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SUPPLEMENTS

Intensity of *Haemoproteus* spp. blood infection differs between wild birds captured using different trapping methods

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Table S1. Comparison of generalized linear mixed models (GLMM), describing the effect of different predictors on the possibility of catching a bird infected with *Haemoproteus* spp. for the sample with all species of birds

Models	Δ_i(BIC)	*df*
Infection status ~ Type + (1 | Species) + (1 | Year)	0.0	4
Infection status ~ Type + Migration distance + (1 | Species) + (1 | Year)	7.5	5
Infection status ~ Type + DayN + Migration distance + (1 | Species) + (1 | Year)	11.8	6
Infection status ~ Type + (1 | Species)	15.1	3
Infection status ~ Type + DayN + DayN*Type + Migration distance + (1 | Species) + (1 | Year)	17.4	7
Infection status ~ Type + DayN + DayN*Type + Leucocytozoon + Plasmodium + (1 | Species) + (1 | Year)	19.4	8
Infection status ~ Type + DayN + DayN*Type + Plasmodium + Migration distance + (1 | Species) + (1 | Year)	20.4	8
Infection status ~ Type + DayN + Plasmodium + Leucocytozoon + Migration distance + (1 | Species) + (1 | Year)	21.1	8
Infection status ~ Type + Migration distance + (1 | Species)	23.8	8
Infection status ~ Type + DayN + DayN*Type + Leucocytozoon + Migration distance + (1 | Species) + (1 | Year)	26.9	9
Infection status ~ Type + DayN + DayN*Type + Leucocytozoon + Plasmodium + Migration distance + (1 | Species) + (1 | Year)	258.7	3

Notes: Δ_i (BIC), the difference between the BIC for a given model and the minimum BIC; *df*, the number of degrees of freedom. In all models, the asterisk denotes the interaction between factors; parentheses indicate a random effect.

Table S2. The result of the generalized linear mixed model (GLMM) for the sample with all bird species

	Infection status		
Predictors	*Odds Ratios*	*CI*	*p*
(Intercept)	0.25	0.13–0.51	**< 0.001**
Type [Passive]	2.01	1.14–3.54	**0.016**
Random Effects			
σ^2	3.29		
$\tau_{00\ \mathrm{Species}}$	1.45		
$\tau_{00\ \mathrm{Year}}$	0.09		
ICC	0.32		
N_{Species}	60		
N_{Year}	5		
Observations	1815		
Marginal R^2 / Conditional R^2	0.007 / 0.324		

Notes: CI — 95 % confidence interval. Random effects: σ^2 = residual variance, τ_{00} = random intercept variance, ICC = intraclass correlation coefficient; R^2 — coefficient of determination. Significant values are in bold.

Table S3. Results of the cumulative link mixed model (CLMM) for the sample with all bird species

	Parasitemia score		
Predictors	*Odds Ratios*	*CI*	*p*
1|2	0.08	0.04–0.17	**< 0.001**
2|3	0.51	0.26–1.00	0.050
3|4	3.42	1.70–6.90	**0.001**
Type [Passive]	0.14	0.07–0.27	**< 0.001**
Random Effects			
σ^2	3.29		
$\tau_{00\ \mathrm{Species}}$	0.62		
ICC	0.16		
N_{Species}	37		
Observations	757		
Marginal R^2 / Conditional R^2	0.040 / 0.192		

Notes: CI — 95 % confidence interval. Random effects: σ^2 = residual variance, τ_{00} = random intercept variance, ICC = intraclass correlation coefficient; R^2 — coefficient of determination. Significant values are in bold.

Table S4. Comparison of cumulative link mixed models (CLMMs), describing the effect of different predictors on parasitemia score of *Haemoproteus* spp. infection for the all-species sample

Models	Δ_i(BIC)	*df*
Score ~ Type + (1 | Species)	0.0	5
Score ~ Type + (1 | Species) + (1 | Year)	5.3	6
Score ~ Type + Migration distance + (1 | Species)	6.6	6
Score ~ Type + DayN + (1 | Species) + (1 | Year)	11.8	7
Score ~ Type + Migration distance + (1 | Species) + (1 | Year)	11.9	7
Score ~ Type + DayN + Migration distance + (1 | Species) + (1 | Year)	18.4	8
Score ~ Type + DayN + DayN*Type + Migration distance + (1 | Species) + (1 | Year)	24.9	9
Score ~ Type + DayN + Plasmodium + Leucocytozoon + Migration distance + (1 | Species) + (1 | Year)	28.7	10
Score ~ Type + DayN + DayN*Type + Leucocytozoon + Migration distance + (1 | Species) + (1 | Year)	29.8	10
Score ~ Type + DayN + DayN*Type + Leucocytozoon + Plasmodium + (1 | Species) + (1 | Year)	30.0	10
Score ~ Type + DayN + DayN*Type + Leucocytozoon + Plasmodium + Migration distance + (1 | Species)	30.0	10
Score ~ Type + DayN + DayN*Type + Plasmodium + Migration distance + (1 | Species) + (1 | Year)	32.4	10
Score ~ Type + DayN + DayN*Type + Leucocytozoon + Plasmodium + Migration distance + (1 | Species) + (1 | Year)	35.2	11
Score ~ Type + (1 | Year)	75.3	5
Score ~ Type + DayN + DayN*Type + Leucocytozoon + Plasmodium + Migration distance + (1 | Year)	96.3	10

Notes: Δ_i (BIC), the difference between the BIC for a given model and the minimum BIC; *df*, the number of degrees of freedom. In all models, the asterisk denotes the interaction between factors; parentheses indicate a random effect.

Table S5. List of species common to the samples of actively and passively captured birds used for GLMM

Shared bird species	Number of actively caught birds	Number of passively caught birds
Acrocephalus palustris	1	64
Erithacus rubecula	38	12
Ficedula hypoleuca	6	67
Ficedula parva	1	2
Fringilla coelebs	3	39
Locustella naevia	1	3
Luscinia luscinia	8	30
Cyanistes caeruleus	1	8
Parus major	1	9
Phoenicurus phoenicurus	11	17
Phylloscopus collybita	10	2
Phylloscopus trochilus	6	25
Sylvia atricapilla	18	109
Sylvia communis	13	98
Curruca curruca	13	25
Troglodytes troglodytes	8	6
Turdus merula	1	56
Total amount	140	572

Table S6. List of species common to the samples of actively and passively captured birds used for CLMM

Shared bird species	Number of actively caught birds	Number of passively caught birds
Curruca curruca	2	11
Ficedula hypoleuca	3	30
Sylvia communis	6	55
Phylloscopus trochilus	1	4
Sylvia atricapilla	8	79
Fringilla coelebs	2	18
Luscinia luscinia	5	18
Phoenicurus phoenicurus	1	1
Cyanistes caeruleus	1	4
Erithacus rubecula	4	1
Total amount	33	221

Table S7. Comparison of generalized linear mixed models (GLMM), describing the effect of different predictors on the possibility of catching a bird infected with *Haemoproteus* spp. for the shared species sample

Models	Δ_i(BIC)	*df*
Infection status ~ Type + (1 | Species) + (1 | Year)	0.0	4
Infection status ~ Type + DayN + Migration distance + (1 | Species) + (1 | Year)	2.3	6
Infection status ~ Type + Migration distance + (1 | Species) + (1 | Year)	4.2	5
Infection status ~ Type + DayN + DayN*Type + Migration distance + (1 | Species) + (1 | Year)	7.8	7
Infection status ~ Type + DayN + Plasmodium + Leucocytozoon + Migration distance + (1 | Species) + (1 | Year)	11.2	8
Infection status ~ Type + DayN + DayN*Type + Plasmodium + Migration distance + (1 | Species) + (1 | Year)	11.7	8
Infection status ~ Type + DayN + DayN*Type + Leucocytozoon + Plasmodium + (1 | Species) + (1 | Year)	11.9	8
Infection status ~ Type + DayN + DayN*Type + Leucocytozoon + Migration distance + (1 | Species) + (1 | Year)	12.6	8
Infection status ~ Type + DayN + DayN*Type + Leucocytozoon + Plasmodium + Migration distance + (1 | Species) + (1 | Year)	16.5	9
Infection status ~ Type + (1 | Species)	19.8	3
Infection status ~ Type + Migration distance + (1 | Species)	24.1	4
Infection status ~ Type + (1 | Year)	76.5	3

Notes: Δ_i(BIC), the difference between the BIC for a given model and the minimum BIC; *df*, the number of degrees of freedom. In all models, the asterisk denotes the interaction between factors; parentheses indicate a random effect.

Table S8. The result of the generalized linear mixed model (GLMM) for sample with the shared bird species

	Infection status		
Predictors	***Odds Ratios***	***CI***	***p***
(Intercept)	0.33	0.12–0.88	**0.026**
Type [Passive]	1.94	0.93–4.05	0.076
Random Effects			
σ^2	3.29		
$\tau_{00\ \text{Species}}$	1.22		
$\tau_{00\ \text{Year}}$	0.39		
ICC	0.33		
N_{Species}	17		
N_{Year}	5		
Observations	712		
Marginal R^2 / Conditional R^2	0.014 / 0.338		

Notes: CI — 95 % confidence interval. Random effects: σ^2 = residual variance, τ_{00} = random intercept variance, ICC = intraclass correlation coefficient; R^2 — coefficient of determination. Significant values are in bold.

Table S9. Comparison of cumulative link mixed models (CLMMs), describing the effect of different predictors on parasitemia score of *Haemoproteus* spp. infection for the same species sample

Models	Δ_i(BIC)	*df*
Score ~ Type + (1 | Species)	0.0	5
Score ~ Type + Migration distance + (1 | Species)	1.5	6
Score ~ Type + (1 | Species) + (1 | Year)	4.3	6
Score ~ Type + Migration distance + (1 | Species) + (1 | Year)	6.1	7
Score ~ Type + (1 | Year)	7.4	5
Score ~ Type + DayN + (1 | Species) + (1 | Year)	9.8	7
Score ~ Type + DayN + DayN*Type + Leucocytozoon + Plasmodium + Migration distance + (1 | Species)	20.7	10
Score ~ Type + DayN + Plasmodium + Leucocytozoon + Migration distance + (1 | Species) + (1 | Year)	20.8	10
Score ~ Type + DayN + DayN*Type + Leucocytozoon + Plasmodium + Migration distance + (1 | Year)	22.1	10
Score ~ Type + DayN + DayN*Type + Leucocytozoon + Plasmodium + (1 | Species) + (1 | Year)	24.7	10

Note: Δ_i(BIC), the difference between the BIC for a given model and the minimum BIC; *df*, the number of degrees of freedom. In all models, the asterisk denotes the interaction between factors; parentheses indicate a random effect.