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SUPPORTING INFORMATION

Insularity effects on the assemblage of the blood parasite community of the birds from the Gulf of Guinea

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Appendix S1 Characteristics of sampling sites and host species.

Table S1.1 Sampling sites and their characteristics: Alt (altitude above sea level in meters), Habitat (P = plantation and F = forest), sampling year(s) and coordinates. N_i/N_{sp}: number of individuals/species captured per site.

Location	*Region*	*Site*	N_i/N_{sp}	*Alt*	*Habitat*	*Year*	*Coordinates*
Island	Annobón	Rio Anganchi	4/1	100	P	2004	0126S 00539E
		Lago Pot	8/3	250	P	2004	0125S 00538E
		Total	*12/3*				
	São Tomé	Abade	26/7	600	P	2013	0015N 00639E
		Alto Douro	69/9	150	P	2002-03-04-13	0012N 00641E
		Angus	2/1	5	P	2004	0020N 00642E
		Bom Sucesso	21/3	1150	P	2002-03-04-05	0017N 00636E
		Contador dam	107/13	600	P	2005-13-14	0019N 00632E
		Duas grotas	4/2	332	P	2013	0013N 00636E
		Lagoa Amélia	41/8	1500	F	2002-03-04-05	0016N 00635E
		Margão	4/2	447	P	2013	0018N 00639E
		Monte Café	8/3	720	P	2002	0018N 00638E
		Monte Carmo	2/1	300	F	2002	0008N 00634E

		Monteforte	50/7	150	P	2013	0020N 00632E
		Pico Calvário	8/2	1590	F	2002	0016N 00634E
		Praia Cruz	152/12	5	P	2013-14	0022N 00642E
		Quija	28/3	650	F	2002-03-04-05	0009N 00633E
		S. Miguel	9/3	400	F	2005	0010N 00630E
		Umbumgu	13/6	300	F	2003-04	0009N 00633E
		Vanguarda	5/3	582	P	2013	0018N 00639E
		Total	*549/25*				
	Boné	Boné de Jóquei	51/1	5	F	2002-03-04	0130N 00725E
	Príncipe	Água Cató-Henry	64/5	40	P	2014	0137N 00724E
		Água Petróleo	8/3	120	P	2002	0140N 00724E
		Bela Vista	93/10	40	P	2002-04-14	0137N 00724E
		Oquê Daniel	80/14	60	P	2014	0136N 00724E
		Praia Cará	38/3	30	P	2003-04	0133N 00721E
		Ribeira Porco	13/5	130	F	2002-03	0132N 00722E
		Sundi	25/6	170	P	2002-03	0140N 00723E
		Total	*321/20*				
	Bioko	Moka	28/6	1015	P	2004	0320N 00840E
		Pico Basilé	37/9	2400	F	2004	0335N 00847E
		Total	*65/12*				
Mainland	Cameroon	Limbe	6/3	90	P	2003	0400N 00912E
		Etinde Trail	9/2	560	F	2003	0403N 00907E
		Buea	23/12	1100	P	2003	0407N 00912E
		Mann's Spring	32/10	2280	F	2003	0408N 00907E
		Total	*70/17*				
	Gabon	Bakoumba	27/6	636	P	2013	0149S 01300E
		Cap Esterias	42/13	0	P	2004	0037N 00920E
		Ipassa-Makokou	37/8	510	P	2005	0030N 01248E
		Kango	25/10	30	P	2004	0009N 01007E
		Lekedi	197/11	605	P	2013	0149S 01301E
		Total	*328/24*				

Table S1.2 Year, month and season of sampling.

Year	*Month*	*Season*	*Region*
2002	October	Rainy	São Tomé
	November	Rainy	São Tomé
	December	Short Dry	São Tomé / Príncipe
2003	January	Short Dry	São Tomé
	February	Short Dry / Dry	São Tomé / Cameroon
	March	Rainy	São Tomé
	April	Rainy	Príncipe
	November	Rainy	São Tomé
	December	Short Dry	São Tomé / Príncipe
2004	January	Short Dry	São Tomé / Bioko
	February	Short Dry / Dry	Annobón / Gabon
	March	Rainy	São Tomé / Príncipe
	December	Short Dry	Príncipe
2005	January	Short Dry / Dry	São Tomé / Gabon
	February	Short Dry	São Tomé
2013	January	Dry	Gabon
	February	Short Dry	São Tomé
2014	January	Short Dry	São Tomé / Príncipe

Table S1.3 All the families and species captured are listed with their status (E = endemic and NE = non-endemic) and their number of lineages (*Plasm* = *Plasmodium* sp.; *Haem* = *Haemoproteus* sp.; *Leuco* = *Leucocytozoon* sp.; NA means that species have not been tested).

Family	Species	N Mainland	N Island	Location	Status	N *Plasm*	N *Haem*	N *Leuco*	N Total
Alcedinidae	*Corythornis cristatus nais*	0	20	Príncipe	E	0	0	0	0
	Corythornis cristatus thomensis	0	7	São Tomé	E	0	0	0	0
	Halcyon malimbica	0	20	Príncipe	NE	0	0	0	0
	Halcyon senegalensis	4	0	Gabon	NE	0	0	0	0
	Ispidina picta	10	0	Gabon	NE	0	1	1	2
Cisticolidae	*Camaroptera chloronota*	4	0	Gabon	NE	1	0	1	2
	Cisticola anonymus	5	0	Gabon	NE	1	0	0	1
	Prinia molleri	0	18	São Tomé	E	0	1	0	1
	Urolais epichlora	0	2	Bioko	NE	0	0	0	0
Columbidae	*Aplopelia larvata*	0	37	São Tomé, Príncipe	NE	0	1	0	1
	Columba malherbii	0	9	São Tomé	E	0	2	0	2
	Streptopelia senegalensis	0	1	Príncipe	NE	NA	NA	0	0
	Treron calva	0	1	Príncipe	NE	NA	NA	0	0
	Turtur afer	15	0	Gabon	NE	1	1	0	2
Estrildidae	*Cryptospiza reichnovii*	4	0	Cameroon	NE	0	1	0	1
	Estrilda astrild	0	99	São Tomé, Príncipe	NE	0	0	1	1
	Estrilda atricapilla	2	0	Gabon	NE	0	0	0	0
	Estrilda melpoda	14	0	Gabon	NE	1	2	0	3
	Estrilda nonnula	0	4	Bioko	NE	0	0	0	0
	Lonchura bicolor	2	0	Gabon	NE	0	1	1	2
	Lonchura cucullata	0	26	São Tomé, Príncipe, Annobón	NE	0	1	0	1
	Lonchura cucullata	20	0	Gabon	NE	1	2	0	3
	Pyrenestes ostrinus	3	0	Gabon	NE	0	0	0	0
	Spermophaga haematina	4	0	Gabon	NE	2	0	0	2
	Uraeginthus angolensis	0	6	São Tomé	NE	NA	NA	0	0
Fringillidae	*Crithagra burtoni*	3	0	Cameroon	NE	0	0	0	0
	Crithagra capistrata	21	0	Gabon	NE	2	0	1	3
	Crithagra concolor	0	3	São Tomé	E	0	1	1	2

	Crithagra mozambica	0	15	São Tomé	NE	3	0	0	3
	Crithagra rufobrunnea	0	219	São Tomé, Príncipe, Boné	E	5	2	3	10
	Linurgus olivaceus	0	4	Bioko	NE	1	0	0	1
	Linurgus olivaceus	2	0	Cameroon	NE	1	0	0	1
Monarchidae	*Terpsiphone atrochalybea*	0	10	Sao Tome	E	0	0	0	0
	Terpsiphone rufiventer	2	0	Cameroon	NE	0	1	0	1
	Terpsiphone smithii	0	6	Annobón	E	0	0	0	0
	Terpsiphone viridis	2	0	Cameroon	NE	0	0	0	0
Nectariniidae	*Cinnyris chloropygius*	6	0	Cameroon, Gabon	NE	2	0	0	2
	Cinnyris reichenowi	0	4	Bioko	NE	0	0	0	0
	Cinnyris reichenowi	4	0	Cameroon	NE	0	1	0	1
	Cyanomitra olivacea	0	38	Príncipe	NE	6	0	0	6
	Cyanomitra olivacea	29	0	Cameroon, Gabon	NE	8	3	5	16
	Cyanomitra oritis	0	6	Bioko	NE	1	0	0	1
	Cyanomitra oritis	5	0	Cameroon	NE	0	0	0	0
	Cyanomitra verticalis	15	0	Gabon	NE	7	0	4	11
	Dreptes thomensis	0	11	São Tomé	E	0	0	2	2
	Nectarinia hartlaubii	0	18	Príncipe	E	5	0	2	7
	Nectarinia newtonii	0	36	São Tomé	E	6	1	2	9
Ploceidae	*Euplectes albonotatus*	0	8	São Tomé	NE	NA	NA	0	0
	Euplectes aureus	0	11	São Tomé	NE	NA	NA	0	0
	Euplectes hordeaceus	0	25	São Tomé	NE	1	0	0	1
	Euplectes hordeaceus	27	0	Gabon	NE	5	2	6	13
	Ploceus cucullatus	0	34	São Tomé	NE	4	0	0	4
	Ploceus cucullatus	51	0	Gabon	NE	4	4	4	12
	Ploceus grandis	0	25	São Tomé	E	1	1	2	4
	Ploceus melanogaster	0	2	Bioko	NE	1	0	0	1
	Ploceus melanogaster	5	0	Cameroon	NE	1	0	1	2
	Ploceus nigerrimus	6	0	Cameroon, Gabon	NE	0	2	1	3
	Ploceus nigricollis	36	0	Gabon	NE	3	3	12	18
	Ploceus princeps	0	68	Príncipe	E	9	0	0	9
	Ploceus sanctithomae	0	23	São Tomé	E	3	0	6	9

	Ploceus velatus	0	9	São Tomé	NE	NA	NA	0	0
	Quelea erythrops	0	2	São Tomé	NE	NA	NA	0	0
	Quelea erythrops	7	0	Gabon	NE	0	3	0	3
Pycnonotidae	*Arizelocichla tephrolaema*	0	8	Bioko	NE	0	1	1	2
	Arizelocichla tephrolaema	5	0	Cameroon	NE	0	0	1	1
	Eurillas latirostris	12	0	Gabon	NE	2	1	5	8
	Eurillas virens	0	6	Bioko	NE	0	0	0	0
	Eurillas virens	14	0	Cameroon, Gabon	NE	4	0	0	4
	Pycnonotus barbatus	6	0	Gabon	NE	3	0	0	3
Sturnidae	*Lamprotornis splendens/ornatus*	0	18	Príncipe	E	1	0	0	1
	Onychognathus fulgidus	0	3	São Tomé	E	NA	NA	0	0
Sylviidae	*Horizorhinus dohrni*	0	6	Príncipe	E	NA	NA	0	0
	Pseudoalcippe abyssinica	0	3	Bioko	NE	0	0	0	0
	Pseudoalcippe abyssinica	5	0	Cameroon	NE	0	2	0	2
Turdidae	*Turdus olivaceofuscus*	0	47	São Tomé, Príncipe	E	6	2	4	12
	Turdus pelios	0	13	Bioko	NE	2	0	1	3
	Turdus pelios	39	0	Cameroon, Gabon	NE	8	2	2	12
Zosteropidae	*Zosterops brunneus*	0	8	Bioko	E	1	2	0	3
	Zosterops feae	0	6	São Tomé	E	0	1	0	1
	Zosterops ficedulinus	0	4	Príncipe	E	1	1	0	2
	Zosterops griseovirescens	0	5	Annobón	E	0	1	1	2
	Zosterops leucophaeus	0	16	Príncipe	E	1	1	0	2
	Zosterops lugubris	0	24	São Tomé	E	0	3	0	3
	Zosterops melanocephalus	3	0	Cameroon	NE	0	0	0	0
	Zosterops senegalensis	0	5	Bioko	NE	1	1	2	4
	Zosterops senegalensis	6	0	Cameroon	NE	0	1	1	2

Appendix S2 Host specificity indices, distribution and prevalence of Haemosporidia lineages in the 13 bird families sampled in the Gulf of Guinea, and further statistical results for the paired-species design excluding some pairs (1 and 5).

Statistical Results

For the paired-species design, we used the package lme4 in R version 3.1.3 (R Core Team, 2015). We tested the insularity effect using generalized linear mixed models on parasite prevalence and diversity with the random effect 'species' nested in 'pair' nested in 'family'.
Because we formed two pairs including species with different genus: pair 1(genus *Turtur*, *Aplopelia* and *Columba*) and pair 5 (genus *Cyanomitra* and *Nectarinia*), we did the statistical analyses including them (in the main text) or excluding them, presented below. In both cases we found the same results.

Insularity effect on prevalence:

a) Haemoproteus

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	-6.138	1.289	-4.762	1.91e-06 ***
Insularity effect	4.185	1.017	4.115	3.87e-05 ***

b) Leucocytozoon

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	-2.5361	0.6018	-4.214	2.51e-05 ***
Insularity effect	3.0648	0.5273	5.813	6.15e-09 ***

c) Plasmodium

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	-1.1032	0.8082	-1.365	0.17224
Insularity effect	0.8665	0.3060	2.832	0.00463 **

Insularity effect on diversity:

a) Haemoproteus

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	-1.7918	0.707	-2.534	0.01128 *
Insularity effect	2.3026	0.752	3.059	0.00222 **

b) Leucocytozoon

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	-0.5792	0.5174	-1.119	0.263034
Insularity effect	1.2979	0.3678	3.529	0.000417 ***

c) Plasmodium

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	0.8375	0.3462	2.419	0.0156 *
Insularity effect	0.1340	0.2588	0.518	0.6047

Table S2.1 All described Haemosporidia lineages from the Gulf of Guinea are listed by genus (P = *Plasmodium*, H = *Haemoproteus* and L = *Leucocytozoon*), with their host specificity indices (STD) and their Genbank accession number. The number of orders (O), families (F), genera (G) and species (Sp) in which the lineages have been found is also given. We present the combined data of i) our sampling (**in bold**) and ii) the additional MalAvi/Genbank data (*in italic*). "*" indicates a new lineage.

Location	Lineage	Genera	O	F	G	Sp	STD	Genbank
Mainland	**ACCTAC01**	P	6	12	17	19	18.45	EU810700
	AFTRU07	P	1	1	1	1	0	EU810631
	AFTRU08	P	1	1	1	1	0	EU810633
	AFTRU4	P	1	1	1	2	2	DQ847261
	ALEDIA01	P	1	1	1	1	0	DQ659552
	ALEDIA02	P	1	2	2	2	4.00	EU810634
	ALPOL02	P	1	4	5	6	7.00	EU810636
	ANLAT01	P	1	2	2	2	4.00	EU770151
	ANLAT03	P	1	2	3	4	4.82	EU810642
	ANLAT04	P	1	2	5	7	7.19	EU810623
	ANLAT05	P	1	1	1	1	0	DQ508377
	ANLAT06	P	1	1	1	2	2.00	DQ508381
	ANLAT07	P	1	1	1	2	2.00	FJ404720
	ANLAT09	P	1	1	2	2	3.00	FJ404719
	ANVIR01	P	1	1	1	1	0	EU810617
	BSR1	P	1	2	2	2	4	AF495548
	BT8	P	1	6	9	14	13.28	AY393792
	BUL04	P	1	1	1	1	0	EU810629
	BUL05	P	1	1	1	1	0	EU810630
	BUL06	P	1	1	1	1	0	EU810627
	BUL07	P	7	23	31	33	31.25	EU810628
	CIANO01	P	1	1	1	1	0	EU810654
	CINCHL01	P	1	2	3	3	4.46	DQ659577
	CINCHL02	P	1	2	2	2	4.00	EU810663
	CINPRE02	P	1	1	1	1	0	KJ446984
	COSUN2	P	1	1	1	2	2.00	DQ847269
	CRICAP01*	P	1	2	2	2	4.00	KT376920
	CYAOLI01	P	1	1	1	1	0	DQ659579
	CYAOLI02	P	1	1	1	1	0	DQ659587
	CYAOLI09	P	1	2	2	2	4.00	FJ404707
	CYAOLI10	P	1	1	1	1	0	FJ404717
	CYAOLI12	P	1	1	1	1	0	FJ424521
	CYAORI02	P	1	1	1	1	0	KJ446986
	CYAVER01	P	1	1	1	1	0	KJ446985
	CYAVER02*	P	1	1	1	1	0	KT376922
	GBCAM1	P	1	3	3	3	5	DQ847267
	GRW02	P	2	5	11	14	12.93	AF254962
	GRW09	P	1	15	47	63	60.97	DQ060773
	GRW11	P	3	14	25	40	35.39	AY831748
	GRW12	P	1	1	1	1	0	DQ368378
	LAMPUR03	P	1	2	2	2	4.00	EU810655
	NEOBS01	P	1	1	1	3	3.00	FJ404705
	NEOBS02	P	1	1	1	1	0	DQ508392
	PBPIP1	P	1	4	4	6	6.38	DQ847258

PHICT01	P	1	2	3	5	5.07	EU810619
PHICT02	P	1	1	2	3	3.46	EU810622
PSB1	P	1	2	2	2	4.00	AF495566
REB12P	P	1	1	1	2	2.00	DQ847259
RFF1	P	1	6	12	24	21.76	DQ847264
RTSR1	P	3	7	11	14	13.19	AF495568
SGS1	P	11	31	67	106	90.33	AF495571
SYAT05	P	4	13	16	22	19.63	DQ847271
SYBOR02	P	1	5	7	9	9.71	DQ368392
SYBOR05	P	1	2	2	2	4.00	DQ368393
SYBOR10	P	2	4	4	5	6.09	DQ368390
SYBOR11	P	1	2	3	3	4.46	DQ368391
TERUF02	P	2	3	3	3	5.46	EU810618
TURAF01	P	1	1	1	1	0	EU810698
TURDUS1	P	3	12	24	31	28.95	AF495576
TURPEL03*	P	1	1	1	1	0	KT376932
TURPEL04*	P	1	1	1	1	0	KT376933
AFTRU1	L	1	1	1	1	0	DQ847205
AFTRU2	L	1	1	1	1	0	DQ847206
AFTRU3	L	1	1	1	1	0	DQ847207
ANLAT10	L	2	3	4	4	5.68	FJ839445
ANLAT12	L	1	1	1	1	0	FJ839447
ANLAT17*	L	1	1	1	1	0	KT376935
ANLAT18*	L	1	1	1	1	0	KT376936
ARITEP02*	L	1	1	1	1	0	KT595662
BT2	L	1	6	10	12	12.66	AY393802
BUL3	L	1	1	1	1	0	DQ847208
CAMCHL01*	L	1	1	1	1	0	KT595663
COSUN1	L	1	1	1	1	0	DQ847216
CYAOLI15*	L	1	1	1	1	0	KT376941
CYAOLI16*	L	1	1	1	1	0	KT376942
CYAOLI17*	L	1	1	1	1	0	KT376943
CYAOLI18*	L	1	1	1	1	0	KT376944
CYAVER03*	L	1	1	1	1	0	KT376946
CYAVER04*	L	1	1	1	1	0	KT376945
EUPHOR02*	L	1	1	1	1	0	KT376947
EUPHOR03*	L	1	1	1	1	0	KT376948
EUPHOR04*	L	1	1	1	1	0	KT376949
HIRUS11	L	1	3	3	4	5.01	KP696494
HYLPRA01*	L	1	1	1	1	0	KT595664
NEOLI02	L	1	1	1	1	0	AF465560
PLACYA02*	L	1	1	1	1	0	KT595666
PLOCUC01*	L	1	1	1	3	3.00	KT376950
PLOCUC03*	L	1	1	1	1	0	KT376951
PLOCUC04*	L	1	1	1	1	0	KT376952
PLOMEL04*	L	1	1	1	1	0	KT595667
PLONIG04*	L	1	1	1	1	0	KT376953
PLONIG05*	L	1	1	1	1	0	KT376954
PLONIG06*	L	1	1	1	2	2.00	KT376955
PLONIG10*	L	1	1	1	1	0	KT376956
PLONIG11*	L	1	1	1	1	0	KT376957
PLONIG12*	L	1	1	1	1	0	KT376958
PLONIG13*	L	1	1	1	1	0	KT376959
PLONIG14*	L	1	1	1	1	0	KT376960
PLONIG15*	L	1	1	1	1	0	KT376961

REB10	L	1	2	3	3	4.46	DQ847222
REB11	L	1	6	7	10	10.72	DQ847223
REB12L	L	1	1	1	1	0	DQ847227
REB6	L	1	2	3	5	5.32	DQ847209
REB7	L	1	3	4	4	5.64	DQ847218
REB8	L	1	2	3	4	4.68	DQ847219
REB9	L	1	1	1	1	0	DQ847224
RECOB3	L	1	9	14	17	17.59	DQ847221
SATEC01	L	1	4	4	4	6.00	JN032654
SFC8	L	1	6	10	16	15.12	DQ847234
SYBOR06	L	1	2	2	2	4	DQ847237
SYBOR07	L	1	1	1	1	0	DQ847238
SYBOR08	L	2	3	3	3	5.46	DQ847239
SYBOR12	L	1	1	1	1	0	DQ847211
SYBOR22	L	1	1	1	1	0	KJ850284
TURPEL02*	L	1	1	1	1	0	KT376972
VIMWE2	L	1	1	1	1	0	DQ847225
WW6	L	1	5	7	8	8.95	DQ847210
YMWD1	L	1	2	2	2	4.00	DQ847220
YMWD2	L	1	1	2	2	3	DQ847226
ZOSSEN04*	L	1	1	1	1	0	KT376976
AFTRU06	H	1	1	1	1	0	EU810734
ALCLEU01	H	1	1	1	1	0	DQ659592
ALCLEU02	H	2	2	3	3	4.72	EU810713
ALCLEU03	H	1	1	1	1	0	EU810712
ALCQUA01	H	1	1	1	1	0	EU810717
ANLAT02	H	1	1	2	2	3.00	EU770153
ANSEI01	H	1	1	1	1	0	EU810742
BESUN1	H	1	1	1	1	0	DQ847183
BLESY01	H	1	1	1	1	0	EU810727
BLNW1	H	1	1	1	1	0	DQ847202
BUL1	H	1	1	1	3	3	DQ847194
BUL2	H	1	2	3	5	5.07	DQ847195
CCF6	H	1	1	1	1	0	DQ368341
CELEC01	H	2	3	3	3	5.46	EU810722
CHAFUL01	H	1	1	1	1	0	EU810738
CINPRE01	H	1	1	1	1	0	EU810743
COLL2	H	1	4	9	11	11.53	DQ060766
CRYRE01	H	1	1	1	1	0	EU810737
CYAOLI03	H	1	1	1	1	0	EU810741
CYAOLI05	H	1	1	1	1	0	FJ404696
CYAOLI06	H	1	1	1	1	0	FJ404698
CYAOLI07	H	1	1	1	1	0	FJ404699
CYAOLI08	H	1	1	1	1	0	FJ404700
DELFRA01	H	1	1	1	1	0	EU810741
DELFRA02	H	1	1	1	1	0	EU810744
ESTMEL02*	H	1	1	1	1	0	KT376902
EUPHOR01*	H	1	1	1	1	0	KT376904
GLSJO01	H	2	2	2	2	5,0	EU810726
HAECOL1	H	1	1	1	1	0	AF495554
HALMAL01	H	1	1	1	1	0	EU810721
HIPOL1	H	1	2	3	4	4.68	DQ000324
ILABY01	H	1	2	2	2	4.00	EU810746
ILABY02	H	1	1	1	1	0	EU810747
LAMPUR01	H	1	1	2	3	3.46	EU810728

	LAMPUR02	H	1	2	2	2	4.00	EU810729
	LAVA1	H	1	2	2	3	3.72	DQ847186
	LONBIC01*	H	1	2	2	2	4.00	KT376905
	LONCUC02*	H	1	1	1	1	0	KT376907
	MALNI01	H	1	1	1	1	0	EU810731
	NIGBI01	H	1	1	1	1	0	EU810736
	PLOCUC05*	H	1	1	1	1	0	KT376908
	PLONIG01	H	1	1	1	1	0	HQ386237
	PLONIG02	H	1	1	1	1	0	HQ386238
	PLONIG03	H	1	1	1	1	0	HQ386239
	PLONIG07*	H	1	2	2	2	4.00	KT376910
	PLONIG08*	H	1	1	1	1	0	KT376911
	PLONIG09*	H	1	1	1	1	0	KT376912
	QUERY01	H	4	8	9	10	11.12	EU810750
	RBQ01	H	1	1	2	2	3.00	AF495567
	RBQ07	H	1	1	1	2	2.00	EF117230
	RBQ11	H	1	1	3	4	4.64	EF117229
	REB1	H	1	1	1	1	0	DQ847180
	REB2	H	1	1	1	2	2.00	DQ847191
	REB3	H	1	1	1	1	0	DQ847196
	REB4	H	1	1	3	4	4.64	DQ847197
	REB5	H	1	1	1	1	0	DQ847198
	RECOB1	H	1	1	1	1	0	DQ847188
	RECOB2	H	1	1	1	1	0	DQ847187
	TERUF01	H	1	2	2	3	3.72	EU810753
	TURAFE02*	H	1	1	1	1	0	KT376914
	VASUN1	H	1	1	1	1	0	DQ847184
	VILWE04	H	1	1	1	3	3.00	EU810751
	VILWE1	H	1	1	1	2	2.00	DQ847181
	VILWE2	H	1	1	1	1	0	DQ847200
	VILWE3	H	1	1	1	3	3.00	DQ847201
	WW1	H	3	7	10	10	10.84	AF254971
	YEWE1	H	1	1	1	5	5	DQ847192
Island	**ANAHAR03***	P	1	1	1	1	0	KT376918
	ANANEW01*	P	1	1	1	1	0	KT376919
	CRIMOZ01*	P	1	1	1	1	0	KT376921
	PLOCUC02*	P	1	1	2	3	3.46	KT376923
	PLOPRI02*	P	1	1	1	1	0	KT376924
	TUROLI01*	P	1	1	1	1	0	KT376926
	TUROLI02*	P	1	1	1	1	0	KT376927
	TUROLI03*	P	1	1	1	1	0	KT376928
	TUROLI04*	P	1	1	1	1	0	KT376929
	TUROLI11*	P	1	1	1	1	0	KT376930
	TUROLI12*	P	1	1	1	1	0	KT376931
	ZOSBRU01*	P	1	1	1	1	0	KT376934
	ANAHAR01*	L	1	1	1	1	0	KT376937
	ANAHAR02*	L	1	1	1	1	0	KT376938
	PLOSAN01*	L	1	1	1	1	0	KT376962
	PLOSAN04*	L	1	1	1	2	2.00	KT376965
	TUROLI06*	L	1	2	2	2	4.00	KT376966
	TUROLI08*	L	1	1	1	1	0	KT376968
	TUROLI09*	L	1	1	1	1	0	KT376969
	TUROLI10*	L	1	1	1	1	0	KT376970
	ZOBOR04	L	1	1	1	4	4.00	JN032615
	ARITEP01*	H	1	1	1	1	0	KT376897

	COLMAL01*	H	1	1	1	1	0	KT376898
	COLMAL02*	H	1	1	1	1	0	KT376899
	CRIRUF05*	H	1	1	1	1	0	KT376901
	PLOGRA01*	H	1	1	1	1	0	KT376909
	PRIMOL01*	H	1	1	1	1	0	KT376913
	TUROLI05*	H	1	1	1	1	0	KT376915
	ZOSGRI01*	H	1	1	1	1	0	KT376916
	ZOSLUG01*	H	1	1	1	2	2.00	KT376917
	ZOSLUG02*	H	1	1	1	1	0	KT595668
	ZOSLUG03*	H	1	1	1	1	0	KT595669
	ZOSMAD01	H	1	3	3	8	6.60	JN661945
Both	**AEMO01**	P	2	9	13	16	15.69	FJ355919
	AFTRU09	P	1	1	1	1	0	EU810611
	AFTRU5	P	3	4	5	6	6.73	DQ847263
	COLL7	P	1	6	11	17	16.03	DQ368376
	CYAOLI04	P	1	2	7	12	11.84	EU810652
	CYAORI01	P	1	2	2	2	4.00	DQ659568
	GRW04	P	3	19	39	61	56.66	AF254975
	GRW06	P	10	27	40	47	42.34	DQ368381
	LINOLI01	P	2	9	16	20	19.33	DQ659554
	MALNI02	P	2	7	10	17	14.06	EU810645
	PLACAS02	P	2	5	6	6	6.51	EU810612
	PLOPRI01	P	1	4	10	11	11.35	DQ659575
	PLOSAN05*	P	1	1	1	2	2.00	KT376925
	PYSUN1	P	1	3	7	13	12.45	DQ847268
	RECOB4	P	1	3	11	16	15.21	DQ847260
	SYBOR09	P	1	5	5	5	7.00	DQ368394
	WW3	P	1	11	16	22	22.15	AF495577
	AFR211	L	1	9	10	13	13.77	KM056529
	AFR212	L	1	5	5	5	7.00	KM056530
	AFR214	L	1	4	7	8	8.87	KM056531
	CRIRUF02*	L	1	4	5	6	7.16	KT376939
	CRIRUF04*	L	1	2	2	2	4.00	KT376940
	TURPEL01*	L	1	1	1	1	0	KT376971
	CRIRUF01*	H	2	4	5	5	6.09	KT376900
	ESTMEL03*	H	2	2	3	3	4.72	KT376903
	LONCUC01*	H	1	1	1	1	0	KT376906
	YEWE2	H	1	2	2	4	4.00	DQ847193
	ZOSSTE01	H	1	1	1	6	6.00	EU810756

Table S2.2 Distribution of Haemosporidia lineages in the 13 bird families sampled in the Gulf of Guinea is indicated with grey cells with the numbers of species infected by the lineages. The lineages are classified by their presence on the mainland (Main), on the islands (Isl) or in both the islands and the mainland (Both). (a) *Plasmodium* sp., (b) *Haemoproteus* sp., (c) *Leucocytozoon* sp.

(a) Plasmodium sp.

	Site	Nectariniidae	Ploceidae	Turdidae	Sylviidae	Fringillidae	Pycnonotidae	Zosteropidae	Estrildidae	Cisticolidae	Sturnidae	Columbidae	Monarchidae	Alcedinidae	Total
GRW09	Main	9	4	9	3	2	14		6	1					48
RFF1	Main		7	1			1		5	7					21
BUL07	Main		1	1	2	1	4	1	4		1				15
SYAT05	Main			7	4	1					1	1			14
GRW02	Main		2		7	2									11
BT8	Main		5	1		1			2				1		10
ACCTAC01	Main		2	4			2				1				9
PHICT01	Main	1					4								5
CINCHL01	Main	4													4
ANLAT03	Main						2			1					3
CYAOLI09	Main	1							1						2
CRICAP01	Main	1				1									2
AFTRU4	Main			2											2
CYAOLI02	Main	1													1
CYAVER02	Main	1													1
AFTRU07	Main			1											1
AFTRU08	Main			1											1
TURPEL03	Main			1											1
TURPEL04	Main			1											1
ANVIR01	Main						1								1
BUL04	Main						1								1
BUL05	Main						1								1
CIANO01	Main									1					1
TURAF01	Main											1			1
GRW04	Both	5	4	2	11	7		7	4	2	2				44
GRW06	Both	1	1	5	7	5	1	3				1		1	25
WW3	Both	1	5	1	4	3	2		1						17
LINOLI01	Both	6	5		1	2				2					16

COLL7	Both	5	7			1	1		1						15
RECOB4	Both	13							2						15
PYSUN1	Both	11	1				1								13
MALNI02	Both		10		1	1		1							13
CYAOLI04	Both	11					1								12
AEMO01	Both	4	5		1				1				1		12
PLOPRI01	Both	7	1								1				9
SYBOR09	Both		1	1	1	1	1								5
PLACAS02	Both	2		1		1									4
AFTRU5	Both			3				1							4
CYAORI01	Both	1	1												2
PLOSAN05	Both		2												2
AFTRU09	Both			1											1
PLOCUC02	Isl		3												3
ANAHAR03	Isl	1													1
ANANEW01	Isl	1													1
PLOPRI02	Isl		1												1
TUROLI01	Isl			1											1
TUROLI02	Isl			1											1
TUROLI03	Isl			1											1
TUROLI04	Isl			1											1
TUROLI11	Isl			1											1
TUROLI12	Isl			1											1
CRIMOZ01	Isl					1									1
ZOSBRU01	Isl							1							1
Total		64	43	18	15	15	7	6	5	2	1	1	1	1	

(b) Haemoproteus sp.

	Site	Ploceidae	Zosteropidae	Nectariniidae	Estrildidae	Turdidae	Columbidae	Fringillidae	Pycnonotidae	Monarchidae	Cisticolidae	Sturnidae	Sylviidae	Alcedinidae	Total
QUERY01	Main	2							1				1		4
RBQ11	Main	4													4
VILWE04	Main	3													3
VILWE3	Main	3													3
TERUF01	Main					1				2					3
RBQ07	Main	2													2
REB2	Main	2													2
PLONIG07	Main	1		1											2
LONBIC01	Main	1			1										2
EUPHOR01	Main	1													1
PLOCUC05	Main	1													1
PLONIG08	Main	1													1
PLONIG09	Main	1													1
CINPRE01	Main			1											1
CYAOLI03	Main			1											1
CYAOLI05	Main			1											1
CYAOLI06	Main			1											1
CRYRE01	Main				1										1
LONCUC02	Main				1										1
ESTMEL02	Main				1										1
AFTRU06	Main					1									1
ILABY01	Main					1									1
TURAFE02	Main						1								1
ZOSSTE01	Both		6												6
CRIRUF01	Both					1		2	1					1	5
YEWE2	Both	1	3												4
ESTMEL03	Both				1		2								3
LONCUC01	Both				1										1
ZOSMAD01	Isl		6	1								1			8
ZOSLUG01	Isl		2												2
ZOSGRI01	Isl		1												1

ZOSLUG02	Isl		1												1
ZOSLUG03	Isl		1												1
PLOGRA01	Isl	1													1
TUROLI05	Isl					1									1
COLMAL01	Isl						1								1
COLMAL02	Isl						1								1
CRIRUF05	Isl							1							1
ARITEP01	Isl								1						1
PRIMOL01	Isl										1				1
Total		6	20	5	5	4	5	3	2	0	1	1	0	1	

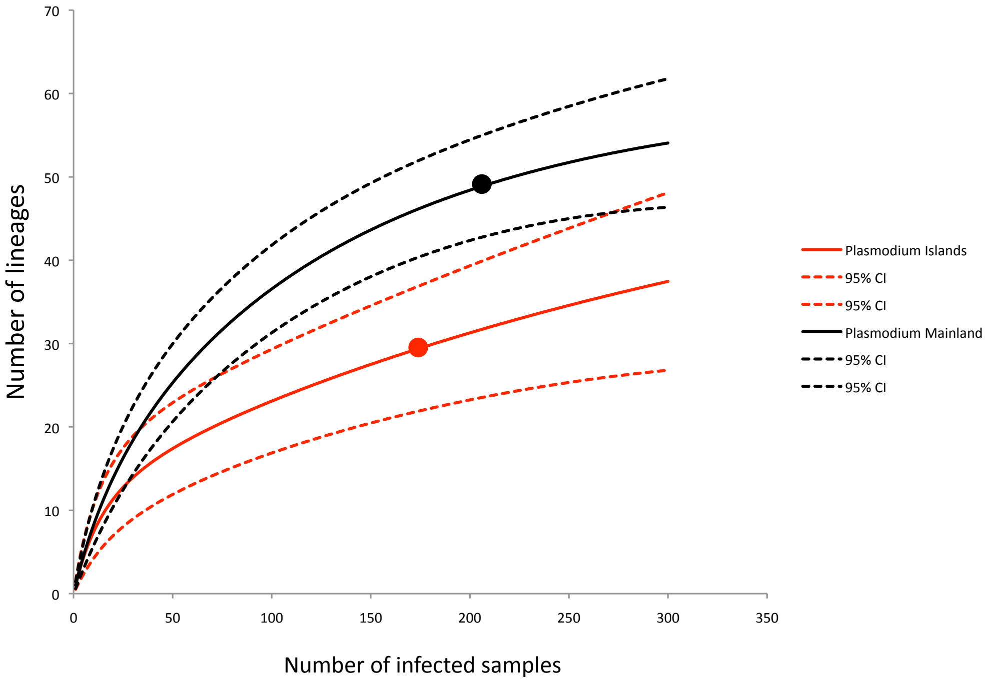
(c) Leucocytozoon sp.

	Site	Ploceidae	Nectariniidae	Pycnonotidae	Turdidae	Zosteropidae	Estrildidae	Fringillidae	Sylviidae	Cisticolidae	Sturnidae	Alcedinidae	Columbidae	Monarchidae	Total
RECOB3	Main	4		2	1	1	1	1	4						14
REB7	Main	1			1			2							4
SATECO01	Main	1	1	1	1										4
ANLAT10	Main	2		1								1			4
HIRUS11	Main	1	2												3
PLOCUC01	Main	3													3
PLONIG06	Main	2													2
CAMCHL01	Main									1					1
HYLPRA01	Main								1						1
ANLAT12	Main			1											1
ANLAT17	Main			1											1
ANLAT18	Main			1											1
ARITEP02	Main			1											1
CYAOLI15	Main		1												1
CYAOLI16	Main		1												1
CYAOLI17	Main		1												1
CYAOLI18	Main		1												1
CYAVER03	Main		1												1
CYAVER04	Main		1												1
EUPHOR02	Main	1													1
EUPHOR03	Main	1													1
EUPHOR04	Main	1													1
PLOCUC03	Main	1													1
PLOCUC04	Main	1													1
PLOMEL04	Main	1													1
PLONIG04	Main	1													1
PLONIG05	Main	1													1
PLONIG10	Main	1													1
PLONIG11	Main	1													1
PLONIG12	Main	1													1
PLONIG13	Main	1													1

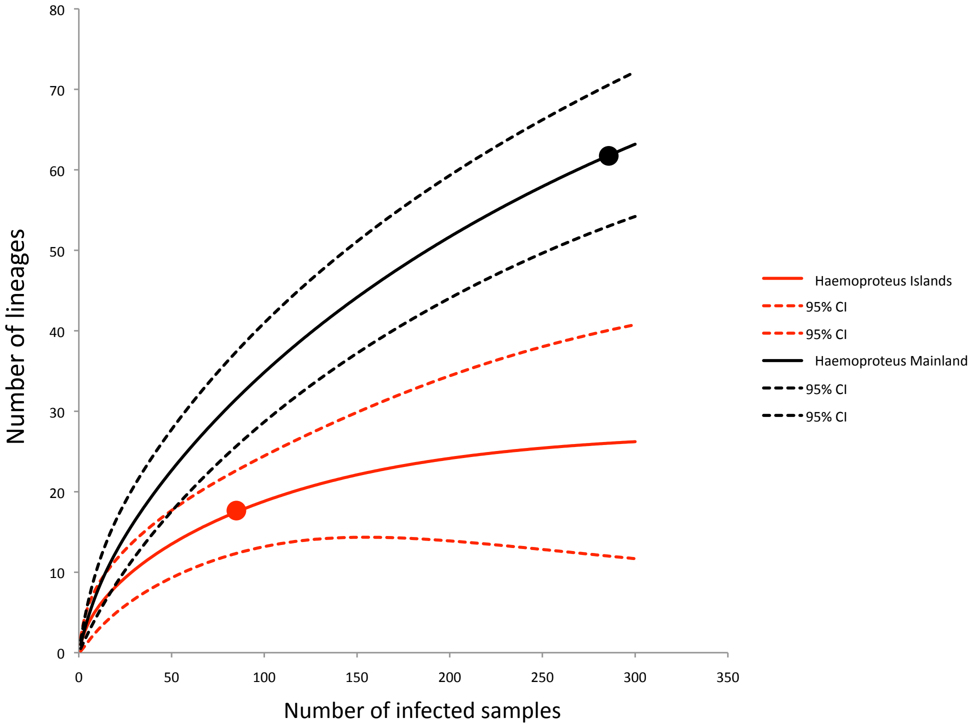
PLONIG14	Main	1													1
PLONIG15	Main	1													1
TURPEL02	Main				1										1
ZOSSEN04	Main					1									1
AFR211	Both	1			1	2	1		1	3	2				11
AFR214	Both	2	1				4	1							8
CRIRUF02	Both	2	1	1				2							6
AFR212	Both			1		1	1								3
CRIRUF04	Both						1	1							2
TURPEL01	Both				1										1
ZOBOR04	Isl					4									4
PLOSAN01	Isl	1													1
PLOSAN04	Isl	2													2
ANAHAR01	Isl		1												1
ANAHAR02	Isl		1												1
TUROLI06	Isl			1	1										2
TUROLI08	Isl				1										1
TUROLI09	Isl				1										1
TUROLI10	Isl				1										1
Total		32	13	9	9	8	7	6	2	4	2	1	0	0	

Figure S2.1 Rarefaction and extrapolation curves with 95% confidence intervals (dashed lines) for a) *Plasmodium* sp., b) *Haemoproteus* sp. and c) *Leucocytozoon* sp. Black lines correspond to mainland estimates and red lines to island estimates. Dots represent the actual number of samples.

a)



b)



c)

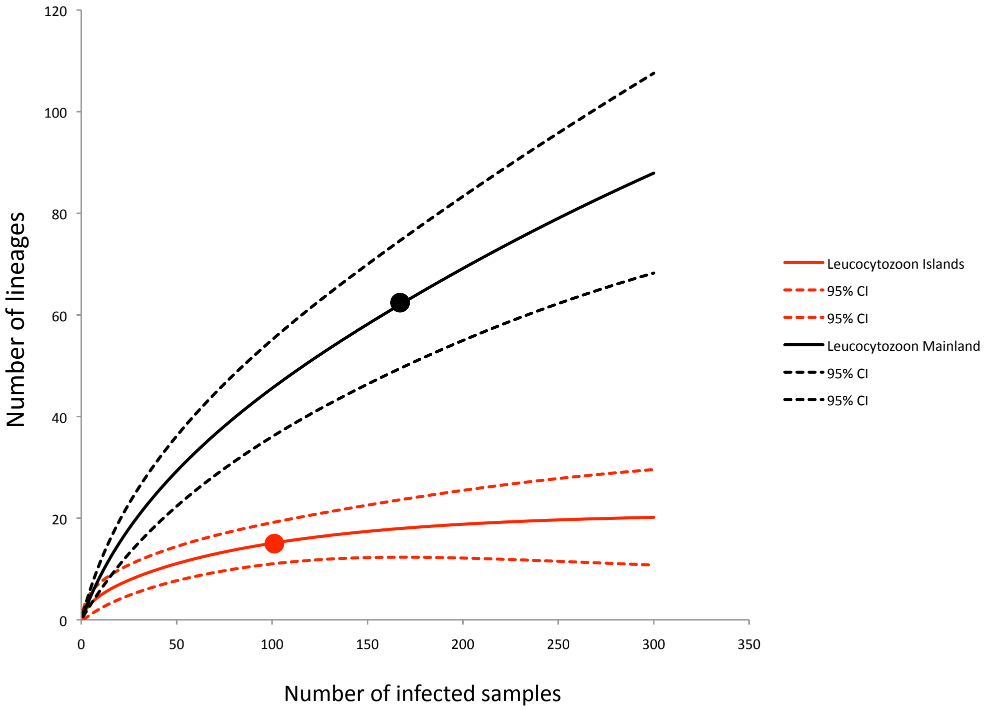
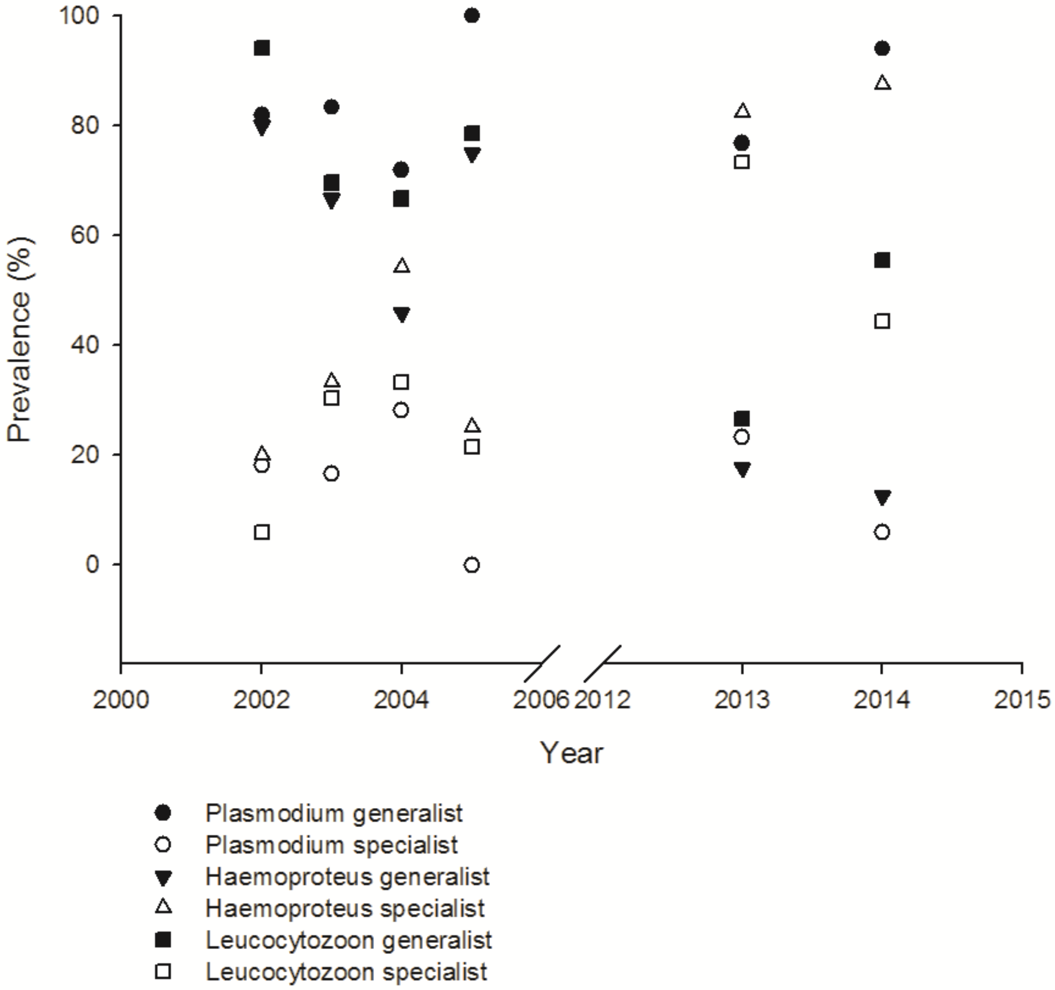

120
100
80
60
40
20
0
Number of lineages
0
50
100
150
200
250
300
350
Number of infected samples
Leucocytozoon Islands
95% CI
95% CI
Leucocytozoon Mainland
95% CI
95% CI

Figure S2.2 Prevalence of generalist and specialist Haemosporidian lineages in the Gulf of Guinea, per genus and per year.



Appendix S3 Phylogenetic analyses and phylogenetic trees.

For the three haemosporidia genera we recovered all the sequences available on MalAvi from the Gulf of Guinea. Relationships between lineages were inferred with Bayesian inference, both as implemented in MrBayes 3.2.6 (Huelsenbeck & Ronquist, 2001; Ronquist & Huelsenbeck, 2003) and in Beast 1.8.2 (Drummond *et al.*, 2012). We used PartitionFinder 1.1.1 (Lanfear *et al.*, 2012) to determine the best-fit partitioning scheme for the cyt *b* dataset (486 bp) and the respective substitution models for each partition, using the Bayesian Information Criterion. For both MrBayes and Beast, we carried out two independent runs of 25 million generations sampled every 2500 generations, for a total of 10000 trees each per run. For the 'burn-in', 25% of the trees were discarded from the posterior distribution. The remaining trees were used to calculate the posterior probabilities (15000 trees). Convergence of the independent runs and the Effective Sampling Size (ESS) of each parameter were assessed in Tracer version 1.5 (Drummond & Rambaut, 2007); ESS above 200 are considered adequate. For the runs in MrBayes, the potential scale reduction factor (PSRF) was also checked, with values close to 1 supporting convergence. Analyses in Beast were used not only to confirm results from MrBayes but also to produce chronograms – ultrametric trees with the splits between lineages occurring along a timescale. As the evolutionary rate of haemosporidians has been difficult to estimate (Bensch *et al.*, 2013), the clock rate has been left at 1.0. This gives a relative time sequence of branching events. The divergence values can be multiplied by any putative rate (in substitutions per site per lineage per million years) in order to be translated in years before present. For the most widely used rate of 1.2% sequence divergence per million year for haemosporidians (Ricklefs & Outlaw, 2010), this means multiplying divergence values by 0.006. Initial runs were performed with different tree priors (Yule, Birth-and-Death) and clock models (strict and uncorrelated relaxed clock). A Bayes factors approach (Kass & Raftery, 1995) rejected, as expected, the strict clock and showed that tree prior choice had no impact. The final analysis used a relaxed-clock model assuming an uncorrelated lognormal clock model (standard deviation prior: exponential with mean 1/3) and a Yule speciation model (uniform prior between 0 and 100).

The relationships between the different haemosporida genera have been extremely hard to resolve (Perkins, 2014). The classical position of *Leucocytozoon* as the outgroup to all other genera was replaced by a basal position for mammalian *Plasmodium* and *Hepatocystis* (Outlaw & Ricklefs, 2011), but it was recently supported again by a study using multiple slow evolving nuclear markers (Borner *et al.*, 2016). Ongoing whole-genome work suggests yet again another arrangement where *Haemoproteus* and *Leucocytozoon* make a basal clade, avian *Plasmodium* is the most recent clade, and the mammal and sauropsid haemosporida are in between (Susan Perkins, pers. comm.). Using a certain but distant outgroup (*Theileria*) we recovered the 'classic' topology, where *Leucocytozoon* is basal to all haemosporida and the mammalian *Plasmodium* and *Hepatocystis* are a sister clade to avian *Plasmodium* and *Haemoproteus.* Nevertheless, this sister relationship had no statistical support making the relationships between all groups unresolved. Using a Bayes factor approach, all possible relationships between *Leucocytozoon*, *Haemoproteus*, and *Plasmodium* were equally likely (Fig. S3.1). We decided to run the final analyses with our Gulf of Guinea dataset, rooting the trees with *Leucocytozoon*.

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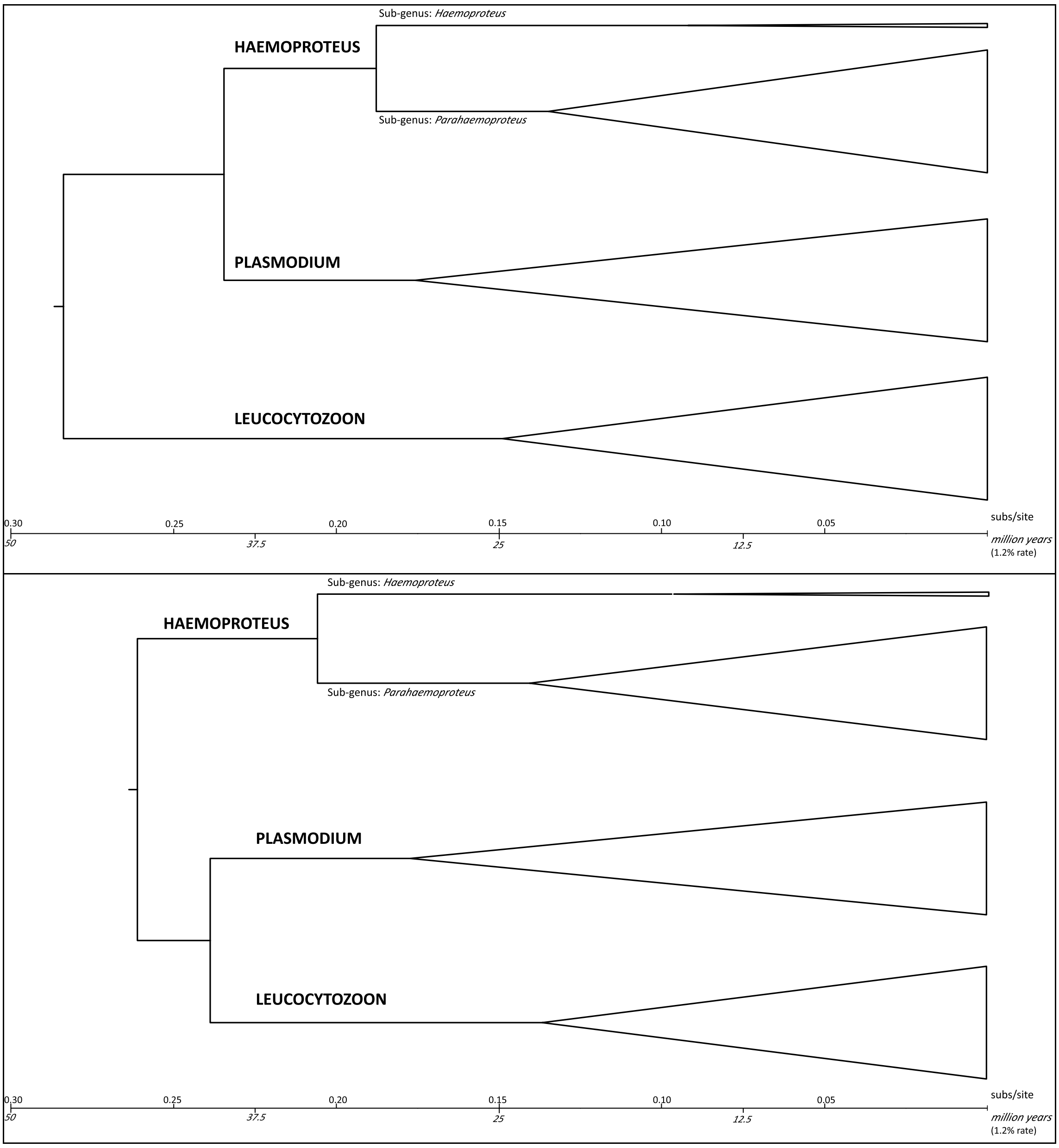
Ronquist, F. & Huelsenbeck, J.P. (2003) MRBAYES3: Bayesian phylogenetic inference under mixed models. *Bioinformatics*, **19**, 475-481.

Figure S3.1 Phylogenetic relationships between the three avian haemosporidian genera inferred from a 486 bp fragment of cyt *b* using the Bayesian approach implemented in MrBayes. Branching order between the genera remains uncertain as the closest known outgroup (*Theileria*) is very distantly related. Top: the classic topology, which was confirmed recently by a study using slowly evolving nuclear markers; it was the topology used in this study. Middle: topology proposed by Outlaw & Ricklefs (2011) where *Leucocytozoon* is not basal, but instead has a high mutation rate compared to the other two genera; bottom: third possibility, which curiously seems to be supported by ongoing genomic studies – in this case avian *Haemoproteus* and *Leucocytozoon* form the basal clade, whereas avian *Plasmodium* is at the tip, with all other mammalian and squamata Haemosporidia in between (not shown). Using the Bayes Factor approach with our Gulf of Guinea dataset, all topologies were equivalent.

Figure S3.2 a) Phylogenetic relationships of the avian Haemosporida genera from the Gulf of Guinea. Bayesian chronogram inferred with BEAST from a 486 bp fragment of cyt *b*. Divergence scale: top, substitutions per site per lineage per million years; bottom – million years before present using the 1.2% molecular clock rate estimated by Ricklefs & Outlaw (2010) for avian Haemosporida. Relationships were inferred for lineages from all genera at the same time, considering *Leucocytozoon* as the basal group (as in Fig. S3.1, top). For clarity, relationships within each genera are also presented separately: b) *Haemoproteus*; c) *Plasmodium*; d) *Leucocytozoon*. Except were a value is given, all branches with posterior probabilities below 0.95 were collapsed. The asterisk on the branch for ZOSMAD01 in figure b) refers to a lineage previously found on other islands (Madagascar, Grande Comore) and on the mainland (East Africa).

Figure S3.1


Sub-genus: *Haemoproteus*
HAEMOPROTEUS
Sub-genus: *Parahaemoproteus*
PLASMODIUM
LEUCOCYTOZOON
0.30
0.25
0.20
0.15
0.10
0.05
subs/site
50
37.5
25
12.5
million years
(1.2% rate)
Sub-genus: *Haemoproteus*
HAEMOPROTEUS
Sub-genus: *Parahaemoproteus*
PLASMODIUM
LEUCOCYTOZOON
0.30
0.25
0.20
0.15
0.10
0.05
subs/site
50
37.5
25
12.5
million years
(1.2% rate)

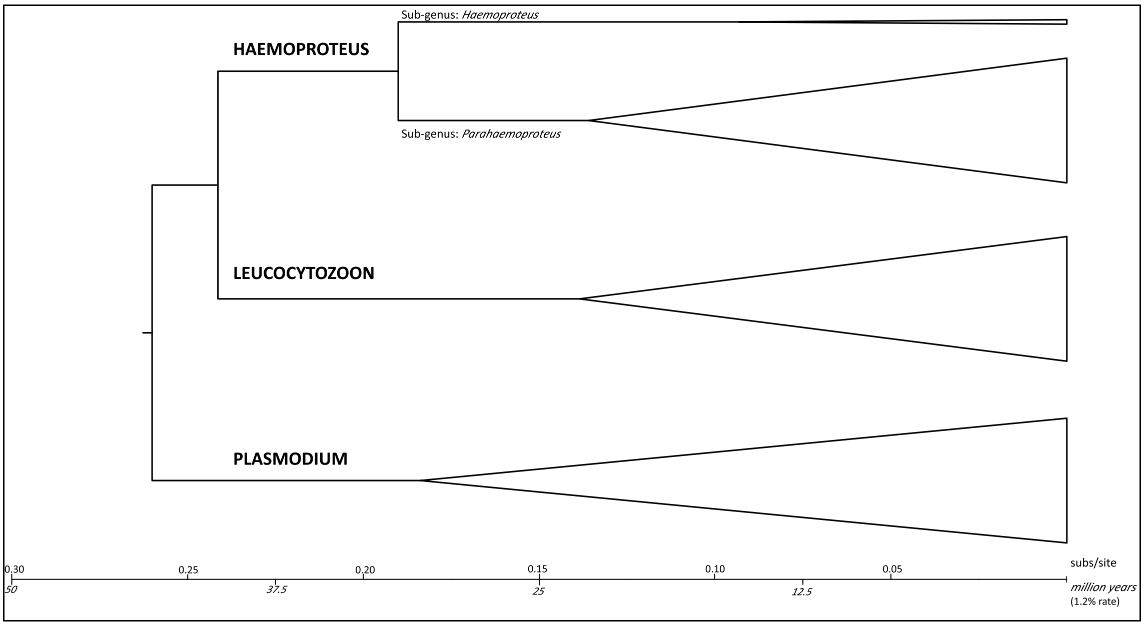

Sub-genus: *Haemoproteus*
HAEMOPROTEUS
Sub-genus: *Parahaemoproteus*
LEUCOCYTOZOON
PLASMODIUM
0.30
0.25
0.20
0.15
0.10
0.05
subs/site
50
37.5
25
12.5
million years
(1.2% rate)

Figure S3.2a

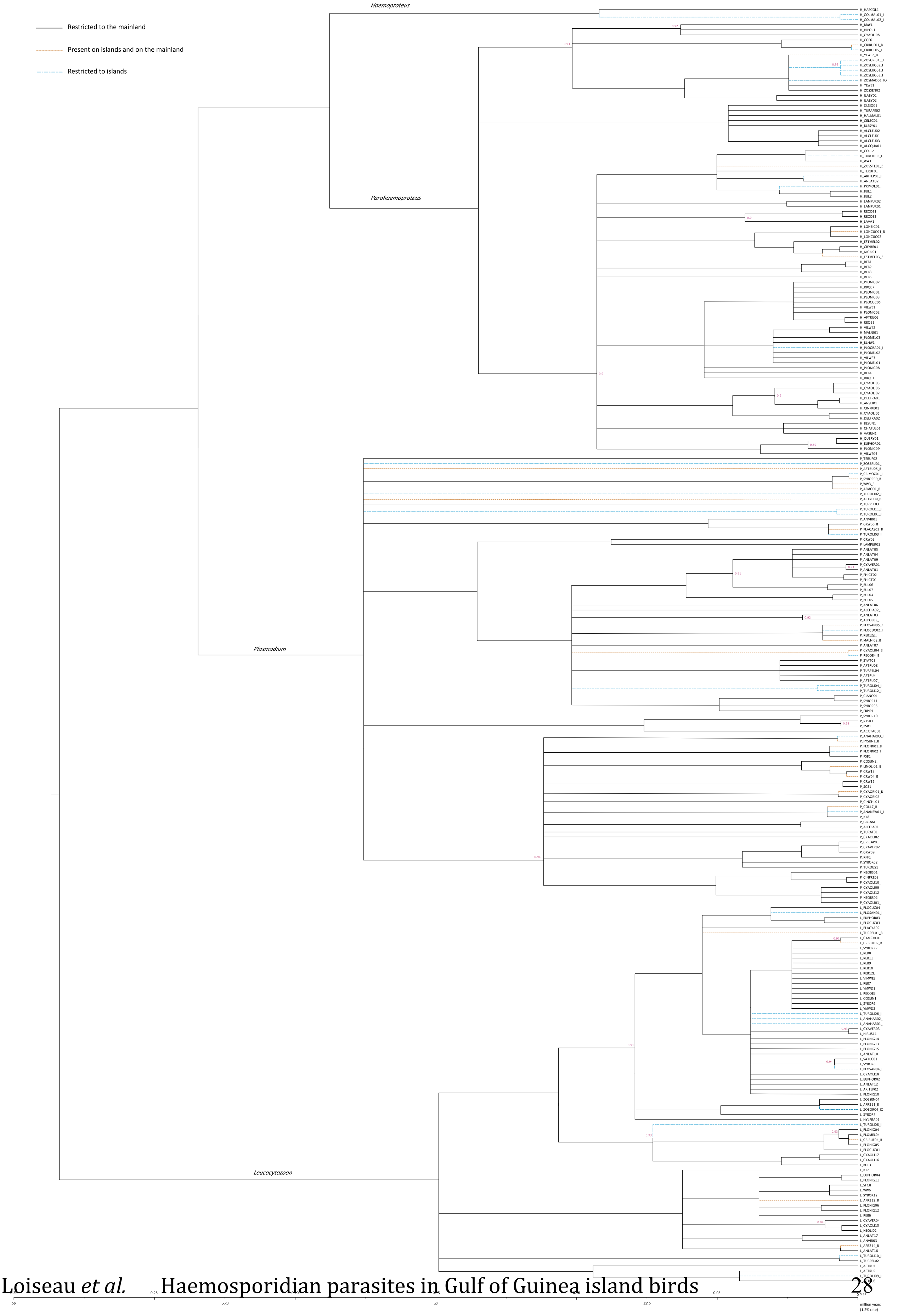

Restricted to the mainland
Present on islands and on the mainland
Restricted to islands
Haemoproteus
Parahaemoproteus
Plasmodium
Leucocytozoon
0.92
0.91
0.89
0.93
0.94
H_HAECOL1
H_COLMAL01_I
H_COLMAL02_I
H_BRW1
H_HIPOL1
H_CYAOLI08
H_CCF6
H_CRIRUF01_B
H_CRIRUF05_I
H_YEWE2_B
H_ZOSGRI01__I
H_ZOSLUG02_I
H_ZOSLUG01_I
H_ZOSLUG03_I
H_ZOSMAD01_IO
H_YEWE1
H_ZOSSEN02_
H_ILABY01
H_ILABY02
H_GLSJO01
H_TURAFE02
H_HALMAL01
H_CELEC01
H_BLESY01
H_ALCLEU02
H_ALCLEU01
H_ALCLEU03
H_ALCQUA01
H_COLL2
H_TUROLI05_I
H_WW1
H_ZOSSTE01_B
H_TERUF01
H_ARITEP01_I
H_ANLAT02
H_PRIMOL01_I
H_BUL1
H_BUL2
H_LAMPUR02
H_LAMPUR01
H_RECOB1
H_RECOB2
H_LAVA1
H_LONBIC01
H_LONCUC01_B
H_LONCUC02
H_ESTMEL02
H_CRYRE01
H_NIGBI01
H_ESTMEL03_B
H_REB1
H_REB2
H_REB3
H_REB5
H_PLONIG07
H_RBQ07
H_PLONIG01
H_PLONIG03
H_PLOCUC05
H_VILWE1
H_PLONIG02
H_AFTRU06
H_RBQ11
H_VILWE2
H_MALNI01
H_PLOMEL03
H_BLNW1
H_PLOGRA01_I
H_PLOMEL02
H_VILWE3
H_PLOMEL01
H_PLONIG08
H_REB4
H_RBQ01
H_CYAOLI03
H_CYAOLI06
H_CYAOLI07
H_DELFRA01
H_ANSEI01
H_CINPRE01
H_CYAOLI05
H_DELFRA02
H_BESUN1
H_CHAFUL01
H_VASUN1
H_QUERY01
H_EUPHOR01
H_PLONIG09
H_VILWE04
P_TERUF02
P_ZOSBRU01_I
P_AFTRU05_B
P_CRIMOZ01_I
P_SYBOR09_B
P_WW3_B
P_AEMO01_B
P_TUROLI02_I
P_AFTRU09_B
P_TURPEL03
P_TUROLI11_I
P_TUROLI01_I
P_ANVIR01
P_GRW06_B
P_PLACAS02_B
P_TUROLI03_I
P_GRW02
P_LAMPUR03
P_ANLAT05
P_ANLAT04
P_ANLAT09
P_CYAVER01
P_ANLAT01
P_PHICT02
P_PHICT01
P_BUL06
P_BUL07
P_BUL04
P_BUL05
P_ANLAT06
P_ALEDIA02_
P_ANLAT03
P_ALPOL02_
P_PLOSAN05_B
P_PLOCUC02_I
P_REB12p_
P_MALNI02_B
P_ANLAT07
P_CYAOLI04_B
P_RECOB4_B
P_SYAT05
P_AFTRU08
P_TURPEL04
P_AFTRU4
P_AFTRU07_
P_TUROLI04_I
P_TUROLI12_I
P_CIANO01
P_SYBOR11
P_SYBOR05
P_PBPIP1
P_SYBOR10
P_RTSR1
P_BSR1
P_ACCTAC01
P_ANAHAR03_I
P_PYSUN1_B
P_PLOPRI01_B
P_PLOPRI02_I
P_PSB1
P_COSUN2_
P_LINOLI01_B
P_GRW12
P_GRW04_B
P_GRW11
P_SGS1
P_CYAORI01_B
P_CYAORI02
P_CINCHL01
P_COLL7_B
P_ANANEW01_I
P_BT8
P_GBCAM1
P_ALEDIA01
P_TURAF01
P_CYAOLI02
P_CRICAP01
P_CYAVER02
P_GRW09
P_RFF1
P_SYBOR02
P_TURDUS1
P_NEOBS01_
P_CINPRE02
P_CYAOLI10_
P_CYAOLI09
P_CYAOLI12
P_NEOBS02
P_CYAOLI01_
L_PLOCUC04
L_PLOSAN01_I
L_EUPHOR03
L_PLOCUC03
L_PLACYA02
L_TURPEL01_B
L_CAMCHL01
L_CRIRUF02_B
L_SYBOR22
L_REB8
L_REB11
L_REB9
L_REB10
L_REB12L_
L_VIMWE2
L_REB7
L_YMWD1
L_RECOB3
L_COSUN1
L_SYBOR6
L_YMWD2
L_TUROLI06_I
L_ANAHAR02_I
L_ANAHAR01_I
L_CYAVER03
L_HIRUS11
L_PLONIG14
L_PLONIG13
L_PLONIG15
L_ANLAT10
L_SATEC01
L_SYBOR8
L_PLOSAN04_I
L_CYAOLI18
L_EUPHOR02
L_ANLAT12
L_ARITEP02
L_PLONIG10
L_ZOSSEN04
L_AFR211_B
L_ZOBOR04_IO
L_SYBOR7
L_HYLPRA01
L_TUROLI08_I
L_PLONIG04
L_PLOMEL04
L_CRIRUF04_B
L_PLONIG05
L_PLOCUC01
L_CYAOLI17
L_CYAOLI16
L_BUL3
L_BT2
L_EUPHOR04
L_PLONIG11
L_SFC8
L_WW6
L_SYBOR12
L_AFR212_B
L_PLONIG06
L_PLONIG12
L_REB6
L_CYAVER04
L_CYAOLI15
L_NEOLI02
L_ANLAT17
L_ANVIR03
L_AFR214_B
L_ANLAT18
L_TUROLI10_I
L_TURPEL02
L_AFTRU1
L_AFTRU2
L_TUROLI09_I
L_AFTRU3
0.25
0.20
0.15
0.10
0.05
0 s.s.l
50
37.5
25
12.5
million years
(1.2% rate)

Figure S3.2b

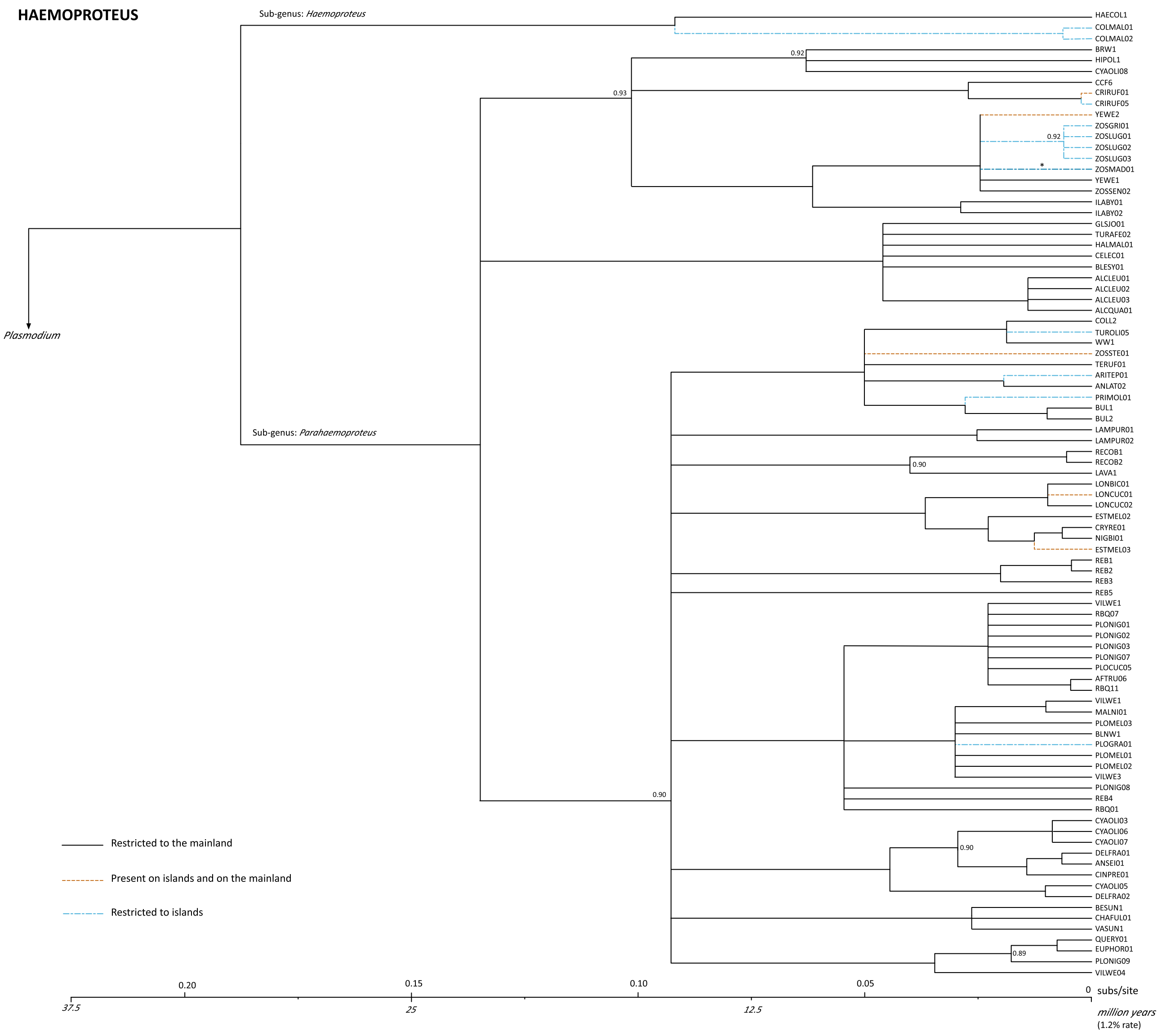

HAEMOPROTEUS
Sub-genus: *Haemoproteus*
Sub-genus: *Parahaemoproteus*
Plasmodium
HAECOL1
COLMAL01
COLMAL02
BRW1
HIPOL1
CYAOLI08
CCF6
CRIRUF01
CRIRUF05
YEWE2
ZOSGRI01
ZOSLUG01
ZOSLUG02
ZOSLUG03
ZOSMAD01
YEWE1
ZOSSEN02
ILABY01
ILABY02
GLSJO01
TURAFE02
HALMAL01
CELEC01
BLESY01
ALCLEU01
ALCLEU02
ALCLEU03
ALCQUA01
COLL2
TUROLI05
WW1
ZOSSTE01
TERUF01
ARITEP01
ANLAT02
PRIMOL01
BUL1
BUL2
LAMPUR01
LAMPUR02
RECOB1
RECOB2
LAVA1
LONBIC01
LONCUC01
LONCUC02
ESTMEL02
CRYRE01
NIGBI01
ESTMEL03
REB1
REB2
REB3
REB5
VILWE1
RBQ07
PLONIG01
PLONIG02
PLONIG03
PLONIG07
PLOCUC05
AFTRU06
RBQ11
VILWE1
MALNI01
PLOMEL03
BLNW1
PLOGRA01
PLOMEL01
PLOMEL02
VILWE3
PLONIG08
REB4
RBQ01
CYAOLI03
CYAOLI06
CYAOLI07
DELFRA01
ANSEI01
CINPRE01
CYAOLI05
DELFRA02
BESUN1
CHAFUL01
VASUN1
QUERY01
EUPHOR01
PLONIG09
VILWE04
0.92
0.93
0.92
*
0.90
0.90
0.90
0.89
Restricted to the mainland
Present on islands and on the mainland
Restricted to islands
0.20
0.15
0.10
0.05
0
subs/site
37.5
25
12.5
million years
(1.2% rate)

Figure S3.2c

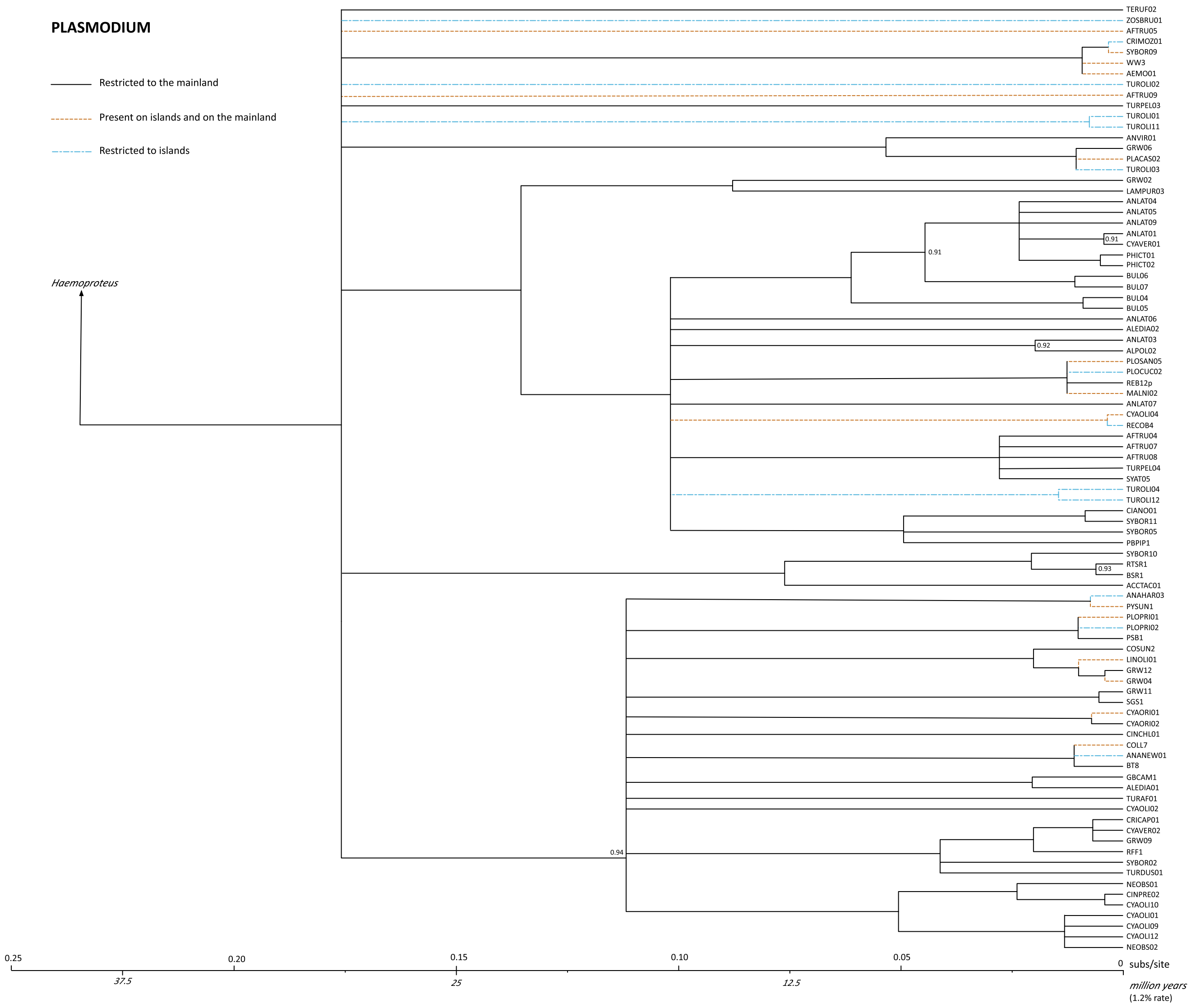
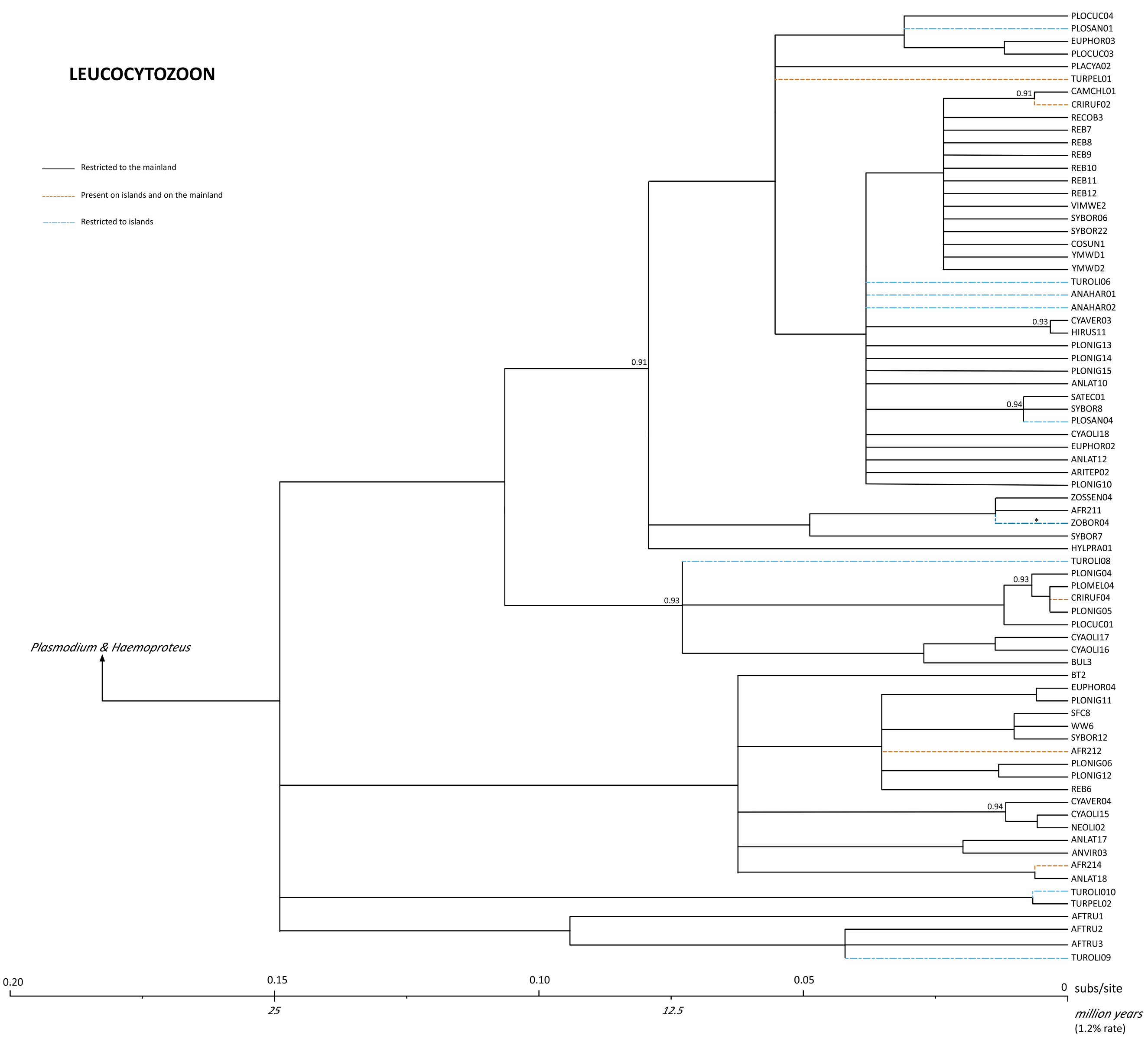

PLASMODIUM
Restricted to the mainland
Present on islands and on the mainland
Restricted to islands
Haemoproteus
TERUF02
ZOSBRU01
AFTRU05
CRIMOZ01
SYBOR09
WW3
AEMO01
TUROLI02
AFTRU09
TURPEL03
TUROLI01
TUROLI11
ANVIR01
GRW06
PLACAS02
TUROLI03
GRW02
LAMPUR03
ANLAT04
ANLAT05
ANLAT09
ANLAT01
0.91
CYAVER01
0.91
PHICT01
PHICT02
BUL06
BUL07
BUL04
BUL05
ANLAT06
ALEDIA02
ANLAT03
0.92
ALPOL02
PLOSAN05
PLOCUC02
REB12p
MALNI02
ANLAT07
CYAOLI04
RECOB4
AFTRU04
AFTRU07
AFTRU08
TURPEL04
SYAT05
TUROLI04
TUROLI12
CIANO01
SYBOR11
SYBOR05
PBPIP1
SYBOR10
RTSR1
0.93
BSR1
ACCTAC01
ANAHAR03
PYSUN1
PLOPRI01
PLOPRI02
PSB1
COSUN2
LINOLI01
GRW12
GRW04
GRW11
SGS1
CYAORI01
CYAORI02
CINCHL01
COLL7
ANANEW01
BT8
GBCAM1
ALEDIA01
TURAF01
CYAOLI02
CRICAP01
CYAVER02
GRW09
0.94
RFF1
SYBOR02
TURDUS01
NEOBS01
CINPRE02
CYAOLI10
CYAOLI01
CYAOLI09
CYAOLI12
NEOBS02
0.25
0.20
0.15
0.10
0.05
0
subs/site
37.5
25
12.5
million years
(1.2% rate)

Figure S3.2d


LEUCOCYTOZOON
Restricted to the mainland
Present on islands and on the mainland
Restricted to islands
Plasmodium & Haemoproteus
PLOCUC04
PLOSAN01
EUPHOR03
PLOCUC03
PLACYA02
TURPEL01
0.91
CAMCHL01
CRIRUF02
RECOB3
REB7
REB8
REB9
REB10
REB11
REB12
VIMWE2
SYBOR06
SYBOR22
COSUN1
YMWD1
YMWD2
TUROLI06
ANAHAR01
ANAHAR02
0.93
CYAVER03
HIRUS11
PLONIG13
PLONIG14
PLONIG15
ANLAT10
0.94
SATEC01
SYBOR8
PLOSAN04
CYAOLI18
EUPHOR02
ANLAT12
ARITEP02
PLONIG10
0.91
ZOSSEN04
AFR211
*
ZOBOR04
SYBOR7
HYLPRA01
TUROLI08
0.93
0.93
PLONIG04
PLOMEL04
CRIRUF04
PLONIG05
PLOCUC01
CYAOLI17
CYAOLI16
BUL3
BT2
EUPHOR04
PLONIG11
SFC8
WW6
SYBOR12
AFR212
PLONIG06
PLONIG12
REB6
0.94
CYAVER04
CYAOLI15
NEOLI02
ANLAT17
ANVIR03
AFR214
ANLAT18
TUROLI010
TURPEL02
AFTRU1
AFTRU2
AFTRU3
TUROLI09
0.20
0.15
0.10
0.05
0
subs/site
25
12.5
million years
(1.2% rate)