

Table 1. Demographic characteristics of the study population

Characteristics	<i>P. falciparum</i>	<i>P. falciparum</i> / <i>P. malariae</i>
	n (%)	n (%)
Age		
Mean± SD	19.8 ± 18.4	19.6 ± 17.1
Gender		
Female	77 (61.6)	64 (51.2)
Male	48 (38.4)	61 (48.8)
Age groups (year)		
< 5	14 (11.2)	19 (15.2)
5-14	55 (44)	55 (44)
≥ 15	56 (44.8)	51 (40.8)
Location		
Ouidah	63 (50.4)	62 (49.6)
Kpomasse	62 (49.6)	63 (50.4)

SD: Standard Deviation; n represents the number of participants and the corresponding percentage value is indicated in brackets.

Table 2. Prevalence of *msp1* and *msp2* allelic families in *P. falciparum* and *P. falciparum* / *P. malariae* isolates

Genes	Allelic family	<i>P. falciparum</i> % (n/N)	<i>P. falciparum</i> / <i>P. malariae</i> % (n/N)	P-value
<i>msp1</i>	K1	0 (0/120)	0 (0/103)	/
	MAD20	0.8 (1/120)	11.7 (12/103)	0.0007
	RO33	26.7 (32/120)	26.2 (27/103)	0.9
	K1 + MAD20	0 (0/120)	0.9 (1/103)	0.2
	K1+ RO33	6.7 (8/120)	5.8 (6/103)	0.8
	MAD20 + RO33	34.2 (41/120)	40.8 (42/103)	0.4
	K1+MAD20 + RO33	31.7 (38/120)	13.6 (14/103)	0.005
	Total K1	38.3 (46/120)	20.4 (21/103)	0.01
	Total MAD20	66.7 (80/120)	67 (69/103)	0.97
	Total RO33	99.2 (119/120)	86.4 (89/103)	0.32
<i>msp2</i>	3D7	10.7 (13/122)	43.3 (42/97)	< 0.0001
	FC27	11.5 (14/122)	11.3 (11/97)	0.9
	3D7 + FC27	77.9 (95/122)	45.4 (44/97)	0.002
	Total 3D7	88.5 (108/122)	88.7 (86/97)	0.99
	Total FC27	89.3 (109/122)	56.7 (55/97)	0.005

n: number of participants positive for allelic family, N: Number of participants positive for each gene and the corresponding percentage value is indicated in front of the brackets

Table 3. Multiplicity of infection of *msp1* and *msp2* in *P. falciparum* and *P. falciparum* / *P. malariae* isolates

Genes	<i>P. falciparum</i>	<i>P. falciparum</i> / <i>P. malariae</i>	P-value
<i>msp1</i>			
<i>Multiple infections</i>	82.5	73.8	0.1
MOI	3.7	2.7	< 0.001
<i>msp2</i>			
<i>Multiple infections</i>	90.2	62.9	< 0.001
MOI	5.8	2.3	< 0.001

MOI: Multiplicity of Infection

Table 4. Multiplicity of infection of *msp1* and *msp2* in *P. falciparum* and *P. falciparum* / *P. malariae* isolates per age groups

Age groups	Multiplicity of infection			
	<i>P. falciparum</i>		<i>P. falciparum</i> / <i>P. malariae</i>	
	<i>msp1</i>	<i>msp2</i>	<i>msp1</i>	<i>msp2</i>
< 5	4.1	6	3.5	3.1
5-14	4.2	6.5	2.7	2.4
≥ 15	3.2	5	2.4	2
P-value	> 0.05	> 0.05	> 0.05	> 0.05

Table 5. Prevalence of *msp1* and *msp2* allelic families of microscopic and submicroscopic infections in the mono-infection *P. falciparum* group

Genes	Allelic family	Microscopic (n=68) % (n/N)	Submicroscopic (n=57) % (n/N)
<i>msp1</i>	K1	0 (0/67)	00 (0/53)
	MAD20	0 (0/67)	1.9 (1/53)
	RO33	11.9 (8/67)	45.3 (24/53)
	K1 + MAD20	0 (0/67)	00 (0/53)
	K1+ RO33	11.9 (8/67)	00 (0/53)
	MAD20 + RO33	35.3 (36/102)	39.6 (21/53)
	K1+MAD20 + RO33	46.3 (31/67)	13.2 (7/53)
	Total K1	58.2 (39/67)	13.2 (7/53)
	Total MAD20	76.1 (51/67)	54.7 (29/53)
	Total RO33	100 (67/67)	98.1 (52/53)
<i>msp2</i>	3D7	5.9 (4/68)	16.4 (9/55)
	FC27	11.8 (8/68)	10.9 (6/55)
	3D7 + FC27	82.4 (56/68)	70.9 (39/55)
	Total 3D7	88.2 (60/68)	87.3 (48/55)
	Total FC27	94.1 (64/68)	81.8 (45/55)

n: Represents the number of microscopic, submicroscopic isolates, and the number of participants positive for allelic family, N: Number of participants positive for each gene and the corresponding percentage value is indicated in front of the brackets

Table 6. Prevalence of *m*sp1 and *m*sp2 allelic families of microscopic and submicroscopic infections in the mixed infections *P. falciparum*/*P. malariae* group

Genes	Allelic family	Microscopic (n=76) % (n/N)	Submicroscopic (n=49) % (n/N)
<i>m</i> sp1	K1	00 (0/69)	00 (0/34)
	MAD20	5.8 (4/69)	23.5 (8/34)
	RO33	23.2 (16/69)	32.4 (11/34)
	K1 + MAD20	0 (0/69)	2.9 (1/34)
	K1+ RO33	7.2 (5/69)	2.9 (1/34)
	MAD20 + RO33	44.9 (31/69)	32.4 (11/34)
	K1+MAD20 + RO33	18.8 (13/69)	2.9 (1/34)
	Total K1	26.1 (18/69)	8.8 (3/34)
	Total MAD20	69.6 (48/69)	61.8 (21/34)
	Total RO33	94.2 (65/69)	70.6 (24/34)
<i>m</i> sp2	3D7	38.5 (25/65)	51.5 (17/33)
	FC27	9.2 (6/65)	15.2 (5/33)
	3D7 + FC27	52.3 (34/65)	30.3 (10/33)
	Total 3D7	90.8 (59/65)	81.8 (27/33)
	Total FC27	61.5 (40/65)	45.5 (15/33)

n: Represents the number of microscopic, submicroscopic isolates, and the number of participants positive for allelic family, N: Number of participants positive for each gene and the corresponding percentage value is indicated in front of the brackets

Table 7. Multiplicity of infection (MOI) of *msp1* and *msp2* of microscopic and submicroscopic infections in *P. falciparum* and *P. falciparum* / *P. malariae* isolates

Genes	<i>P. falciparum</i> isolates group (n=125)			<i>P. falciparum</i> / <i>P. malariae</i> isolates group (n=125)		
	microscopic	submicroscopic	P-value	microscopic	submicroscopic	P-value
<i>msp1</i>						
MOI	4.4	2.9	<0.05	3	2	<0.05
<i>msp2</i>						
MOI	6.5	4.7	< 0.05	2.6	1.8	> 0.05

Supplementary data. Table 1. Names and sequences of primers

Name of primers	Sequences of primers (5' to 3')
M1-OF	CTA GAA GCT TTA GAA GAT GCA GTA TTG
M1-OR	CTT AAA TAG TAT TCT AAT TCA AGT GGA TCA
K1	AAA TGA AGA AGA AAT TAC TAC AAA AGG TGC
K2	GCT TGC ATC AGC TGG AGG GCT TGC ACC AGA
MAD20-1	AAA TGA AGG AAC AAG TGG AAC AGC TGT TAC
MAD20-2	ATC TGA AGG ATT TGT ACG TCT TGA ATT ACC
RO33-1	TAA AGG ATG GAG CAA ATA CTC AAG TTG TTG
RO33-2	CAT CTG AAG GAT TTG CAG CAC CTG GAG ATC
M2-OF	ATG AAG GTA ATT AAA ACA TTG TCT ATT ATA
M2-OR	CTT TGT TAC CAT CGG TAC ATT CTT
3D7-1/ FC27-1	GCT TAT AAT ATG AGT ATA AGG AGA A
FC27-2	GCA TTG CCA GAA CTT GAA
3D7-2	CTG AAG AGG TAC TGG TAG A