

1 **Spring reproductive success influences autumnal malarial load in a passerine**  
2 **bird**

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## Abstract

24 Although avian haemosporidian parasites are widely used as model organisms to study  
25 fundamental questions in evolutionary and behavioral ecology of host-parasite interactions, some of  
26 their basic characteristics, such as seasonal variations in within-host density, are still mostly unknown.  
27 In addition, their interplay with host reproductive success in the wild seems to depend on the  
28 interaction of many factors, starting with host and parasite species and the temporal scale under  
29 study. Here, we monitored the parasitemia of two haemosporidian parasites – *Plasmodium relictum*  
30 (lineage SGS1) and *P. homonucleophilum* (lineage SW2) – in two wild populations of great tits (*Parus*  
31 *major*) in Switzerland over three years, to characterize their dynamics. We also collected data on birds'  
32 reproductive output – laying date, clutch size, fledging success – to determine whether they were  
33 associated with parasitemia before (winter), during (spring) and after (autumn) breeding season.  
34 Parasitemia of both species dramatically increased in spring, in a way that was correlated to  
35 parasitemia in winter. Parasitemia before and during breeding season did not explain reproductive  
36 success. However, the birds which fledged the more chicks had higher parasitemia in autumn, which  
37 was not associated with their parasitemia in previous spring. Our results tend to indicate that high  
38 haemosporidian parasite loads do not impair reproduction in great tits, but high resource allocation  
39 into reproduction can leave birds less able to maintain low parasitemia over the following months.

40

41 **Keywords:** avian malaria, annual variations, relapses, recrudescence, recurrences, parasitemia, life  
42 history traits, bird

## Introduction

44 The assumed impact of parasitic infections on animal fitness is at the basis of several evolutionary  
45 theories such as the Hamilton-Zuk (Hamilton & Zuk, 1982) or the terminal investment (Stearns, 1989)  
46 hypotheses. A recent meta-analysis highlighted the overall negative cost of parasites on reproductive  
47 success (Hasik & Siepielski, 2022). This meta-analysis focused on the infection status as a binary  
48 variable (parasitized versus non-parasitized), as is the case of many studies. However, the parasite  
49 load might better represent the host's ability to control the infection (resistance) and might be a finer  
50 correlate of its physiological or energetical costs (Stjernman et al., 2008; Risely et al., 2018; Sánchez  
51 et al., 2018; Methling et al., 2019). A negative association between parasite load and reproductive  
52 success was shown in several host-parasite systems (Madsen et al., 2005; Asghar et al., 2011;  
53 Gooderham & Schulte-Hostedde, 2011; Hicks et al., 2019; Schoepf et al., 2022) but some studies also  
54 show an absence or a positive correlation (Siikamäki et al., 1997; Edler et al., 2004; Raveh et al., 2011;  
55 Kulma et al., 2014; Delefortrie et al., 2022).

56 The different results obtained from studies sometimes involving similar host-parasite pairs could  
57 be explained by a number of factors. For instance, the results can vary with the host's sex. Several  
58 studies have reported a negative relationship between parasite load and reproductive success only in  
59 males (Sundberg, 1995; Dawson & Bortolotti, 2001; Gooderham & Schulte-Hostedde, 2011; but see  
60 Hicks et al., 2019). The age of the infected individuals could also partly blur the signal, since it has been  
61 shown that in some species, individuals nearing the end of their lives may invest heavily in  
62 reproduction (i.e., terminal investment hypothesis, Velando et al., 2006; Duffield et al., 2018), and in  
63 others, that the age-reproductive success relationship follows a bell-shaped curve (Lecomte et al.,  
64 2010; Saraux & Chiaradia, 2022). The fluctuation of parasite loads over time may also pose a significant  
65 challenge. A large diversity of parasites, ranging from viruses to eukaryotic organisms, exhibit highly  
66 dynamic patterns of replication rate, leading to temporal fluctuations of within-host load (e.g., Hasker  
67 et al., 2013; Pigeault et al., 2018; Colangeli et al., 2020). These fluctuations can occur on short-term  
68 scales, such as daily variations, as well as on long-term scales, spanning months or even years  
69 (Martinez-Bakker & Helm, 2015; Prior et al., 2020). Although the parasite load experienced by the host  
70 during the breeding period is most likely to have a direct (e.g. pathogenicity, resource exploitation)  
71 influence on host's reproductive success (e.g. Madsen et al., 2005; Asghar et al., 2011; Gooderham &  
72 Schulte-Hostedde, 2011; Hicks et al., 2019; Schoepf et al., 2022), the parasite load before the breeding  
73 season may also have indirect effects, by influencing for instance premating trade-offs in resource  
74 allocation (i.e. carry over effect, Harrison et al., 2011; e.g. Marzal et al., 2013). **On the other hand, as**  
75 **life-history theory assumes that components of reproductive effort are costly, investment in**

76 reproduction may have longer-term consequences for the host's ability to clear or at least to control  
77 parasite replication rate (Williams, 1966; Stearns, 1989; Sheldon & Verhulst, 1996). This was notably  
78 shown in great tits, collared flycatcher and Soay sheep, in which increased reproductive effort was  
79 later associated with higher loads of haemosporidian parasites and strongyle nematodes (Richner et  
80 al., 1995, Oppliger et al., 1996, Christe et al. 2012, Nordling et al., 1998; Leivesley et al., 2019). However,  
81 the association between natural reproductive effort and parasite load several months after the  
82 reproductive event was rarely investigated.

83 In this study, we used a longitudinal approach to assess whether the parasite load, quantified a  
84 few months before and during the breeding season, could explain host reproductive output, and  
85 whether reproductive effort could predict parasite load later in the year. To do this, we used avian  
86 malaria as a biological system. For over a century, this vector borne disease has been used in studies  
87 of host-parasite interactions (Pigeault et al., 2015, Rivero & Gandon, 2018) and provides an excellent  
88 model for exploring the influence of parasitic infections on host life-history traits (e.g., Oppliger et al.,  
89 1997; Asghar et al., 2015; Pigeault, Cozzarolo, et al., 2018). To date, the vast majority of studies that  
90 investigated the influence of malaria infection on bird reproduction used the infection status (i.e.,  
91 parasitized versus non-parasitized) as a predictor of diverse reproductive parameters (e.g., Sanz et al.,  
92 2001; Norte et al., 2009; Podmokła et al., 2014; Zylberberg et al., 2015; Pigeault, Cozzarolo, et al.,  
93 2018). The few non-interventional studies that have examined the influence of parasitemia (i.e.,  
94 quantity of haemosporidian parasites in the peripheral blood of the host) on the reproductive success  
95 of birds have reported contrasting results (e.g., Siikamäki et al., 1997; Edler et al., 2004; Asghar et al.,  
96 2011; Kulma et al., 2014). On the other hand, drug-induced reduction of parasitemia usually results in  
97 higher reproductive success (e.g., Merino et al., 2000; Marzal et al., 2005; Knowles et al., 2010;  
98 Schoepf et al., 2022).

99 A possible explanation for the difference in results between the non-interventional studies and  
100 those in which the parasitemia was experimentally reduced is that only its experimental reduction can  
101 ensure that treated birds have a permanently lower parasitemia than control individuals. Indeed,  
102 avian malaria is characterized by radical temporal variations in parasitemia. After transmission of the  
103 parasite by a mosquito, parasitemia increases rapidly and reaches a maximum in 10-20 days (Pigeault  
104 et al., 2018; Palinauskas et al., 2018). Activation of the host immune system then controls avian  
105 malaria parasite replication rate, but in most cases, it is not able to eliminate it completely, leading to  
106 the establishment of the chronic phase of the infection (Valkiūnas, 2005; Asghar et al., 2012) during  
107 which parasites persist at low densities for several months or years. However, this chronic phase can  
108 be regularly interrupted by recrudescence events when parasitemia increases significantly over a short  
109 period of time (three to seven days, Cornet et al., 2014; Pigeault et al., 2023). Consequently, the results

110 of non-interventional studies investigating the relationship between haemosporidian parasitemia and  
111 host reproductive success will be highly dependent on the timing of measurements.

112 Our non-interventional study was carried out over a period of three years, during which field  
113 sessions were organized to capture and recapture great tits in order to (i) monitor annual infection  
114 dynamics, (ii) study the link between parasitemia and reproductive success, and (iii) investigate the  
115 influence of investment in reproduction on parasitemia measured later in the year. **Two great tit**  
116 **populations, characterized by different haemosporidian communities – in particular, the most**  
117 **prevalent *Plasmodium* species in each population is not found in the other one – and different overall**  
118 **reproductive parameters (Pigeault, Cozzarolo et al. 2018), were studied here.** Although commonly  
119 mentioned in the literature, but rarely reported, we predict a significant increase of parasitemia in  
120 spring, illustrating spring recurrences (or spring relapses, Applegate, 1971). In light of the studies  
121 which showed a trade-off between activation of the great tit's immune system and their reproduction  
122 (e.g., Ots & Hõrak, 1998; Grzędzicka, 2017; Kubacka & Cichoń, 2020), we predict a negative  
123 relationship between winter and/or spring parasitemia and reproductive success. Finally, in view of  
124 the energy expenditure associated with reproduction (Visser & Lessells, 2001; Nilsson & Råberg,  
125 2001), we also predict that infected individuals who invest substantially in reproduction will later  
126 experience higher parasitemia (Hanssen et al., 2005).

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## Material and Methods

### 128 Study area and host species

129 The study was carried out between 2017 and 2019 in two populations of great tits (*Parus major*)  
130 breeding in nest-boxes located near the University of Lausanne (Dorigny Forest, 46°31'025.60700 N,  
131 6°34'040.71400 E, altitude: 380 m) and 15 km apart in the Marais des Monod (46°34'019.95300 N,  
132 6°23'059.20400 E, altitude: 660 m), both in Switzerland. **As in Pigeault, Cozzarolo, et al. (2018), we**  
133 **monitored nest-boxes during each breeding season (from March to June), collecting breeding**  
134 **parameters: laying date, clutch size and fledging success.** We trapped breeding great tits in the nest  
135 boxes to determine whether they were infected by haemosporidian parasites and, if so, we  
136 molecularly identified the parasites involved in the infection (see Appendix 1). We also measured  
137 birds' mass and tarsus length to calculate the scaled mass index of each individual as a proxy for body  
138 condition (SMI, Peig & Green, 2009). **We categorized the birds' age as "first-year" or "older" based on**  
139 **whether they already had their first post-nuptial molt or not, by looking at their wing feathers.** To  
140 correct for between-year differences in average breeding time, laying date was standardized by using  
141 the first year of the study as a reference (2017, 1 April = day 1). The differences in laying date between

142 2017 and each subsequent year were subtracted from the actual laying date of that particular year  
143 (see Allander & Bennett, 1995).

144 In addition to the spring monitoring, birds were also captured with mist nets during winter  
145 (between January and end of March) and autumn (between mid-October and mid-December). Three  
146 capture sessions were done in winter and in autumn in the Dorigny Forest, while for logistic reasons  
147 it was only possible to perform two sessions per season in the Marais des Monod. We also took blood  
148 samples and morphometric measurements on all caught individuals. No capture session was carried  
149 out in summer because we know from previous attempts that it is very difficult to capture great tits  
150 during this period in our study area.

### 151 **Molecular analyses**

152 Only birds captured at least twice in a focal year and diagnosed as infected by *Plasmodium* parasite  
153 on at least one of their capture dates were retained for analyses (see **Appendices, section 1** for  
154 diagnosis and parasite identification protocol). The quantification of parasitemia in all the blood  
155 samples was carried out using qPCR (see **Appendices, section 2**). Parasitemia was calculated with  
156 relative quantification values (RQ). RQ can be interpreted as the fold-amount of target gene  
157 (*Plasmodium* 18S rDNA) with respect to the amount of the reference gene (avian 18S rDNA) and is  
158 calculated as  $2^{-(Ct\_Plasmodium - Ct\_bird)}$ . For convenience, RQ values were standardized by  $\times 10^4$  factor. Since  
159 some individuals were trapped and blood sampled several times per season, we calculated the  
160 average parasitemia of individuals for each season when we wanted to compare it between seasons.

### 161 **Statistical analysis**

162 We used a mixed model procedure with a normal error structure and bird individual fitted as a  
163 random factor to test for an effect of month of capture on change in parasitemia ('lme4' package,  
164 Bates et al., 2014). Sex, age, *Plasmodium* lineage and year were added as fixed factors into the model.  
165 As parasitemia could be expected to be a non-linear function of month of capture, because of spring  
166 recurrences, the quadratic term month of capture was added to assess whether it significantly  
167 improved the model fit. In order to study the influence of the parasitemia measured in winter and  
168 spring on the reproductive parameters and the impact of reproductive parameters on the parasitemia  
169 measured in autumn, **we calculated the average parasitemia of individual birds within each season of each**  
170 **year. In fact, some individuals were captured several times in the winter or in autumn of a focal year, while**  
171 **others were captured only once, so we used average seasonal parasitemia to reduce data complexity.**  
172 Then, for a focal year, we used generalized linear models (glm), with an error structure appropriate to  
173 each response variable (see **Appendices, Table S1**), to study the impact of winter and spring  
174 parasitemia on bird's reproductive parameters. We also used a glm to evaluate the influence of the

175 birds' reproductive parameters on their parasitemia measured in the autumn. Previous studies  
176 showed that co-infection by at least two different haemosporidian parasite genera was highly  
177 prevalent in the two great-tits populations monitored here (Pigeault, Cozzarolo, et al., 2018). As co-  
178 infection with *Plasmodium* and *Leucocytozoon* may affect life history traits of great tits (see Figure 2 in  
179 Pigeault, Cozzarolo, et al., 2018), birds were also screened for *Leucocytozoon* infection (see **Appendix 1,**  
180 **section 1**). However, detection of *Leucocytozoon* was not achieved for 12 individuals. Given the relatively  
181 small size of our dataset and the fact that including *Leucocytozoon* infection status as an explanatory  
182 variable did not change the conclusions of our study, all the analyses with *Leucocytozoon* infection status  
183 fitted as an explanatory variable are presented in the **Appendix (Section 3)**.

184 All statistical analyses were carried out using the R statistical software (v. 4.1.3). The raw data and  
185 the R script used for the analyses and to produce the figures are available on the figshare repository  
186 (10.6084/m9.figshare.23695422).

## 187 **Ethics statement**

188 This study was approved by the Ethical Committee of the Vaud Canton veterinary authority  
189 (authorization number is 1730.4).

## 190 **Results**

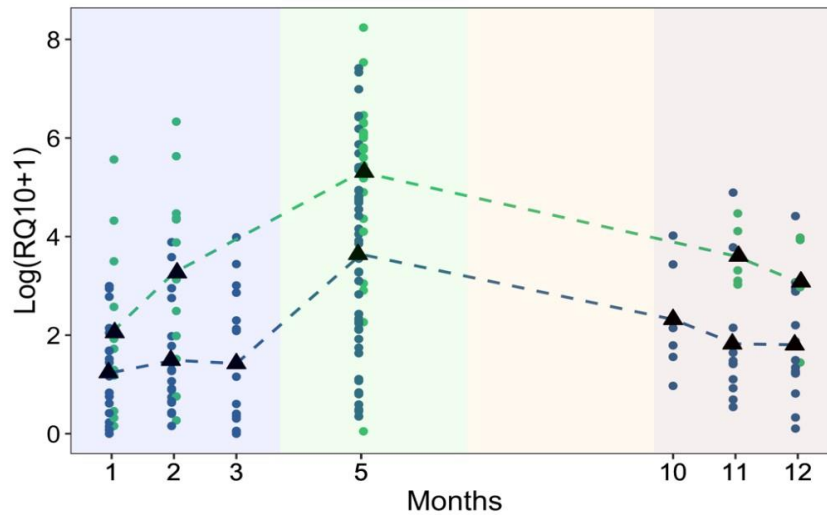
### 191 **Variations in parasitemia**

192 We followed the annual infection dynamics in 70 individuals (31 females and 39 males). We  
193 detected four lineages of *Plasmodium* [BT7 (*Plasmodium* sp.): 2, TURDUS1 (*P. circumflexum*): 4, SW2  
194 (*P. homonucleophilum*): 20, SGS1 (*P. relictum*): 43] and one lineage of *Haemoproteus* [PARUS1 (*H.*  
195 *majoris*): 1] but we focused our subsequent analyses on the two most prevalent lineages (i.e. SW2 and  
196 SGS1). The parasite communities were very different in both sites. The SW2 lineage was only observed  
197 in the Marais des Monod while hosts infected by SGS1 were only captured in the Dorigny forest.

198 A significant influence of month of capture on the parasitemia was observed but only when month  
199 was added as a quadratic term in the model (model 1, month:  $\chi^2 = 62.17$ ,  $p < 0.0001$ , month<sup>2</sup>:  $\chi^2 =$   
200  $63.205$ ,  $p < 0.0001$ , Figure 1). We indeed observed that the parasitemia followed a bell-shaped  
201 function: peaking during spring and decreasing thereafter (**Figure 1**). When spring captures were  
202 removed from our analyses, we no longer observed an influence of month on parasitemia (model 2,  
203 month:  $\chi^2 = 1.21$ ,  $p = 0.271$ , month<sup>2</sup>:  $\chi^2 = 1.09$ ,  $p = 0.315$ ).

204 Although the general shape of infection for both lineages was similar, we observed that host  
205 infected by SW2 showed higher parasitemia than those infected by SGS1 (model 1,  $\chi^2 = 31.69$ ,  $p <$   
206  $0.0001$ , mean RQ10  $\pm$  se, SW2 = 294  $\pm$  99, SGS1 = 148  $\pm$  87, Figure 1). Parasitemia differed between

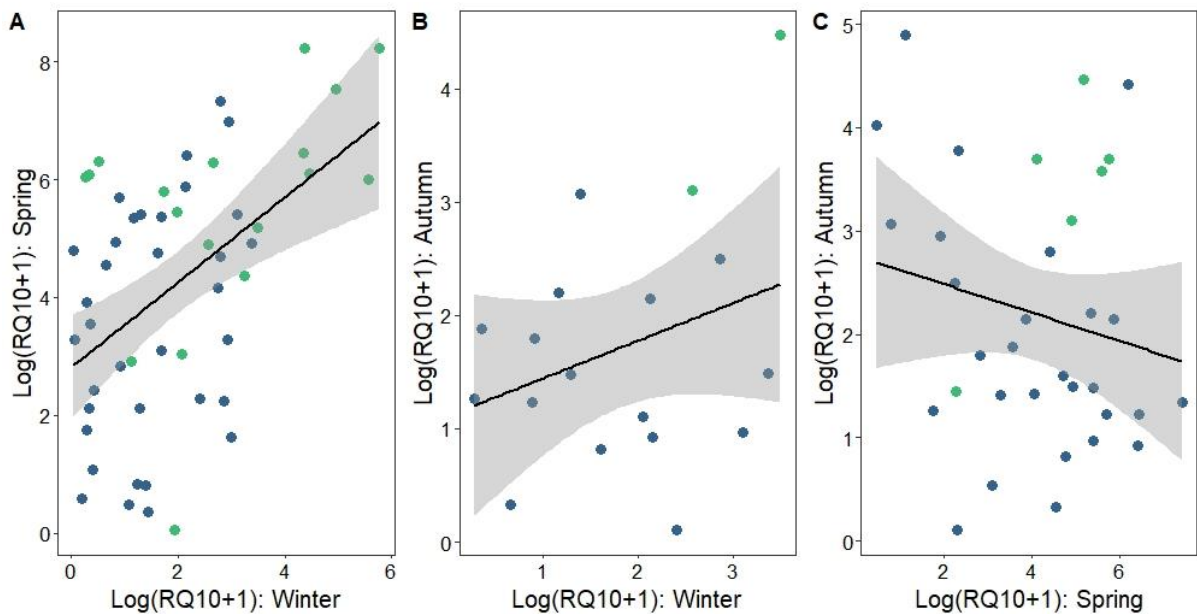
207 years (model 1,  $\chi^2 = 9.44$ ,  $p = 0.002$ , mean  $RQ_{10} \pm se$ , 2017 =  $174 \pm 69$ , 2018 =  $83 \pm 31$ , 2019 =  $247 \pm$   
 208 145) but we did not observe any difference between host sex and age (model 1, sex:  $\chi^2 = 1.41$ ,  $p =$   
 209 0.235, age:  $\chi^2 = 0.002$ ,  $p = 0.967$ ).



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 211 **Figure 1 – Annual variation of avian malaria within-host infection load.** Each point represents the  
 212 parasitemia (Log  $RQ_{10+1}$ ) of an individual caught at least twice during a same year. Blue dots  
 213 correspond to individuals infected with *P. relictum* SGS1, green dots correspond to individuals  
 214 infected with *P. homonucleophilum* SW2. The colored rectangles represent the seasons. Blue: winter,  
 215 green: spring, yellow: summer, light red: autumn. Months: 1 = January, 2 = February, 3 = March, 5 =  
 216 May, 10 = October, 11 = November, 12 = December.

217 After calculating the average parasitemia of hosts within each season, we observed a significant  
 218 relationship between winter and spring parasitemia (model 3,  $\chi^2 = 6.16$ ,  $p = 0.010$ ). The most infected  
 219 hosts in winter exhibited higher parasitemia in spring (**Figure 2**). Conversely, we did not observe any  
 220 relationship between winter and autumn parasitemia or between spring and autumn (model 4-5,  $\chi^2$   
 221 = 0.62,  $p = 0.445$ ,  $\chi^2 = 0.04$ ,  $p = 0.837$ , respectively, **Figure 2**). **We could not look for a correlation**  
 222 **between parasitemia in autumn and subsequent winter, because of the low sample size (N = 2).** As  
 223 observed previously in the analysis of the annual dynamics of *Plasmodium* infection, within each  
 224 season, the parasitemia was higher in individuals infected by SW2 than in birds infected by SGS1  
 225 (model 3:  $\chi^2 = 8.40$ ,  $p = 0.006$ , model 4:  $\chi^2 = 4.77$ ,  $p = 0.049$ , model 5:  $\chi^2 = 6.55$ ,  $p = 0.016$ ).





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**Figure 2 – Relationship between parasitemia measured at different season.** (A) Relationship between parasitemia in spring and winter, (B) autumn and winter and (C) autumn and spring. Blue dots correspond to individuals infected with *P. relictum* SGS1, green dots correspond to individuals infected with *P. homonucleophilum* SW2.

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### Relationship between parasitemia and reproductive parameters

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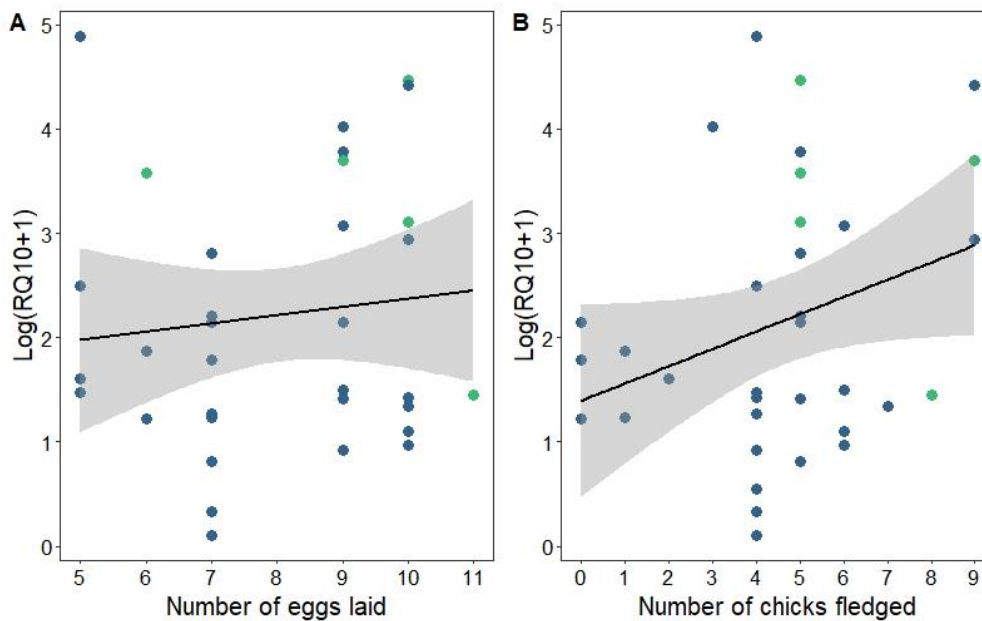
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Parasitemia recorded during the winter period did not influence the laying date (model 6,  $\chi^2 = 0.244$ ,  $p = 0.623$ ), the investment in the reproduction or the reproductive success of the hosts (model 7, clutch size:  $\chi^2 = 0.103$ ,  $p = 0.748$ , model 8, number of fledged chicks:  $\chi^2 = 0.479$ ,  $p = 0.489$ ). We also did not observe any relationship between parasitemia measured during the reproductive period and any reproductive parameters (model 9-11, laying date:  $\chi^2 = 0.037$ ,  $p = 0.847$ , clutch size:  $\chi^2 = 0.141$ ,  $p = 0.707$ , number of fledged chicks:  $\chi^2 = 0.001$ ,  $p = 0.975$ ). However, the number of fledged chicks was higher in hosts infected by SW2 than in birds infected by SGS1 (model 11,  $\chi^2 = 7.60$ ,  $p = 0.006$ , mean  $\pm$  se, SW2 =  $6.22 \pm 0.46$ , SGS1 =  $4.20 \pm 0.32$ ). Finally, the clutch size did not impact the parasitemia measured later in autumn (model 12,  $\chi^2 = 1.340$ ,  $p = 0.247$ , **Figure 3A**), but we observed a significant effect of the number of fledged chicks (model 12,  $\chi^2 = 5.91$ ,  $p = 0.015$ ). Individuals with high fledging success also had higher parasitemia the following autumn (**Figure 3B**). We observed a negative relationship between individual SMI and autumn parasitemia (model 12,  $\chi^2 = 4.66$ ,  $p = 0.031$ ). The birds with the lowest body condition were those that had the highest parasitemia (**Figure S1**). However, there was no relationship between the breeding success (i.e., the number of fledged chicks) of birds in spring and their body condition a few months later in autumn (model 13,  $\chi^2 = 0.55$ ,  $p = 0.457$ ).



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**Figure 3 – Influence of reproductive parameters monitored in spring and parasitemia measured a few months later in autumn.** Relationship between (A) the number of eggs laid or (B) the number of chicks fledged and parasitemia (Log RQ10+1). Blue dots correspond to individuals infected with *P. relictum* SGS1, green dots correspond to individuals infected with *P. homonucleophilum* SW2.

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## Discussion

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Using data collected from two wild populations of great tits infected by two different *Plasmodium* lineages, we highlighted that parasitemia increased drastically between winter and spring, and we found that increased reproductive allocation in spring is associated with higher parasitemia in autumn.

Numerous studies have attempted to characterize the yearly fluctuations of infection prevalence in different bird populations. They either found no seasonality in probability of infection (Himalayan bird community; Ishtiaq et al., 2017), a link with migration (Hellgren et al., 2013; Pulgarín-R et al., 2019), or seasonality patterns that vary across *Plasmodium* lineages (Neto et al., 2020) and geographical regions (Cosgrove et al., 2008; Lynton-Jenkins et al., 2020; Neto et al., 2020). On the other hand, little is known about annual within-host variation in parasitemia. In a wild bird community in Slovakian woodlands, *Plasmodium* sp. parasitemia peaked in summer (Šujanová et al., 2021) while *Plasmodium relictum* parasitemia in captive house sparrows (*Passer domesticus*) in Spain varied monthly without clear seasonal pattern (Garcia-Longoria et al., 2022). In the present study, we report that, for two *Plasmodium* lineages, the parasitemia followed a bell-shaped function. It increased more than tenfold between winter and spring, and then decreased in autumn to winter levels. Our study illustrates a phenomenon described by Applegate & Beaudoin in the 70s but rarely documented since: spring recurrences (or spring relapses Applegate, 1970). Spring recurrences can be due to several

270 factors likely acting on bird's physiology or immunity, such as resource availability (Cornet, Bichet, et  
271 al., 2014), environmental stressors (Becker et al., 2020; Pigeault et al., 2023), immune challenges, co-  
272 infections with other parasites (Palinauskas et al., 2011; Reinoso-Pérez et al., 2020; Garcia-Longoria et  
273 al., 2022) and energy allocation to other functions such as reproduction (Christe et al., 2012).

274 Although various factors may be responsible for triggering recurrences of infection, we have  
275 demonstrated that the spring parasitemia of birds was positively correlated to their parasitemia  
276 recorded in winter. However, contrary to our predictions, we did not observe any effect of both winter  
277 and spring parasitemia on bird reproductive parameters. Indeed, individuals with extremely high  
278 parasitemia ( $RQ > 1000$ ) did not lay more eggs nor fledged more chicks than those with very low  
279 parasitemia ( $RQ < 1$ ). This result is not consistent with a premating trade-off in resource allocation  
280 (i.e., carry-over effect) or with a reallocation of host resources towards immunity during the mating  
281 period (Stearns, 1989; Harrison et al., 2011; Stahlschmidt et al., 2013; Albery et al., 2020).

282 Interestingly, while the parasitemia in winter is a significant predictor of the intensity of the spring  
283 recurrence, we did not observe any relationship between parasitemia measured in winter or in spring  
284 and parasitemia recorded the following autumn. This result suggests that between spring and autumn,  
285 biotic and/or abiotic parameters may have modified the interactions between *Plasmodium* and its  
286 host. Infections by new parasites during spring or summer periods could directly or indirectly influence  
287 the within-host infection dynamics of *Plasmodium* (Cellier-Holzem et al., 2010). Our study was not  
288 designed to test this hypothesis, but we noted that the birds recaptured in the autumn were all  
289 infected with the same lineage of *Plasmodium* that was identified in the spring. Further, we did not  
290 record any new haemosporidian parasite infection. However, we cannot exclude the possibility that,  
291 during the breeding season, the birds were infected by other parasites (e.g. gastrointestinal  
292 nematodes, viruses; regarding co-infections with other *Leucocytozoon*, see **Appendices, section 3**).

293 Inter-individual variability in reproductive investment may also explain why there was no  
294 relationship between the parasitemia measured at the beginning of the reproductive period and that  
295 measured several months later in autumn. Because immunity and reproduction compete for host  
296 resources, in resource-limited environments, hosts that reproduce should have fewer resources to  
297 allocate to immune defense which may ultimately influence within-host infection dynamics. Increased  
298 allocation to reproduction was found to be associated with increased load of gastrointestinal  
299 nematodes in wild Soay sheep during both late gestation and early lactation (Leivesley et al., 2019).  
300 Brood manipulation studies on birds showed that increased allocation to reproduction was associated  
301 with greater parasite loads and less effective immune responses at the end of the breeding period  
302 (Richner et al., 1995, Oppliger et al., 1997, Knowles et al., 2009; Christe et al., 2012). Here, we observed  
303 birds with the highest reproductive success tended to be those with the highest parasitemia 6-8

304 months later. Although supported by a small sample size ( $n = 36$ ), this result suggests a long-term  
305 effect of investment in reproduction on the ability of hosts to control the replication rate of blood  
306 parasites.

307 Finally, in addition to seasonal variations, we observed a significant difference in the parasitemia  
308 in birds, depending on the *Plasmodium* lineage involved in the infection. Hosts infected with *P.*  
309 *homonucleophilum* SW2 had a higher parasitemia than hosts infected with *P. relictum* SGS1,  
310 irrespective of the time of year when the blood samples were taken. This result is consistent with that  
311 of an earlier study conducted on the same great tits populations in 2009-2011 (Rooyen et al., 2013).  
312 Interestingly, we also found that birds infected by *P. homonucleophilum* showed higher reproductive  
313 success than those infected by *P. relictum*. The fact that *P. relictum* SGS1 is a very generalist and  
314 widespread lineage (147 host species and worldwide distribution according to MalAvi database; Bensch et  
315 al. 2009) compared to the relatively less common *P. homonucleophilum* SW2 (33 host species, found only  
316 in Afro-Eurasia) might correlate with these differences, in line with the hypothesis of a trade-off between  
317 generalism and virulence in parasites (Leggett et al. 2013). Peak parasitemia (a proxy for virulence) was  
318 negatively correlated with host breadth (a proxy for generalism) in primate malaria parasites (Garamszegi  
319 2006), but, to our knowledge, there is no such evidence for avian haemosporidians. However, there does  
320 not seem to be a trade-off between generalism and prevalence in avian *Plasmodium* (Hellgren et al. 2009).  
321 Alternatively, *P. relictum* might also have been infecting the Dorigny population for longer than *P.*  
322 *homonucleophilum* has been infecting the Monod population; if this is the case, birds may have had more  
323 time to evolve specific immune defenses to limit the virulence of *P. relictum*. Our data do not allow to  
324 determine whether the differences observed between hosts infected by these two *Plasmodium*  
325 species are the result of differences inherent to the two blood parasites, of the vertebrate host genetic  
326 background, of their environment, or interactions between all these factors. Indeed, the individuals  
327 infected with *P. homonucleophilum* all originated from the Monod marshlands, whereas the birds  
328 infected with *P. relictum* all came from the Dorigny forest. Although these two populations are only  
329 15km apart, we have never observed birds migrating between the two populations and the habitats  
330 are very different (large marshy forest massif versus periurban forest patches on the campus of the  
331 University of Lausanne, respectively).

332 In conclusion, our monitoring of haemosporidian parasitemia in great tits across seasons  
333 evidenced a spring recurrence, the triggers of which are still to be determined. Further, our study  
334 supported the idea that strong allocation in reproduction incurs costs later in life, without evidence  
335 that higher parasitemia prior to and during breeding season reduce reproductive success.  
336 Interestingly, we found this pattern in two great tit populations, infected by two different *Plasmodium*  
337 species.

338

## Supplementary Information

339 Appendices include:

340 Section 1: Haemosporidian parasite detection

341 Section 2: Quantification of parasitemia

342 Section 3: Results of the analyses with *Leucocytozoon* infection status fitted as explanatory variable

343 Table S1: Description of the statistical models presented in the main text.

344 Figure S1: Relationship between scale mass index and parasitemia in birds captured in autumn

345

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347

### Conflict of interest disclosure

348 The authors declare that they comply with the PCI rule of having no conflicts of interest in relation to the  
349 content of the article.

350

### Data, scripts, code, and supplementary information availability

351 Data and scripts are available online: <https://doi.org/10.6084/m9.figshare.23695422>. Supplementary  
352 information can be found on the bioRxiv preprint server in the Supplementary Material section under this  
353 link: <https://doi.org/10.1101/2023.07.28.550923>.

354

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