL TABLE 2

Allelic size range, number of alleles, expected heterozygosity, and microsatellite loci genotyping success

Locus	Chromosome	Range (bp)	A	H_e	Genotyping success (%)
TA1	6	151–202	17	0.89	83.0
TA60	13	66–99	10	0.79	99.0
TA40	10	202–292	26	0.84	97.0
POLYα	4	125–191	20	0.88	93.5
ARA2	11	59–80	8	0.80	98.5
Pfg377	12	90–105	6	0.63	98.5
TA109	6	148–208	18	0.83	99.0
TA87	6	75–126	16	0.86	96.5
TA42	5	179–233	8	0.35	89.0
2490	10	75–90	5	0.40	91.5
TA81	5	103–136	11	0.84	98.0
PfPK2	12	153–192	14	0.83	94.5

A = number of alleles per locus; H_e = expected heterozygosity.

SUPPLEMENTAL TABLE 3

Microsatellite allele frequencies and sample sizes (n) for 12 microsatellite loci

Marker	bp	All infections (N = 200)	Dominant infections (N = 74)
		Frequency	Frequency
TA1	151	0.012	0.016
	154	0.006	–
	157	0.006	0.016
	160	0.084	0.082
	163	0.145	0.131
	166	0.187	0.197
	169	0.151	0.098
	172	0.133	0.131
	175	0.072	0.049
	178	0.066	0.082
	181	0.036	0.082
	184	0.024	–
	187	0.018	0.016
	190	0.018	0.033
	193	0.030	0.033
	196	0.006	0.016
	202	0.006	0.016
	n	166	61
TA60			
	66	0.020	0.027
	72	0.278	0.284
	75	0.222	0.230
	78	0.030	0.027
	81	0.248	0.176
	84	0.152	0.162
	87	0.030	0.054
	90	0.005	0.014
	93	0.010	0.014
	99	0.005	0.014
	n	198	74
TA40			
	202	0.010	–
	205	0.010	0.014
	208	0.021	0.028
	211	0.010	–
	214	0.010	0.014
	217	0.010	0.014
	220	0.067	0.085
	223	0.021	0.028
	226	0.077	0.113
	229	0.005	0.014
	235	0.026	0.042
	238	0.021	0.028
	241	0.253	0.183
	244	0.278	0.211
	247	0.057	0.085
	250	0.010	0.028
	253	0.026	0.014
	256	0.016	0.028
	259	0.005	–
	262	0.005	0.014
	265	0.005	0.014
	274	0.005	0.014
	283	0.005	–
	286	0.026	0.028
	289	0.010	–
	292	0.010	–
	n	194	71
POLYα			
	125	0.005	0.014
	131	0.011	–
	137	0.005	–
	140	0.005	–
	143	0.043	0.043
	146	0.027	0.029
	149	0.054	0.043
	152	0.267	0.257
	155	0.155	0.129
	158	0.107	0.071
	161	0.091	0.071
	164	0.043	0.057
	167	0.043	0.071
	170	0.032	0.014
	173	0.043	0.071
	176	0.037	0.071
	179	0.011	0.014
	185	0.011	0.014
	188	0.005	0.014
	191	0.005	0.014
	n	187	70
ARA2			
	59	0.0812	0.081
	62	0.066	0.066
	65	0.3401	0.340
	68	0.1929	0.193
	71	0.1827	0.183
	74	0.0863	0.086
	77	0.0305	0.031
	80	0.0203	0.020
	n	197	74
PfG377			
	90	0.025	0.014
	93	0.046	0.081
	96	0.279	0.311

(continued)

SUPPLEMENTAL TABLE 3
Continued

Marker	bp	All infections (*N* = 200)	Dominant infections (*N* = 74)
		Frequency	Frequency
	99	0.543	0.500
	102	0.096	0.081
	105	0.010	0.014
	n	197	74
TA109			
	148	0.005	0.014
	151	0.005	–
	154	0.010	–
	157	0.005	–
	160	0.172	0.176
	163	0.192	0.203
	166	0.015	0.014
	169	0.015	0.027
	172	0.182	0.176
	175	0.237	0.284
	178	0.015	–
	181	0.005	–
	184	0.056	0.054
	187	0.010	0.014
	190	0.005	–
	196	0.061	0.041
	199	0.005	–
	208	0.005	–
	n	198	74
TA87			
	75	0.010	–
	81	0.005	0.014
	84	0.005	–
	87	0.005	–
	90	0.031	–
	93	0.062	0.110
	96	0.150	0.164
	99	0.171	0.123
	102	0.218	0.219
	105	0.140	0.151
	108	0.098	0.110
	111	0.067	0.069
	114	0.005	0.014
	117	0.010	0.014
	120	0.010	–
	126	0.010	0.014
	n	193	73
TA42			
	179	0.006	–
	185	0.803	0.779
	188	0.017	0.029
	194	0.006	–
	197	0.140	0.162
	200	0.006	–
	209	0.017	0.029
	233	0.006	–
	n	178	68
2490			
	75	0.011	0.014
	81	0.175	0.143
	84	0.760	0.743
	87	0.033	0.071
	90	0.022	0.029
	n	183	70
TA81			
	103	0.005	–
	106	0.020	0.055
	109	0.036	0.027
	112	0.077	0.069
	115	0.235	0.233
	118	0.214	0.164
	121	0.194	0.192
	124	0.092	0.110

(continued)

SUPPLEMENTAL TABLE 3
Continued

Marker	bp	All infections (*N* = 200)	Dominant infections (*N* = 74)
		Frequency	Frequency
	127	0.097	0.096
	130	0.026	0.055
	136	0.005	–
	n	196	73
PfPK2			
	153	0.005	0.014
	156	0.027	0.014
	159	0.164	0.167
	162	0.233	0.292
	165	0.259	0.181
	168	0.122	0.153
	171	0.058	0.097
	174	0.016	–
	177	0.032	0.014
	180	0.042	0.028
	183	0.016	0.014
	186	0.005	–
	189	0.016	0.028
	192	0.005	–
	n	189	72

Supplemental Table 4

Patterns of genetic diversity in Bongo District for dominant infections

Population	n	h	A ± SE	R_s ± SE	H_e ± SE
Vea/Gowrie catchment area	42	42	8.67 ± 3.34	8.45 ± 3.24	0.76 ± 0.17
Vea	26	26	7.42 ± 2.81	6.14 ± 2.01	0.76 ± 0.13
Gowrie	16	16	5.75 ± 2.09	5.45 ± 1.94	0.72 ± 0.23
Soe catchment area	32	32	8.00 ± 3.59	7.97 ± 3.58	0.75 ± 0.19
Soe Sanabisi	10	10	5.08 ± 1.93	5.07 ± 1.92	0.72 ± 0.23
Soe Boko	22	22	7.08 ± 2.81	5.96 ± 2.09	0.74 ± 0.17
Total	74	74	10.50 ± 4.82	10.44 ± 4.78	0.76 ± 0.18

A = number of alleles per locus; h = number of haplotypes; H_e = expected heterozygosity; n = number of isolates; R_s = allelic richness estimate.

Supplemental Table 5

Multilocus linkage disequilibrium in Bongo District for one marker/chromosome for 55 dominant infections with no missing data.

chr5	chr6	chr10	chr12	I^S_A (P value)
TA42	TA109	TA40	PFG377	0.0120 (0.066)
TA42	TA109	2490	PFG377	0.0105 (0.145)
TA42	TA109	TA40	PfPK2	0.0083 (0.127)
TA42	TA109	2490	PfPK2	0.0062 (0.254)
TA42	TA87	TA40	PFG377	0.0106 (0.091)
TA42	TA87	2490	PFG377	0.0077 (0.209)
TA42	TA87	TA40	PfPK2	0.0088 (0.108)
TA42	TA87	2490	PfPK2	0.0050 (0.288)
TA42	TA1	TA40	PFG377	0.0168 (0.022)*
TA42	TA1	2490	PFG377	0.0166 (0.055)
TA42	TA1	TA40	PfPK2	0.0151 (0.028)*
TA42	TA1	2490	PfPK2	0.0141 (0.070)
TA81	TA109	TA40	PFG377	0.0046 (0.230)
TA81	TA109	2490	PFG377	0.0097 (0.103)
TA81	TA109	TA40	PfPK2	0.0030 (0.312)
TA81	TA109	2490	PfPK2	0.0077 (0.138)
TA81	TA87	TA40	PFG377	0.0028 (0.311)
TA81	TA87	2490	PFG377	0.0066 (0.178)
TA81	TA87	TA40	PfPK2	0.0036 (0.276)
TA81	TA87	2490	PfPK2	0.0066 (0.171)
TA81	TA1	TA40	PFG377	0.0034 (0.294)
TA81	TA1	2490	PFG377	0.0112 (0.074)
TA81	TA1	TA40	PfPK2	0.0037 (0.272)
TA81	TA1	2490	PfPK2	0.0111 (0.061)

*$P < 0.05$