Host migration and environmental temperature influence avian haemosporidian prevalence: a molecular survey in a Brazilian Atlantic Rainforest

Raquel A. Rodrigues[1], Gabriel M. F. Felix[2], Mauro Pichorim[3], Patrícia A. Moreira[4], Érika M. Braga[1*]

Table S2. Backward selection of the main effects influencing the probability of infection by *Plasmodium* sp. The full random structure was maintained in all models. The Plas.Glmm1 model starts with all main effects (fixed factors), which were sequentially removed. In each step we removed the main effect that explained the small amount of deviance (indicated on the fixed factor column). The procedure was repeated until no effect could be removed without causing significant loss of model fit (indicated by the p value column). In this case, this happened only when temperature was removed from the model.

Model	Fixed Factors	Deviance	Chisq	DF	P
Plas.Glmm1	Full⊦	243.03			
Plas.Glmm2	- Age	243.03	0.002	1	0.959
Plas.Glmm3	- Preciptation	243.09	0.063	1	0.800
Plas.Glmm4	- Migratory status	244.72	1.621	1	0.202
Plas.Glmm5	- Nest shape	245.80	1.080	1	0.298
Plas.Glmm6	- Body mass	248.18	2.378	1	0.122
Plas.Glmm7	- Breeding period	249.43	1.251	2	0.534
Plas.Glmm8 (null)	- Temperature	257.62	8.195	1	0.004**

⊦Full model: *Plasmodium* sp. Infection status ~ Intercept + Age + Precipitation + Migratory Status + Nest Shape + Body mass + Breeding Period + Temperature + (Intercept|Season/Month) + (Intercept|Order/Family/Genus/Species), family = binomial (link = "logit").