**Dynamics of resting metabolic rate and innate immune response in malaria-infected Eurasian siskins**

Maria Erokhinaa,b\*, Andrey Bushuevb, Vaidas Palinauskasc, Elena Platonovaa, Vadim Khaitovd,e, Alexander Davydova, Andrey Mukhina

*a Biological Station Rybachy of Zoological Institute RAS, Rybachy, 238535, Russia*

*b Department of Vertebrate Zoology, Faculty of Biology, Lomonosov Moscow State University, Moscow, 119234, Russia*

*c Nature Research Centre, Vilnius, 08412, Lithuania*

*d St. Petersburg State University, St. Petersburg, 199034, Russia*

*e* *Kandalaksha State Nature Reserve, Kandalaksha, 184042, Russia*

\* Corresponding author. Biological Station Rybachy of Zoological Institute RAS, Rybachy, 238535, Russia

*E-mail addresses:* erokhina.marija96@gmail.com (M. Erokhina)

**Abstract**

Avian malaria, caused by parasites of the genus *Plasmodium*, is prevalent among wild bird populations worldwide and can have significant impacts on avian health and populations. With the rise in global temperatures due to climate change, there has been a concern about the spread of southern species of malaria parasites to new regions, potentially affecting previously unexposed bird populations. In our experiment, we studied the course of the malaria in two groups of juvenile siskins (*Spinus spinus*) infected with two different species of malaria parasites originating from distinct geographical regions. The first group received an infection with *Plasmodium relictum* (SGS1 lineage), a parasite with established transmission in the Northern Palearctic region. The second group was exposed to *Plasmodium ashfordi* (GRW2 lineage), a parasite with documented transmission in Central and Southern Africa but not yet confirmed in the Northern Palearctic. To assess the impact of these diverse malarial species on the physiological well-being of siskins, we employed two key physiological parameters: resting metabolic rate (RMR) and interleukin-6 (IL-6) levels. RMR measurement offers insights into the energetic cost associated with disease, while IL-6 serves as a crucial pro-inflammatory cytokine that triggers the acute phase response during infection within the context of the innate immune system. Our experimental findings reveal distinct outcomes during the acute phase of SGS1 infection, characterized by a reduction in resting metabolic rate and decreased IL-6 levels in siskins. A partially similar pattern for IL-6 was observed in the GRW2-infected group during the acute phase, although this effect was not sustained during the later stages of infection. Furthermore, the dynamics of resting metabolic rate in siskins from the GRW2-infected group exhibited significant differences from those observed in the SGS1 group. In summary, our study did not provide conclusive evidence that tropical malaria has more severe consequences for infected siskins. However, we did observe similarities with previous studies with SGS1 infected birds and point out notable variations in the disease progression between the two infected birds` groups, highlighting the complexity of host-parasite interactions in the context of avian malaria infections.

*Keywords*: Avian malaria, *Plasmodium relictum*, *Plasmodium ashfordi*, Experimental infection, Metabolic rate, Innate immunity.

**1. Introduction**

Each year, billions of birds undertake a remarkable journey from their breeding to wintering areas and back. The final autumn destination for most migrating Western Palearctic passerines is Central and Southern Africa, encompassing tropical and subtropical regions (Newton, 2010; Shirihai & Svensson, 2018). Due to their movement across various geographic areas during migration, migratory birds encounter a diverse range of blood-sucking insects along their routes. These insects may serve as vectors and can carry different species and strains of haemosporidian parasites, with transmission restricted to the distribution range of their competent vector. Specifically, migrating birds may become infected with malaria parasites of the *Plasmodium* genus (Plasmodiidae, Haemosporida), which are prevalent in the African region. Infected birds that manage to survive and return to their breeding grounds in the Northern Palearctic serve as reservoirs for new infections, as malaria parasites can persist in individuals for years (Bensch et al., 2007; Rooyen, Lalubin, Glaizot, & Christe, 2013). This scenario presents a potential threat to birds belonging to resident or short-distance migratory species that have not co-evolved with malaria parasite species whose transmission extends beyond their habitats. It is well-known that *Plasmodium* parasites can be of high virulence when introduced to naïve populations that have not co-evolved with avian malaria species (Van Riper III, Van Riper, Goff, & Laird, 1986). Furthermore, avian malaria outbreaks happen regularly in zoos, where captive birds (penguins particularly) are for the first time exposed to locally transmitting *Plasmodium* parasites (Cocumelli et al., 2021; González-Olvera et al., 2022; Meister, Richard, Hoby, Gurtner, & Basso, 2021).

Upon invading a vertebrate host organism, the parasite penetrates tissue cells of various organs, initiating multiplication. No parasites can be seen in the red blood cells during this period (so-called pre-patent period). This process precedes the subsequent stage, known as the acute phase, which is usually marked by a sharp increase of infected erythrocytes in the peripheral blood (Valkiūnas, 2005). Similar to any other infection, avian malaria triggers the process of an immune response, which demands energy, affects host metabolism (Eraud, Duriez, Chastel, & Faivre, 2005; Martin, Scheuerlein, & Wikelski, 2003) and energy reserves (Bonneaud et al., 2003; Demas, Drazen, & Nelson, 2003). Excessive and inappropriate immune response can be detrimental, leading to immunopathology (Graham, Allen, & Read, 2005; Sorci & Faivre, 2009). Hence, despite its benefits of controlling parasite infections, immune defense comes at a high cost and a trade-off should exist between immunity and other energy-demanded physiological processes in the organism (Norris & Evans, 2000; Owen-Ashley & Wingfield, 2007; Sheldon & Verhulst, 1996; Zuk & Stoehr, 2002).

One approach for assessing the energetic costs of immune response is to measure the resting metabolic rate (RMR), which reflects the expense of the self-maintenance (Ricklefs, Konarzewski, & Daan, 1996). However, measuring the precise metabolic cost of immunity is challenging due to its intricate integration with other physiological systems within the organism (Lochmiller & Deerenberg, 2000). That implies that RMR measured in our study reflected not only the immune response itself but also the energetic consequences of collateral damages caused by malaria, such as free hemoglobin and heme utilization, replenishment of destroyed red blood cells (RBCs) and tissue damages, and other related factors.

Successful recovery following primary malaria infection and the development of acquired immunity depends on the first line of non-specific defense: innate immunity, specifically the activation of many pro- and anti-inflammatory cytokines (Gowda and Wu, 2018). IL-6 is one of the proinflammatory cytokines that triggers the acute phase reaction and is produced shortly after infection as part of the induced innate immune response ~~in vertebrates~~ (Karel A. Schat, 2014; Owen-Ashley & Wingfield, 2007). The IL-6 system is regarded as highly conserved in vertebrates and IL-6 demonstrates low species specificity in experiments (Zimmerman, 2014). While there is scarce information about the role of this cytokine in avian malaria models, a recent meta-analysis of IL-6 levels in malaria infected human patients and several studies on murine models suggest that IL-6 can serve as a marker for malaria severity (Carapau et al., 2007; Wilairatana et al., 2022; Wunderlich et al., 2012) and even could be used to differentiate malaria from other febrile disease in humans, though more studies are needed (Wilairatana et al., 2022).

In this study, we compared the impact of malaria infection on the physiological parameters of a common European passerine short-distance migrant – the Eurasian siskin (*Spinus spinus*) infected with two different avian haemosporidian parasites: *Plasmodium relictum* (lineage SGS1) and *Plasmodium ashfordi* (lineage GRW2). The first one is widespread in the Palearctic region, a generalist with a broad range of avian host species and high variability in developed levels of parasitemia depending both on host species and on host individuals (Martínez-de la Puente, Santiago-Alarcon, Palinauskas, & Bensch, 2021; Palinauskas, Valkiūnas, Bolshakov, & Bensch, 2008, 2011). Experiments conducted with juvenile siskins revealed that during SGS1 malaria infection, they usually exhibit high levels of parasitemia (i.e., the quantity of infected erythrocytes) during the acute stage. However, considerable individual variation was observed, with some birds displaying a deficient number of infected erythrocytes (Mukhin et al., 2016; Palinauskas et al., 2008). Overall, this lineage is considered as severe and highly pathogenic, with a high potential for mortality in susceptible birds (Valkiūnas et al., 2018). *Plasmodium ashfordi* (GRW2) is also a generalist malarial parasite primarily transmitted in Africa. In Europe, this parasite has only been detected in adults of long-distance migrating birds after their return from wintering grounds in tropical Africa (Bensch, Hellgren, & Pérez‐Tris, 2009). Experimental infections with *P. ashfordi* demonstrated its ability to develop high levels of parasitemia and lethality of its natural host great reed warbler (*Acrocephalus arundinaceus*)(Asghar et al., 2012), as well as in siskins (Asghar et al., 2016).

Given the contradictory data on metabolic responses in birds during parasitic infection (Robar, Murray, & Burness, 2011), particularly during malaria infection, we can anticipate three possible scenarios for RMR changes during infection: i) RMR might increase in all infected juvenile siskins due to immune response against proliferating malaria parasites. Moreover, the intensity of the immune reaction could be higher in birds infected with GRW2 – an evolutionary unfamiliar malarial parasite for European resident bird species like siskins. Consequently, this could lead to elevated RMR levels; ii) RMR might decrease, especially during the acute stage when there is active destruction of erythrocytes and digestion of hemoglobin (Hb) by multiplying parasites. Red blood cells primarily serve to transport oxygen to tissues; thus, progressing anemia could reduce the blood's oxygen-binding capacity, disrupting oxygen transportation. This view is supported by the results of Hayworth (1987) and aligns with general knowledge of the *Plasmodium* parasite life cycle (Stager, 2021), although several studies have not confirmed it (Hahn, 2018; Stager, 2021); iii) Changes in RMR should correlate with parasitemia levels. This assumption directly follows from the previous scenario. On one hand, increased erythrocyte destruction leads to a more pronounced disruption of oxygen transportation. On the other, this should activate the processes of hematopoiesis, which is potentially energy consuming (but see Sun et al., (2020). To provide a rough estimation of the acute immune response during infection, we used IL-6 level as the marker. We assume that an increase of IL-6 will be detected during the acute phase of malaria, followed by a decrease in birds that survive the crisis and acquire chronic infection.

Considering the lack of experimental data on both RMR and, especially, IL-6 levels during malaria infection in birds, our minimum expectation was to observe different average group reactions for the studied parameters in response to *P. relictum* SGS1 and *P. ashfordi* GRW2. This assumption is based on the distinct co-evolutionary backgrounds of the host and two parasite species.

**2. Materials and methods**

*2.1 Study site, host species*

The study was conducted at the Biological Station Rybachy of the Zoological Institute of the Russian Academy of Sciences (located at 55°09’N, 20°51’E), from July to October 2020. For our study, we selected siskins due to their status as a Palearctic bird species with a limited migratory range, which likely has not come into contact with parasites of African origin. Additionally, this species is common and abundant in the study area and proved itself a convenient candidate for experiments with malaria infection. Birds captured on their autumn migration were examined for the presence of haemosporidian parasites using microscopy and PCR-based diagnostic methods (see below).

Sixty juvenile siskins were randomly divided into three equal groups: one control and two experimental groups, referred to as SGS1, GRW2 and Control. Each bird was housed in an individual plastic cage within a vector-free room with a constant ambient temperature (+23°C) and light-dark photoperiod (L:D) as 17:7, mimicking the natural photoperiod on 1st July. Water and food were provided *ad libitum*.

*2.2 Experimental infections of birds and collection of blood*

We used two species of *Plasmodium* parasites for experimental infections: *P.* *relictum* (lineage SGS1) and *P. ashfordi* (lineage GRW2). The first one, SGS1, was initially isolated in 2018 from a naturally infected wild common rosefinch (*Carpodacus erythrinus*). Several juvenile siskins were infected from this bird, and since then they served as living donors of SGS1. The southern malaria strain, *P. ashfordi,* was collected from a wild wood warbler (*Phylloscopus sibilatrix*) during its spring migration in 2020. Its blood was cryopreserved according to Garnham (1966) and then thawed prior to the start of the experiment.

To multiply the parasites, a number of juvenile siskins (2 for SGS1, 3 for GRW2) were inoculated with infected blood obtained from SGS1 and GRW2 donors. For each experimental group, a mixture of infected donor blood, 3.7% sodium citrate (used as an anticoagulant) and 0.9% saline (all at a ratio of 4:1:5) was prepared as described by (Iezhova, Valkiūnas, & Bairlein\*, 2005). Experimental birds received an injection of 150 μl of this mixture into their pectoral muscle. All control birds underwent the same procedure, with the exception that the inoculated blood originated from an uninfected donor.

Starting with the inoculation procedure and continuing every sixth day after, no more than two capillaries (approximately 150 μl) of blood were collected from the wing vein (ulnar) of each experimental bird. Two drops of this blood were used to prepare two smears, a fraction of blood was centrifuged at 10,000 rpm to separate plasma and red blood cells. Subsequently, plasma was aspirated and transferred into cryo-tubes, then stored at -196º in liquid nitrogen. The remained blood was stored in SET-buffer (0.05 M Tris, 0.15 M NaCl, 0.5 M EDTA, pH 8.0) for molecular analyses, as described by Hellgren, Waldenström, and Bensch (2004).

The blood smears were air-dried, fixed in absolute methanol, and stained with Giemsa according to the standard protocol (Valkiūnas, 2005). These smears were then examined under a light microscope at 1000x magnification using oil immersion. The intensity of parasitemia was determined as a percentage by directly counting the number of parasites per 1000 erythrocytes, or per 10,000 erythrocytes if infections were light, as recommended by Godfrey Jr., Fedynich, and Pence (1987).

Care and handling of animals was under current laws of Russia. All culling of experimental birds was permitted by the Forest and Nature Protection Agency of Kaliningrad Region, Russia (№ 26 of 13/06/2018), whose permits were based on the decisions made by the Specialized Committee of the Scientific Council of the Zoological Institute RAS and Russian Foundation for Basic Research. Experimental procedures were approved by the Scientific Council of the Zoological Institute RAS.

*2.3 DNA extraction and PCR-based method*

We followed a standard ammonium-acetate protocol (Sambrook, 1989) to extract total DNA from the collected blood samples. For PCR-based analysis, we followed nested-PCR protocol using primers specific to avian *Plasmodium* and *Haemoproteus* parasites (Hellgren et al., 2004). To control for false amplification, we used positive (DNA of *P. relictum*) and negative (nuclease-free water) controls. The parasite DNA amplification outcomes were assessed by running electrophoresis on a 2% agarose gel.

To determine the genetic lineages of used parasites, we sequenced fragments from both 5′ and 3′ ends using an ABI PRISM TM 3100 capillary sequencing robot (Applied Biosystems, USA). Obtained sequences were aligned using BioEdit software (Hall, 1999) and identified using the BLAST-program in GenBank and the MalAvi database (Bensch et al., 2009).

*2.4 Measurements of metabolic rate*

To determine the maintenance metabolic rate exhibited by healthy birds, we measured their RMR before inoculation. We designate it as the basal metabolic rate (BMR) because it fulfills all the criteria for BMR measurement (McNab, 1997). This measurement represents the minimal energetic metabolism necessary to maintain normothermia in a resting endotherm in the postabsorptive state and within the thermoneutral zone of ambient temperatures (McNab, 1997). Subsequently in the text, we consistently refer to the initial metabolic rate of birds as BMR, and post-inoculation metabolic rates as RMR. Both BMR and RMR were estimated by flow-through respirometry. The average duration between the capture of all birds and the initial measurement of BMR was 25 days. The average number of days between the capture and inoculation procedure was 31.1 days for all birds.

Each day, at about 21:00, we placed up to four birds into the individual polypropylene chambers with a volume of 1.3 liters. These chambers, with birds inside them, were then placed within a thermostat to maintain the ambient temperature of 27 °C, which is within the thermoneutral zone of siskins (V. Gavrilov & Gavrilov, 2019; V. M. Gavrilov, 2014). Four separate membrane air pumps pushed the outside air through the chambers containing indicating silica gel, facilitating the removal of water vapor from the incoming air. The treated air was subsequently directed into the chambers with the birds, achieving a flow rate of approximately 350-400 ml/min. The air pumps were connected to the uninterruptible power supply system so that possible power outages wouldn`t suffocate birds in chambers.

To measure the metabolic rate of several birds throughout one night, we used an airflow-switching system that automatically alternated between the chamber containing a bird and the empty reference chamber into the respirometer. Each bird was measured for 20 min (10 min for the reference chamber) in each cycle.

After the chamber with a bird, the air entered a 50 ml tube containing Drierite® desiccant (USA), then passed through the mass flow-meter of the FoxBox respirometer (Sable Systems, USA). A portion of the airflow was subsampled through the O2 gas analyzer of the FoxBox respirometer, using a Dwyer GFC-1106 flow controller (Dwyer Instruments, USA) operating at a rate of 120 ml/min. The desiccant was replaced daily, as insufficiently dehumidified air can result in an underestimation of measured oxygen concentration (Melanson et al., 2010). To minimize the system`s washout time, the volume of all pathways downstream of the animal chambers, including the desiccant chamber, was minimized (Frappell, Blevin, & Baudinette, 1989; Lighton & Halsey, 2011).

The fractional concentrations of O2 were recorded with a sampling interval of 4 seconds. We discarded the first five minutes of measurements as a washout time. To estimate the BMR and RMR, we used a 5-minute minimum running average. Before starting all experiments, the gas analyzer was zero-calibrated with 6.0 nitrogen. Before each measurement session, the gas analyzer was calibrated using atmospheric air. The volume of oxygen consumed by the birds was calculated according to Eq. 1a in Koteja (1996), assuming a fixed respiratory quotient (RQ) of 0.8. This value was then converted into energy expenditure (kJ/day) using the energetic equivalent of 20.1 kJ per 1 L of oxygen consumed (Table 12-1 in Brody and Lardy (1946)). At about 7:00, birds were released from their chambers and weighed with an accuracy of 0.1 g. We used this morning’s body mass in the regression analysis, as well as to calculate the mass-specific and mass-independent RMR.

The mean value of BMR in siskins after the capture was 22.03 kJ/day with a mean body mass of 12.87 g. There were no differences in BMR between experimental and control birds (ANOVA: P = 0.065) and between sexes (ANOVA: P = 0.639). Among experimental birds there were no differences in BMR between SGS1 and GRW2 infected siskins (ANOVA: P = 0.0614).

*2.5 Analysis of IL-6 level*

We determined IL-6 levels in birds` blood plasma by enzyme-linked immunosorbent assay using a commercial test system Chicken Interleukin 6, IL-6 ELISA Kit according to the manufacturer’s instructions (Puda Scientific Co., Ltd, China). This test system was developed for the quantitative measurement of IL-6 in serum, plasma and tissue homogenates of chickens. This is a “sandwich” type ELISA kit, its detection range is 0,1-32 pg/ml, and its sensitivity is 0.1 pg/ml. Optical density was measured on a Bio-Rad 680 microplate photometer (USA) at a wavelength of 450 nm. The ELISA Kit required a sample volume of 10 µL of plasma, which was diluted with 40 µL of Sample Diluent provided within the kit.

*2.5 Statistical analysis*

All statistical analyses, data processing and visualizations were performed with functions of the statistical programming language R v. 4.2.3 (R Core Team, 2023).

To describe the dynamics of parasitemia, RMR, IL-6 level, as well as the link between parasitemia and mentioned physiological parameters we used generalized additive mixed models (GAMMs). GAMMs are an extension of generalized additive models (GAM). As GAM, GAMMs incorporates smooth functions, which enable to model non-linear relationships between covariate and response but effect of groupping (random) factor included as well (Wood, 2017). Smooth function

Within all our analysis the bird’s individual ring number (ID) was used as a random grouping factor (Pedersen E. J., 2019). For each response variable, we fitted two models. The first one included one common smoother for all treatment levels (Control, SGS1 and GRW2), while the second model incorporated distinct smoothers, each corresponding to a different treatment. Both models within each response variable were compared using the Akaike information criterion (AIC). The model with the lowest AIC value was considered the final one.

In the GAMM applied for the description of RMR dynamics, we used log10-transform RMR as a response variable and as an explanatory variables we used the belonging to a specific experimental or control group and bird’s body mass (log10-transformed Mb) was included as a covariate for potential allometric relationships. Smoothers were added for the DPI in order to account for the repeated measures over time. For modeling the dynamics of IL-6 we used log10-transformed IL-6 level and as an explanatory variable we used belonging to a specific experimental or control group. For RMR and IL-6 level GAMMs were constructed based on Gaussian distribution ~~(both variables were log10-transformed prior to analysis)~~. For modeling the dynamics parasitemia, again, only belonging to a specific experimental or control group was used as explanatory variable. Since parasitemia, our response variable, cannot have negative values, we used a negative binomial distribution to model it using GAMM.

In order to provide analysis of association of the estimated physiological parameters with malaria parasite infection, we, again, applied GAMM. For log10-transformed RMR we utilized as an explanatory variable the cumulative parasitemia (the sum of approximately calculated parasitemia levels related to the day of RMR measurements for each bird, see below) and, as in the model for RMR dynamics, log10-transformed body mass and belonging to the treatment group. However, our respirometer's design allowed us to simultaneously test only four birds per night. This circumstance, coupled with our decision to collect blood samples every sixth day after the inoculation from the entire experimental or control group at once, posed challenges for subsequent statistical analysis when a combination of RMR and parasitemia level was necessary. To estimate the level of parasitemia on the day of RMR measurement, we calculated the parasitemia's dependence on the date, assuming that over relatively short time intervals (six days), the parasitemia development curve could be approximated as linear. This equation was derived for each RMR measurement from parasitemia data on the two days closest to it (one day before and one after the metabolic trial). This approximately estimated parasitemia was utilized to compute the cumulative parasitemia for our model investigating the association between RMR and parasitemia. Additionally, we sought to assess the relationship between IL-6 levels and cumulative parasitemia levels also using the GAMM. In this model, log10-transformed IL-6 served as the dependent variable, while cumulative parasitemia level, experimental group, and log10-transformed body mass was employed as independent variables. As with all other models, individual bird ring number was included as a random effect variable

To assess the significant differences between our GAMMs for each studied physiological parameters, we employed a pairwise comparison of the estimated smoothers and their associated confidence intervals. This approach enabled us to compare trends across different factor levels for all pairs of treatment groups over time. By examining the difference between trends, we could determine if any observed discrepancies were statistically significant. If the difference between trends for compared groups is negligible, it will be indistinguishable from zero, suggesting that the treatment (infection with one of the two lineages of parasites and the control group) did not induce a discernible change in response within either compared group. In contrast, when the shifts in trends occur, the CI excludes zero, and this allows us to draw conclusions about the differences between the groups without the necessity of calculating the P-value. For a more detailed description of the applied method see Mundo, Tipton, and Muldoon (2022) and <https://fromthebottomoftheheap.net/2017/10/10/difference-splines-i/>.

In order to reveal the relationship between infection intensity and IL-6 level at the moment of their estimation, we applied linear mixed effect model (LMM). This model incorporated dependent variable log-transformed IL-6, log-transformed parasitemia and factor variable which stand for the belonging to one of the two experimental groups, as well as individual birds ring random factor. For LMM analysis we used function lmer() from the package “lme4” (Bates et al., 2015).

For all models`, validity was assessed using residual and quantile-quantile plots. Function appraise() from the package “gratia” (Simpson, 2023) was used for the diagnostic analysis. For GAM-based analysis we applied function gam() from the package “mgcv” (Wood, 2017).

We checked the stability of RMR during the development of parasitemia by assessing its repeatability (Lessells & Boag, 1987; Nakagawa & Schielzeth, 2010). We estimated repeatability of RMR using linear mixed-effects models (LMM), fitted by the function rpt() from the “rptR” package (Stoffel et al., 2017). The individual ring number (ID) was set as a random effect and log10 (RMR) as a response factor. Since RMR highly depends on body mass (Mb), we estimated adjusted RMR repeatability (Nakagawa & Schielzeth, 2010) using log10(Mb) as the covariate. Both the number of parametric bootstraps for estimation of standard error (SE) of repeatability (R) and the number of permutations for estimation of the P-value were set to 1e4.

**3. Results**

*3.1 Parasitemia development*

All experimental birds were susceptible to the infections. The development of parasitemia in the SGS1 group was typical, with a prepatent period of about 6 days post inoculation (DPI) and a peak occurring on the 18th DPI, with a mean parasitemia 50.5% (±7.1%, here and thereafter SE are given). Minimal parasitemia during the acute stage was 0.1% and the maximum reached 90%. By the end of the experiment, all birds had less than 1% parasitemia except one bird with 3.5%. In the GRW2 group, the prepatent period exceeded 6 DPI, with the peak occurring with a slight delay on the 24th DPI with a mean parasitemia of 33.2% (±6.7). The acute stage was prolonged and by the end of the experiment in eight birds out of ten survived parasitemia remained above 1%. The mortality rate for birds with the SGS1 was 50% (10 birds) and 45% (9 birds) for the GRW2 group. The control group experienced a mortality rate of 25% (5 birds).

GAMM fitted with two different smoothers for two parasite species (AIC = 1326) was better in comparison with GAMM including one common smoother for both species (AIC = 1362). The model parameters are given in Table 1.

No significant difference in the mean parasitemia level between the two parasite species was revealed in the fitted model (Table 1. parametric terms). The general patterns of parasitemia dynamics were similar for both species (Fig. 1, A). Although, in the case of SGS1, the parasitemia was significantly higher than that of GRW2 at the beginning of the disease development, at the end of the experiment, the parasitemia level of the second species became significantly higher than that of the first (Fig. 1, B).

*3.2 Analysis of metabolic rates` dynamics*

For the description of RMR the best GAMM, the model with different smoothers (AIC = -753) was better than the model with common for all groups smoother (AIC = -700). This suggests that RMR dynamics differed for each siskin group (SGS1, GRW2 and Control). The smoothers for all groups were significantly curved (i.e., differed from the horizontal straight line, Table 2), indicating an unstable RMR level over the observation time within each group. (Fig 2. A-C).

In the Control group, there was a slight increase in RMR during the first two weeks after the inoculation, whereas in both experimental groups, RMR exhibited a dramatic decrease.

In the SGS1 group, immediately after the inoculation, a decline in RMR was observed, followed by subsequent growth. By the end of the experiment, on average, RMR was higher than it was initially (Fig. 2, A). The RMR level in the SGS1 group was significantly lower than in the Control one during the period of 3-23 DPI, but later (32-50 DPI) the RMR level in the SGS1 group was higher than in the Control (Fig. 2, B).

In GRW2 birds, RMR at first decreased (Fig 2, A): during 3-14 DPI it was significantly lower than in the Control group (Fig. 2, B). However, during the following days there were no significant differences between GRW2 and Control groups (Fig. 2. B).

The comparison of RMR dynamics in two inoculated groups (SGS1 vs GRW2, Fig 2, B) reveals significantly higher RMR levels in GRW2 birds during 17-26 DPI. However, later for a short period (during 46-49 DPI) an opposite pattern was recorded.

*3.3* *Analysis of IL-6 level dynamics*

The best GAMM for IL-6 changes were, as for parasitemia and RMR, with different smoothers for each group of siskins (AIC = -353, for the model with common smoother AIC = -251). The parameters of the model are presented in Table 3.

After the inoculation procedure in the Control group of birds, the level of IL-6 began to decrease from its initial levels. It was the lowest on the 3rd week, after which it began to rise (Fig. 3, A). A similar pattern was revealed in the IL-6 dynamics between birds from the SGS1 group. The concentration of IL-6 decreased during several days after inoculation. However, at the end of the experiment, the average concentration was even higher than the initial level, due to some birds exhibiting several times higher levels of IL-6 from their zero-day values (Fig. 3, A). The IL-6 concentration in the SGS1 group was significantly higher than in the Control group at the beginning and near the end of the survey (Fig. 3, B). Nonetheless, during the middle of the observation period, the IL-6 concentration was significantly lower than in the Control group (Fig. 3, B).

The dynamics of IL-6 in the GRW2 group were more complex. It displayed two peaks: one during the first half of the observation period and another in the second half (Fig. 3, A). The IL-6 concentration in the SGS1 group was significantly higher than in the GRW2 group for a brief period at the beginning of the study (0-2 DPI) and during the last days of observations (45-53 DPI). From 6 to 22 DPI, IL-6 concentrations were significantly higher in the GRW2 group than in the SGS1 group, but no significant differences were found between groups 23-44 DPI.

*3.4* *Analysis of physiological parameters relationships with parasitemia levels*

For the analysis of RMR and associated approximate cumulative parasitemia, the optimal GAMM was the one with a shared smoother for both experimental groups (AIC = X). This suggests that birds in both infected groups exhibited similar changes in their RMR during the accumulation of parasitemia. Initially, RMR increased during the early stages of the disease but then stabilized (see Fig. X). This is supported by the observation that the smooth function for both infected groups deviated from zero, indicating that RMR did not remain constant as parasitemia accumulated. Additionally, RMR appeared to be slightly higher in GRW2 infected birds, although the confidence intervals of the modeled curves overlapped.

For the analysis of the relationship between IL-6 and cumulative parasitemia, once again, the GAMM with the same smoother function performed better (AIC = X), indicating generally similar trends for both groups. As the accumulated parasitemia value increases for each bird, the IL-6 level remains relatively constant, as indicated by a smoother which is equal to zero (Fig. X). However, within SGS1 infected birds, the average IL-6 level is higher than in the group infected with the GRW2 parasite.

The relationship between infection intensity and IL-6 levels measured on exactly the same DPI varied between the two experimental groups. Among GRW2 infected birds, no clear correlation was observed. However, for SGS1 infected siskins, a negative relationship can be traced. This suggests that for this experimental group of birds as parasitemia levels increase, IL-6 levels decrease. Alternatively, it's possible that high parasitemia levels are only attainable when IL-6 levels are low.

**Я бы предложил убрать весь этот кусок**

*3.5 Analysis of repeatabilities*

The repeatabilities of mass-independent RMR in Control, SGS1 and GRW2 groups were R = 0.207±0.114 (P = 0.009), R = 0.359±0.136 (P = 0.007) and R = 0 (P = 0.997; there was singular fit in the model since the variance of the random effect was close to zero). The repeatabilities of log10(Mb) in Control, SGS1 and GRW2 groups were R = 0.464±0.122 (P < 0.001), R = 0.695±0.102 (P < 0.001) and R = 0.139±0.108 (P = 0.07), respectively.

**4. Discussion**

*4.1 Parasitemia development*

Both *P. relictum* SGS1 and *P. ashfordi* GRW2 avian malaria parasite species are considered generalists with a wide range of potential host species. According to published papers, both exhibit high levels of parasitemia during primary infections of juvenile siskins (Palinauskas et al., 2008; Videvall et al., 2017). Palinauskas et al. (2011) was the first to report susceptibility to infected blood inoculation and the formation of gametocytes of *P. ashfordi* in Northern Palearctic bird species, including *S. spinus* and *Loxia curvirostra*. The development of the *P. relictum* SGS1 parasite was more rapid than that of *P. relictum* GRW2. The acute stage started and ended earlier and more simultaneously in SGS1-infected birds than in GRW2. The long prepatent period of *P. ashfordi* in our study corresponds to the idea of a more extended prepatent period for most parasites of *Novyella* subgenus, to which *P. ashfordi* belongs (Garnham, 1966; Palinauskas et al., 2011; Valkiūnas, 2005). The prolonged prepatent period of *P. ashfordi* observed in our experiment aligns with findings from other studies and supports the notion of an extended prepatent period for most parasites of the *Novyella* subgenus, to which *P. ashfordi* belongs (Garnham, 1966; Palinauskas et al., 2011; Valkiūnas, 2005). In addition to the prolonged hidden stage in this group, high levels of parasitemia persisted until the end of our experiment on Day 54 post-infection (DPI). Previous studies with siskins infected with *P. ashfordi* commonly ended on DPI 30-33, during which authors observed a decline in parasitemia levels from its peak but noted that parasitemia remained high. However, whether this persistence is attributable to host-parasite interactions or specific characteristics of the parasite species, such as a late peak in parasitemia, remains unclear (Videvall et al., 2017).

*4.2 Oxygen consumption during different malaria infections in siskins*

A traditional view suggests that RMR should be positively linked to parasite loads (Bordes & Morand, 2011). However, this statement still lacks experimental evidence, and available data contradict each other. A recent meta-analysis of research data that investigated the impact of parasitic load on the RMR of various animal groups indicated that, in most cases, the RMR of hosts increased after parasite infestation (Robar et al., 2011). Nonetheless, the overall effect of parasites was weak and not statistically significant. As the author suggests, the lack of consistent effect of parasites on hosts` energy metabolism in analyzed articles may be explained by different host-parasite systems used in described experiments (Robar et al., 2011)

We are aware of only three studies that focus on the impact of haemosporidian parasites on hosts` metabolic rates, and their results contradict each other. The first was conducted on two-year-old domestic canaries (*Serinus canaria*), where birds were infected with *Plasmodium relictum* of unknown genetic lineage. It was shown that during the peak of parasitemia, oxygen consumption decreased under both thermoneutral and low-temperature conditions (Hayworth, Charles van Riper, & Weathers, 1987). The study by Hahn et al. (2018) on infected great reed warblers (*Acrocephalus arundinaceus*) did not find any difference in RMR and maximal metabolic rate (MMR) between non-infected and experimentally infected birds with *Plasmodium relictum*  (lineage GRW4), during both acute and chronic stages. Hahn et al. (2018) concluded that low-level parasitemia (less than 1%) during avian malaria did not affect the aerobic performance of birds. A recent study by Stager et al. (2021) on the wild pink-sided junco *(Junco hyemalis mearnsi*) demonstrated that the presence of haemosporidian parasites (*Haemoproteus* or *Plasmodium*) did not correlate with any of the measured physiological indices, particularly with the RMR of the birds. The authors concluded that there was a minor cost of haemosporidian infection on either junco aerobic performance or energy budgets.

The results of our study reveal that oxygen consumption in immunologically naïve birds after malaria infection differs depending on the malaria parasite. In the *P. relictum* SGS1 group, the decrease of RMR coincided with the acute phase of parasitemia. This is similar to the result reported by Hayworth et al. (1987), who observed a significant decrease in oxygen consumption in canaries during the crisis period of *P. relictum* infection. Since the destruction of erythrocytes at this time is most pronounced, it is reasonable to assume that hematological parameters, such as hematocrit and hemoglobin, should be negatively affected by proliferating parasite (Hammond, Chappell, Cardullo, Lin, & Johnsen, 2000; Stager et al., 2021). Our study did not measure hematocrit level or hemoglobin concentration – parameters that reflect blood`s capacity to carry oxygen, because the amount of blood collected from each experimental bird was constrained. Several studies indicated a decrease in hematocrit in experimentally infected birds during the acute phase of the *Plasmodium* infection (Ilgūnas, Bukauskaitė, et al., 2019; Ilgūnas, Palinauskas, Platonova, Iezhova, & Valkiūnas, 2019; LaPointe, Atkinson, & Samuel, 2012; Palinauskas et al., 2008; Paulman & McAllister, 2005; Williams, 2005), as well as in hemoglobin concentration (Krams et al., 2013; Palinauskas, Žiegytė, Šengaut, & Bernotienė, 2022). Videvall et al. (2020) reported a negative correlation between parasitemia levels and the expression of genes involved in oxygen binding and transportation processes in siskins infected with *P. relictum* SGS1. Interestingly, in the earlier study with siskins and *P. ashfordi* GRW2, Videvall et al. (2015) observed a significant expression of genes responsible for metabolic functions and oxidation-reduction processes during both peak and decreasing parasitemia stages. Afterwards, during the late stage of malaria, when parasitemia decreased, catabolic processes became predominant compared to the peak of parasitemia. Comparing the result of these two studies, Videvall et al. (2020) noted similarities in functions of expressed genes in SGS1-infected (Videvall et al., 2020) and GRW2-infected siskins (Videvall et al., 2015). They also demonstrated that highly-virulent SGS1 induced a strong transcriptome response, while the low-virulent GRW4 – minor. Given the high levels of parasitemia observed in both *P. relictum* SGS1 and *P. ashfordi* GRW2 in our experiment, we can conclude that both parasites substantially affect the physiological state of experimental siskins.

The pathological consequences of malaria vary depending on host and parasite species, their interactions, environmental factors, host individual traits, and parasite isolates – all of which can affect the disease outcome (Cornet & Sorci, 2014). In the study by Hahn et al. (2018), no correlation was observed between parasitemia intensity and birds' aerobic performance and the peak parasitemia recorded in this study was lower than 1% of parasitized erythrocytes. In contrast, in Hayworth et. al. (1987) it ranged from 1.32% to 50%. Hayworth et. al. (1987) found a significant positive correlation between level of parasitemia at the peak and the relative decrease in oxygen consumption during low temperature conditions, though it was not significant in the thermoneutral zone. It appears evident that the higher is the parasitemia, the more detrimental consequences it has on bird`s health in general, and consequently, strongly it should affect host metabolic rate in particular.

In the light of these considerations, it is curious that for siskins from the GRW2 group, our GAMM also showed a period of lowered RMR, albeit short. During that time period (6-12 DPI) the average level of parasitemia was relatively small, indicating that acute phase had not appeared yet. But, starting on day 12 DPI, both RMR and parasitemia began to rise. We assume two possible explanations for this: a) the average parasitemia in the GRW2 group during the crisis was 33%, which is almost two times less than parasitemia in the SGS1 group (50%). This lower parasitemia level in group GRW2 may not have caused sufficient erythrocyte destruction to reduce the metabolic rate. However, we cannot definitively claim that one parasitemia is less severe than the other, especially when both are so high. Additionally, it is noteworthy that relying solely on parasitemia levels within the bloodstream may not consistently offer an accurate assessment of malaria severity. For example, in the case of *P. elongatum* (subgenus *Huffia*), characterized by typically low-level parasitemia (generally below 1%), it can induce significant pathology (Valkiūnas et al., 2008). This arises from its impact on the erythropoietic system within the bone marrow, a consequence of the destruction of stem cells by exoerythrocytic stages (Palinauskas et al., 2016). b) the increase in RMR might indicate the activation of immune response or, at least, an increase in energy expenditure during the acute phase of an unfamiliar tropical malaria infection. This is suggested by the rise in RMR coincided with the peak parasitemia in birds GRW2 birds 24 DPI. After 30 DPI, the difference between the two experimental groups in RMR became statistically insignificant, with the tendency for birds from the SGS1 group to have a higher rate of metabolism. Interestingly, we observed an increase in oxygen consumption in the Control group after the inoculation of uninfected blood. This increase lasted for about 2 weeks, after which RMR decreased and, by the 5th week, became indistinguishable from the initial level. We see a possible reason for this in: a) stress, because with the beginning of the experiment, birds were regularly subjected to handling, which may have caused a short term stress additional to chronic stress from captivity (Li et al., 2019; Thompson, Brown, & Downs, 2015); b) immune response due to the inoculation with uninfected blood, since blood itself can cause an inflammatory response (Ellis et al., 2015; Garraud et al., 2016). We cannot exclude the possibility that these factors were acting simultaneously.

Despite the high peak of parasitemia in birds infected with *P. relictum* SGS1, repeatabilities of both body mass and mass-independent RMR during the course of the disease in this group were significant and even exceeded the corresponding repeatabilities in the Control group. However, both corresponding repeatabilities in birds infected with *P. ashfordi* GRW2 did not differ significantly from zero, suggesting that GRW2malaria infection causes more significant changes in bird physiology compared to SGS1.

*4.3 Il-6 level in the blood of infected siskins*

Recent research suggests that in addition to the direct harm inflicted by the parasite, such as red blood cell destruction, the immune system's response plays a central role in malaria-induced damage. This occurs predominantly during acute inflammation, triggered by the immune system to eradicate the parasites. However, while inflammation aids in parasite clearance, heightened levels of pro-inflammatory cytokines can exacerbate immunopathology, contributing to severe tissue damage.

In the SGS1 group, siskins exhibited a consistent decline in IL-6 levels during the initial two weeks post-infection. However, towards the later stages of the experiment, it's noteworthy that IL-6 began to increase, reaching levels several times higher than those observed at the start of the experiment. In contrast to SGS1, birds infected with GRW2 parasite tended to increase their IL-6 level in plasma soon after the infection and up to 12 DPI. As shown in figure 1, the week between 12 DPI and 18 DPI was a period when parasites began to multiplicate rapidly. This coincided with the transition from the increase of IL-6 levels to its decrease in GRW2-infected siskins. It seems like birds in both groups tended to decrease IL-6 level in response to the rapid multiplication of the parasite. This aspect is particularly intriguing because, contrary to our findings, the majority of studies conducted on malaria-infected humans have linked elevated levels of IL-6 with malaria severity (reviewed in Wilairatrana, 2022). It seems like we observed somewhat similar to results obtained in the master`s degree project by Esteban Henao (2019) conducted on siskins also infected with *P. relictum* SGS1. The author showed that the expression level of IL-15 on 8 DPI was negatively correlated with the rapidly growing parasitemia level, and highly parasitized birds express less IL-15, approaching the expression level of uninfected birds. This resemblance to our results for siskins from the SGS1 group is notable, although we observed a decrease in interleukin levels in both the Control and SGS1-infected groups. IL-15 is required for type 1 cytokine production, natural killer cells and dendritic cells responses, and, as it was demonstrated on *P.* *chabaudi* infected mice, for the synthesis of malaria-specific antibodies (Ing, Gros, & Stevenson, 2005). The authors suggested that infected birds may express less IL-15 in order to control for hyperreactivity of immune response to the growing number of parasitic antigens (Esteban Henao, 2019). However, despite the different roles of the IL-15 and IL-6 cytokines in immune response, mechanisms of suppressing their expression and lowering the final level in the blood may still be the same. That means, that observed in our study decrease in IL-6 might be the result of malaria-related immunosuppression and/or activation of a tolerogenic way of immune response by the host itself in order to avoid immunopathology (Calle, Mordmüller, & Singh, 2021; Esteban Henao, 2019).

Analysis of birds` transcriptome response to malaria showed that expressed genes were associated with innate and adaptive immunity and their expression was active during the peak of parasitemia and less or not active during the malaria late stages (Paxton et al., 2023; Videvall et al., 2020). Paxton et al. (2023) showed that Hawaiʻi ‘amakihi (*Chlorodrepanis virens*) from a highly susceptible population that succumbed to *P. relictum* GRW4 in experiment, as well as those that recovered, exhibited different gene expression profiles at different stages of malaria. Birds that did not survive the infection had a dysregulation of the innate immune system, resulting in increased levels of gene expression at the middle and late stages of infection. In contrast, survivors showed the upregulation of genes of both innate and adaptive immunity at the peak of parasitemia. We cannot make a comprehensive assessment of gene expression solely based on IL-6 levels. However, in light of the findings by Paxton et al. (2023), it is remarkable that by the end of our experiment, a majority of birds infected with the GRW2 parasite had very low levels of IL-6, the lowest among all three groups of birds. In contrast, several birds from the SGS1 group that survived until the end of the experiment had several times higher levels of IL-6 in their blood plasma after they survived the critical moment at the peak parasitemia. Research indicates that malaria might indirectly increase vulnerability to and complications of other diseases (Scott, 2011). Human patients with malaria are more prone to bacteraemia (Lee, 2018), and while anti-malaria interventions reduce malaria-related deaths, they also lead to a decline in overall morbidity and mortality, suggesting a broader influence on health (Aregawi, 2017). Our experiments involved wild birds. Despite implementing quarantine measures for all birds prior to the experiments, we were unable to completely rule out or diagnose concurrent infections that could potentially influence the results. We assume that the observed elevation of IL-6 in some birds from the SGS1 group may indicate the resurgence of an unidentified chronic disease, which manifested following malaria-induced immune dysregulation.

Pro-inflammatory cytokines play a crucial role in eliminating malaria parasites and their up-regulation is associated with resistance mechanism within host immune response (…). Several works with deliberate suppression of inflammatory response in experimental animals infected with *Plasmodium* parasite have shown the reduce of the cost of infection, mortality and malaria virulence, while significant increase in parasitemia (…). Immunosuppression is considered as one of the tolerance mechanisms aimed to minimize the harm of inflammation, though the mechanisms of it remains yet unexplored (Calle, 2021).

In the control birds, there was also a decrease of IL-6 levels right after the inoculation. This appears inconsistent with the idea that control birds experience prolonged immune activation due to a single injection of birds` blood free from malaria. Instead, it seems that the primary factor influencing changes in RMR and IL-6 levels in control siskins was the chronic stress arising from captivity and handling. Chronic stress can have immunosuppressive effects, contrary to the acute stress, which typically has immunoenhancing properties (reviewed in Dhabhar and Mcewen (1997)), (but see Martin et al. (2011)).

IL-6 is a multifunctional cytokine with roles in acute-phase immune response, immune regulation, and hematopoiesis (Van Snick, 1990; Heinrich, 1990). Consequently, the regular procedure of blood sampling may influence IL-6 levels in the plasma of experimental birds during subsequent blood collection, potentially exacerbating the hemolytic effects of high parasitemia levels. To date, no studies have investigated the long-term effects of regular blood loss on interleukin serum concentrations in either mammals or birds. However, several studies have examined the impact of blood loss during surgical procedures on serum IL-6 levels in humans. These studies have shown a positive correlation between IL-6 levels and factors such as operation duration, amount of blood loss, and extent of tissue injury, with peak levels typically observed within 48 hours post-surgery (Sakamoto, 1994; Igarashi, 1996). Regular blood sampling may also impact metabolic rate, in addition to serum IL-6 levels. However, there is limited research on the effects of blood loss on resting metabolic rate (RMR). Sun et al (2019) simulated blood loss caused by hematophagous parasites in tree swallow nestlings (*Tachycineta bicolor*) and found no decrease in hemoglobin levels or changes in RMR due to blood loss alone. Interestingly, they observed a positive correlation between ectoparasite load and increased RMR, suggesting that continuous blood loss from feeding ectoparasites and the simultaneous production of red blood cells by parasitized birds may contribute to elevated RMR (Schindler, 1986). In our study, we sampled no more than 150 μl of blood each six days (see Materials and methods). Though acute blood removal may have some effects on bird fitness, the research suggest that its impact is generally limited. (reviewed in Sheldon et al. 2008; Orzechowski et al. 2019; Sun, 2021; but see Brown and Brown (2009)). We cannot exclude possible adverse effect of this invasive procedure itself on our measured parameters. Not all the highly parasitized, and therefore with high hemolysis level birds died during the experiment. The effect of blood sampling can be speculated through the control group of birds, as they had not experienced hemolysis from malaria parasite activity, only regular blood loss due to blood sampling. However, it still overlaps with effects from stress from captivity and handling, as discussed earlier. Интерлейкиновая анемия, ИЛ-6 и гемопоэз – стоит ли тут про это расписывать?

*4.4. RMR and IL-6 association with parasitemia level*

To link the measurements of infected birds' RMR with parasitemia, we employed an estimation of the cumulative parasitemia timed to the RMR measurements. Given the imperfections in our experimental design, we had to manipulate the parasitemia approximation, as outlined in the Methods section. We implied that this approximately calculated cumulative parasitemia, an uncommon parameter in avian malaria studies, would provide a rough estimate of the parasite burden that each bird had been experienced in total up to the moment of RMR measurement. Our findings indicate that RMR was indeed influenced by cumulative parasitemia in both groups of infected birds. According to the best-fitting GAMM, the trends in RMR changes were similar between the two infected groups, albeit with a slight difference in RMR levels. Specifically, GRW2 infected birds exhibited slightly higher RMR compared to SGS1 infected siskins. However, it's noteworthy that the confidence intervals of the modeled curves overlapped, suggesting some degree of uncertainty in this observation. Remarkably, according to this model, both SGS1 and GRW2 infected siskins exhibited an increase in RMR as the cumulative parasitemia levels rose. While this trend aligns with the previously discussed modeled dynamics of RMR changes for the GRW2 infected group, though the model still indicated a brief initial decrease in RMR, which was promptly followed by an increase, it seems to contradict with our conclusions for the SGS1 infected birds, where the initial decrease in RMR was clearly visible on the model`s curve. The cumulative parasitemia parameter does not directly reflect the time passed since the moment of infection, unlike the DPI. However, with the progression of infection, cumulative parasitemia consistently increased over time. The absence of RMR measurements, particularly during the acute phase of parasitemia, while the most measurements occurred after peak parasitemia, may have contributed to the emergence of a trend indicating increased oxygen consumption within infected birds.

The analysis of the relationship between IL-6 and cumulative parasitemia within both groups exhibited overall similar trends. Interestingly, as the accumulated parasitemia increased for each bird, the IL-6 level remained relatively constant, as indicated by a smoother that is equal to zero. Again, as in the previous analysis, the GAMM`s curve for IL-6 association with cumulative parasitemia reflects the general trend of IL-6 level within the both infected group of birds. And, according to this model, the IL-6 level appeared to be more or less constant with growing cumulative level of experienced by each bird parasitemia. However, within the SGS1 infected birds, the average IL-6 level was notably higher compared to the group infected with the GRW2 parasite.

In summary, interpreting our models of the relationship between RMR, IL-6, and parasite level can be challenging. It's possible that accumulated parasitemia better reflects the individual course of the disease, while DPI characterizes a more generalized group response, which may vary depending on the bird species. Further research into these relationships is warranted to better understand the complexities of the host-parasite interaction.

The analysis of the LMM relationship between infection intensity and IL-6 levels measured on the same DPI revealed differences between the two experimental groups. While no clear correlation was observed among GRW2 infected birds, a negative relationship can be traced for SGS1 infected siskins. This negative relationship implies that when the parasitemia levels were high in this group of birds, the IL-6 levels were low. This confirms with our speculations based on the model curve of the IL-6 changes over time of the experiment, where we described a decrease in IL-6 level during the beginning of the acute phase of parasitemia. Though, as it was already discussed in previous section, we cannot provide clear mechanism of this depletion.

Experimental birds infected with avian malaria parasites exhibited distinct dynamics of physiological parameters not only compared with control birds, but also between experimental birds where birds were infected with parasites of different *Plasmodium* species. SGS1 infected siskins had both reduced RMR and IL-6 levels during the acute stage of parasitemia, which is consistent with previous findings in other studies. Conversely, GRW2 infected birds demonstrated rather erratic shifts in both RMR and IL-6 levels, which were challenging to interpret in the context of parasitemia development. At the same time, the repeatability of mass-independent RMR and body mass was lower in GRW2 infected birds, than in SGS1 infected birds. We can confidently assert that different avian *Plasmodium* parasites can exert varying effects on the health parameters of their avian hosts. These disparities may also arise from the intricate co-evolutionary dynamics between the host and the parasite. Specifically, in the case of siskins, it's important to consider that they have likely co-evolved with the SGS1 parasite, which has adapted to their local environment. On the other hand, the GRW2 parasite originates from Africa and can be considered exotic for siskins. ~~This difference in evolutionary history and geographic origin may contribute to the varying impacts of these parasites on the health of siskin hosts. This dynamic interplay between host and parasite becomes especially noteworthy when considering the potential introduction of exotic parasites to regions outside their natural range.~~ In the context of climate change and anthropological impacts, the transmission of tropical-origin parasites to northern latitudes has become a matter of concern. Should such transmission occur, it could lead to unpredictable outcomes for local bird populations. Furthermore, our findings with SGS1-infected siskins align closely with the limited existing research that has explored the effects of *Plasmodium* *relictum* parasites on aerobic performance and cytokine expression in avian hosts. Specifically, we observed similar patterns of cytokine expression and aerobic performance alterations as reported in previous studies. Our work helps to elucidate the complexities of the eco-physiological consequences of avian malaria infection and highlights the need for continued interdisciplinary research to fully comprehend the implications of these infections on avian health and population dynamics.

\*\*\* Ниже то, что не вошло в текст \*\*\*

During the asexual development of the blood stage, the parasite was shown to play a clear role in suppressing the host's immune system, affecting both the development and function of humoral and cell-mediated immunity (Calle, 2021). However, most of the evidences of immunosuppressive function of malaria was observed in human and murine malaria models (…).

Blood stages of *Plasmodium yoelli* was shown to impair the initiation of immune response, inhibition of IL-12, which is involved in initiating a cellular immune response, and, in contrast, increasing the anti-inflammatory IL-10 secretion in mice dendritic cells (Ocaña-Morgner, 2016).

**Acknowledgments**

We are grateful to Natalya Gazatova, who conducted all the immunoassays on blood plasma. We also extend our thanks to our colleagues at the Biological Station "Rybachy" for their assistance with species identification and bird ringing, as well as to the students of Immanuel Kant Baltic Federal University for their help in caring for the experimental birds. Data collection and analysis were supported by the Russian Science Foundation grant (grant number 20-14-00049).

Asghar, M., Palinauskas, V., Zaghdoudi-Allan, N., Valkiūnas, G., Mukhin, A., Platonova, E., . . . Hasselquist, D. (2016). Parallel telomere shortening in multiple body tissues owing to malaria infection. *Proc. R. Soc. B., 283*(1836). doi:<https://doi.org/10.1098/rspb.2016.1184>

Asghar, M., Westerdahl, H., Zehtindjiev, P., Ilieva, M., Hasselquist, D., & Bensch, S. (2012). Primary peak and chronic malaria infection levels are correlated in experimentally infected great reed warblers. *Parasitology, 139(10)*(10), 1246-1252. doi:<https://doi.org/10.1017/S0031182012000510>

Bensch, S., Hellgren, O., & Pérez‐Tris, J. (2009). MalAvi: a public database of malaria parasites and related haemosporidians in avian hosts based on mitochondrial cytochrome b lineages. *Mol. Ecol. Resour., 9*(5), 1353-1358. doi:<https://doi.org/10.1111/j.1755-0998.2009.02692.x>

Bensch, S., Waldenström, J., Jonzán, N., Westerdahl, H., Hansson, B., Sejberg, D., & Hasselquist, D. (2007). Temporal dynamics and diversity of avian malaria parasites in a single host species. *J. Anim. Eco.*, 112-122. doi:<https://doi.org/10.1111/j.1365-2656.2006.01176.x>

Bonneaud, C., Mazuc, J., Gonzalez, G., Haussy, C., Chastel, O., Faivre, B., & Sorci, G. (2003). Assessing the cost of mounting an immune response. *Infect. Ecol. Epidemiol., 161*(3), 367-379. doi:<https://doi.org/10.1086/346134>

Bordes, F., & Morand, S. (2011). The impact of multiple infections on wild animal hosts: a review. *Infection ecology & epidemiology, 1*(1), 7346. doi:<https://doi.org/10.3402/iee.v1i0.7346>

Brody, S., & Lardy, H. A. (1946). Bioenergetics and growth. Reinhold. *J. Phys. Chem., 50*(2), 168-169. doi:<https://doi.org/10.1021/j150446a008>

Calle, C. L., Mordmüller, B., & Singh, A. (2021). Immunosuppression in malaria: do *Plasmodium falciparum* parasites hijack the host? *Pathogens, 10*(10), 1277. doi:<https://doi.org/10.3390/pathogens10101277>

Carapau, D., Kruhofer, M., Chatalbash, A., Orengo, J. M., Mota, M. M., & Rodriguez, A. (2007). Transcriptome profile of dendritic cells during malaria: cAMP regulation of IL‐6. *Cell. Microbiol., 9*(7), 1738-1752. doi:<https://doi.org/10.1111/j.1462-5822.2007.00910.x>

Cocumelli, C., Iurescia, M., Diaconu, E. L., Galietta, V., Raso, C., Buccella, C., . . . De Liberato, C. (2021). *Plasmodium matutinum* causing avian malaria in lovebirds (*Agapornis roseicollis*) hosted in an Italian zoo. *Microorganisms, 9*(7), 1356. doi:<https://doi.org/10.3390/microorganisms9071356>

Cornet, S., & Sorci, G. (2014). Avian malaria models of disease. *Encyclopedia of malaria, M. Hommel and PG Kremsner (eds.). Springer New York, New York City, New York*, 1-11.

Demas, G. E., Drazen, D. L., & Nelson, R. J. (2003). Reductions in total body fat decrease humoral immunity. *Proc. R. Soc. B., 270*(1518), 905-911. doi:<https://doi.org/10.1098/rspb.2003.2341>

Dhabhar, F. S., & Mcewen, B. S. (1997). Acute stress enhances while chronic stress suppresses cell-mediated immunityin vivo: A potential role for leukocyte trafficking. *Brain Behav. Immun., 11*(4), 286-306. doi:<https://doi.org/10.1006/brbi.1997.0508>

Ellis, V. A., Cornet, S., Merrill, L., Kunkel, M. R., Tsunekage, T., & Ricklefs, R. E. (2015). Host immune responses to experimental infection of *Plasmodium relictum* (lineage SGS1) in domestic canaries (*Serinus canaria*). *Parasitol. Res., 114*(10), 3627-3636. doi:<https://doi.org/10.1007/s00436-015-4588-7>

Eraud, C., Duriez, O., Chastel, O., & Faivre, B. (2005). The energetic cost of humoral immunity in the collared dove, *Streptopelia decaocto*: is the magnitude sufficient to force energy‐based trade‐offs? *Funct. Ecol., 19*(1), 110-118. doi:<https://doi.org/10.1111/j.0269-8463.2005.00934.x>

Esteban Henao, M. C. (2019). *Analysis of cytokine expression in avian peripheral blood in response to malaria infections*. Retrieved from <http://lup.lub.lu.se/student-papers/record/8998936>

Frappell, P., Blevin, H., & Baudinette, R. (1989). Understanding respirometry chambers: what goes in must come out. *J. Theor. Biol., 138*(4), 479-494. doi:<https://doi.org/10.1016/S0022-5193(89)80046-3>

Garnham, P. C. C. (1966). *Malaria parasites and other Haemosporidia*. Oxford: Blackwell Scientific Publications Ltd.

Garraud, O., Tariket, S., Sut, C., Haddad, A., Aloui, C., Chakroun, T., . . . Cognasse, F. (2016). Transfusion as an inflammation hit: knowns and unknowns. *Front. immunol., 7*, 534. doi:<https://doi.org/10.3389/fimmu.2016.00534>

Gavrilov, V., & Gavrilov, V. (2019). Scaling of total evaporative water loss and evaporative heat loss in birds at different ambient temperatures and seasons. *Int. J. Avian Wildl. Biol., 4*(2), 40-53. doi:<https://doi.org/10.15406/ijawb.2019.04.00150>

Gavrilov, V. M. (2014). Ecological and scaling analysis of the energy expenditure of rest, activity, flight, and evaporative water loss in *Passeriformes* and non-*Passeriformes* in relation to seasonal migrations and to the occupation of boreal stations in high and moderate latitudes. *Q. Rev. Biol., 89*(2), 107-150. doi:<https://doi.org/10.1086/676046>

Godfrey Jr., R. D., Fedynich, A. M., & Pence, D. B. (1987). Quantification of hematozoa in blood smears. *J. Wildl. Dis., 23*(4), 558-565. doi:<https://doi.org/10.7589/0090-3558-23.4.558>

González-Olvera, M., Hernandez-Colina, A., Himmel, T., Eckley, L., Lopez, J., Chantrey, J., . . . Jackson, A. P. (2022). Molecular and epidemiological surveillance of *Plasmodium* spp. during a mortality event affecting Humboldt penguins (*Spheniscus humboldti*) at a zoo in the UK. *Int. J. Parasitol. Parasites Wildl., 19*, 26-37. doi:<https://doi.org/10.1016/j.ijppaw.2022.06.010>

Graham, A. L., Allen, J. E., & Read, A. F. (2005). Evolutionary causes and consequences of immunopathology. *Annu. Rev. Ecol. Evol. Syst., 36*, 373-397. doi:<https://doi.org/10.1146/annurev.ecolsys.36.102003.152622>

Hahn, S., Bauer, S., Dimitrov, D., Emmenegger, T., Ivanova, K., Zehtindjiev, P., & Buttemer, W. A. (2018). Low intensity blood parasite infections do not reduce the aerobic performance of migratory birds. *Proc. R. Soc. B: Biol. Sci., 285*(1871), 20172307. doi:<https://doi.org/10.1098/rspb.2017.2307>

Hall, T. A. (1999). *BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT.* Paper presented at the Nucleic acids symposium series.

Hammond, K. A., Chappell, M. A., Cardullo, R. A., Lin, R.-S., & Johnsen, T. S. (2000). The mechanistic basis of aerobic performance variation in red junglefowl. *J. Exp. Biol., 203*(13), 2053-2064. doi:<https://doi.org/10.1242/jeb.203.13.2053>

Hayworth, A. M., Charles van Riper, I., & Weathers, W. W. (1987). Effects of *Plasmodium relictum* on the metabolic rate and body temperature in canaries (*Serinus canarius*). *J. Parasitol.*, 850-853. doi:<https://doi.org/10.2307/3282431>

Hellgren, O., Waldenström, J., & Bensch, S. (2004). A new PCR assay for simultaneous studies of Leucocytozoon, Plasmodium, and Haemoproteus from avian blood. *J. Parasitol., 90*(4), 797-802. doi:<https://doi.org/10.1645/GE-184R1>

Iezhova, T. A., Valkiūnas, G., & Bairlein\*, F. (2005). Vertebrate host specificity of two avian malaria parasites of the subgenus *Novyella*: *Plasmodium nucleophilum* and *Plasmodium vaughani*. *J. Parasitol., 91*(2), 472-474. doi:<https://doi.org/10.1645/GE-3377RN>

Ilgūnas, M., Bukauskaitė, D., Palinauskas, V., Iezhova, T., Fragner, K., Platonova, E., . . . Valkiūnas, G. (2019). Patterns of *Plasmodium homocircumflexum* virulence in experimentally infected passerine birds. *Malar. J., 18*(1), 1-14. doi:<https://doi.org/10.1186/s12936-019-2810-2>

Ilgūnas, M., Palinauskas, V., Platonova, E., Iezhova, T., & Valkiūnas, G. (2019). The experimental study on susceptibility of common European songbirds to *Plasmodium elongatum* (lineage pGRW6), a widespread avian malaria parasite. *Malar. J., 18*, 1-11. doi:<https://doi.org/10.1186/s12936-019-2926-4>

Ing, R., Gros, P., & Stevenson, M. M. (2005). Interleukin-15 enhances innate and adaptive immune responses to blood-stage malaria infection in mice. *Infect. Immun., 73*(5), 3172-3177. doi:<https://doi.org/10.1128/iai.73.5.3172-3177.2005>

Karel A. Schat, B. K. a. P. K. (2014). *Avian immunology*. Boston: Academic Press.

Koteja, P. (1996). Measuring energy metabolism with open-flow respirometric systems: which design to choose? *Funct. Ecol.*, 675-677. doi:<https://doi.org/10.2307/2390179>

Krams, I., Suraka, V., Rantala, M., Sepp, T., Mierauskas, P., Vrublevska, J., & Krama, T. (2013). Acute infection of avian malaria impairs concentration of haemoglobin and survival in juvenile altricial birds. *J. Zool., 291*(1), 34-41. doi:<https://doi.org/10.1111/jzo.12043>

LaPointe, D. A., Atkinson, C. T., & Samuel, M. D. (2012). Ecology and conservation biology of avian malaria. *Ann. N. Y. Acad. Sci., 1249*(1), 211-226. doi:<https://doi.org/10.1111/j.1749-6632.2011.06431.x>

Lessells, C. M., & Boag, P. T. (1987). Unrepeatable Repeatabilities: a common mistake. *The Auk, 104*(1), 116-121. doi:<https://doi.org/10.2307/4087240>

Li, M., Zhu, W., Wang, Y., Sun, Y., Li, J., Liu, X., . . . Li, D. (2019). Effects of capture and captivity on plasma corticosterone and metabolite levels in breeding Eurasian tree sparrows. *Avian Res., 10*, 16. doi:<https://doi.org/10.1186/s40657-019-0155-8>

Lighton, J., & Halsey, L. (2011). Flow-through respirometry applied to chamber systems: pros and cons, hints and tips. *Comp. Biochem. Physiol. Part A Mol. Integr. Physiol., 158*(3), 265-275. doi:<https://doi.org/10.1016/j.cbpa.2010.11.026>

Lochmiller, R. L., & Deerenberg, C. (2000). Trade‐offs in evolutionary immunology: just what is the cost of immunity? *Oikos, 88*(1), 87-98. doi:<https://doi.org/10.1034/j.1600-0706.2000.880110.x>

Martin, L. B., Kidd, L., Liebl, A. L., & Coon, C. A. (2011). Captivity induces hyper-inflammation in the house sparrow (*Passer domesticus*). *J. Exp. Biol., 214*(15), 2579-2585. doi:<https://doi.org/10.1242/jeb.057216>

Martin, L. B., Scheuerlein, A., & Wikelski, M. (2003). Immune activity elevates energy expenditure of house sparrows: a link between direct and indirect costs? *Proc. R. Soc. B: Biol. Sci., 270*(1511), 153-158. doi:<https://doi.org/10.1098/rspb.2002.2185>

Martínez-de la Puente, J., Santiago-Alarcon, D., Palinauskas, V., & Bensch, S. (2021). *Plasmodium relictum*. *Trends Parasitol., 37*(4), 355-356. doi:<https://doi.org/10.1016/j.pt.2020.06.004>

McNab, B. K. (1997). On the utility of uniformity in the definition of basal rate of metabolism. *Physiol. Zool., 70*(6), 718-720. doi:<https://doi.org/10.1086/515881>

Meister, S. L., Richard, O. K., Hoby, S., Gurtner, C., & Basso, W. U. (2021). Fatal avian malaria in captive Atlantic puffins *(Fratercula arctica*) in Switzerland. *Int. J. Parasitol. Parasites Wildl., 14*, 97-106. doi:<https://doi.org/10.1016/j.ijppaw.2020.12.007>

Melanson, E. L., Ingebrigtsen, J. P., Bergouignan, A., Ohkawara, K., Kohrt, W. M., & Lighton, J. R. (2010). A new approach for flow-through respirometry measurements in humans. *Am. J. Physiol. Regul., 298*(6), R1571-R1579. doi:<https://doi.org/10.1152/ajpregu.00055.2010>

Mukhin, A., Palinauskas, V., Platonova, E., Kobylkov, D., Vakoliuk, I., & Valkiūnas, G. (2016). The strategy to survive primary malaria infection: an experimental study on behavioural changes in parasitized birds. *PLoS One, 11*(7), e0159216. doi:<https://doi.org/10.1371/journal.pone.0159216>

Mundo, A. I., Tipton, J. R., & Muldoon, T. J. (2022). Generalized additive models to analyze nonlinear trends in biomedical longitudinal data using R: Beyond repeated measures ANOVA and linear mixed models. *Statistics in medicine, 41*(21), 4266-4283. doi:<https://doi.org/10.1002/sim.9505>

Nakagawa, S., & Schielzeth, H. (2010). Repeatability for Gaussian and non‐Gaussian data: a practical guide for biologists. *Biol. Rev., 85*(4), 935-956. doi:<https://doi.org/10.1111/j.1469-185X.2010.00141.x>

Newton, I. (2010). *The Migration Ecology of Birds*. Oxford: Academic Press.

Norris, K., & Evans, M. R. (2000). Ecological immunology: life history trade-offs and immune defense in birds. *Behav. Ecol., 11*(1), 19-26. doi:<https://doi.org/10.1093/beheco/11.1.19>

Owen-Ashley, N. T., & Wingfield, J. C. (2007). Acute phase responses of passerine birds: characterization and seasonal variation. *J. Ornithol., 148*, 583-591. doi:<https://doi.org/10.1007/s10336-007-0197-2>

Palinauskas, V., Valkiūnas, G., Bolshakov, C. V., & Bensch, S. (2008). *Plasmodium relictum* (lineage P-SGS1): effects on experimentally infected passerine birds. *Exp. Parasitol., 120*(4), 372-380. doi:<https://doi.org/10.1016/j.exppara.2008.09.001>

Palinauskas, V., Valkiūnas, G., Bolshakov, C. V., & Bensch, S. (2011). *Plasmodium relictum* (lineage SGS1) and *Plasmodium ashfordi* (lineage GRW2): the effects of the co-infection on experimentally infected passerine birds. *Exp. Parasitol., 127*(2), 527-533. doi:<https://doi.org/10.1016/j.exppara.2010.10.007>

Palinauskas, V., Žiegytė, R., Iezhova, T. A., Ilgūnas, M., Bernotienė, R., & Valkiūnas, G. (2016). Description, molecular characterisation, diagnostics and life cycle of *Plasmodium elongatum* (lineage pERIRUB01), the virulent avian malaria parasite. *Int. J. Parasitol., 46*(11), 697-707. doi:<https://doi.org/10.1016/j.ijpara.2016.05.005>

Palinauskas, V., Žiegytė, R., Šengaut, J., & Bernotienė, R. (2022). Experimental study on primary bird co-infection with two *Plasmodium relictum* lineages—pSGS1 and pGRW11. *Animals, 12*(15), 1879. doi:<https://doi.org/10.3390/ani12151879>

Paulman, A., & McAllister, M. M. (2005). *Plasmodium gallinaceum*: clinical progression, recovery, and resistance to disease in chickens infected via mosquito bite. *Am. J. Trop. Med., 73*(6), 1104-1107.

Paxton, K. L., Cassin-Sackett, L., Atkinson, C. T., Videvall, E., Campana, M. G., & Fleischer, R. C. (2023). Gene expression reveals immune response strategies of naïve Hawaiian honeycreepers experimentally infected with introduced avian malaria. *J. Hered., 114*(4), 326–340. doi:<https://doi.org/10.1093/jhered/esad017>

Pedersen E. J., M. D. L., Simpson G.L., Ross N. (2019). Hierarchical generalized additive models in ecology: an introduction with mgcv. *PeerJ, 7*, e6876. doi:<https://doi.org/10.7717/peerj.6876>

Ricklefs, R. E., Konarzewski, M., & Daan, S. (1996). The relationship between basal metabolic rate and daily energy expenditure in birds and mammals. *Am. Nat., 147*(6), 1047-1071. doi:<https://doi.org/10.1086/285892>

Robar, N., Murray, D. L., & Burness, G. (2011). Effects of parasites on host energy expenditure: the resting metabolic rate stalemate. *Can. J. Zool., 89*(11), 1146-1155. doi:<https://doi.org/10.1139/z11-084>

Rooyen, J. v., Lalubin, F., Glaizot, O., & Christe, P. (2013). Avian haemosporidian persistence and co-infection in great tits at the individual level. *Malar. J., 12*(1), 1-8. doi:<https://doi.org/10.1186/1475-2875-12-40>

Sambrook, J., Fritsch, E. F., Maniatis, T. (1989). *Molecular colning: A laboratory manual*. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press.

Sheldon, B. C., & Verhulst, S. (1996). Ecological immunology: costly parasite defences and trade-offs in evolutionary ecology. *Trends Ecol. Evol., 11*(8), 317-321. doi:<https://doi.org/10.1016/0169-5347(96)10039-2>

Shirihai, H., & Svensson, L. (2018). *Handbook of Western Palearctic Birds, Volume 1: Passerines: Larks to Warblers*. London, UK: Bloomsbury Publishing.

Simpson, G. L. (2023). R Package: gratia. Retrieved from <https://gavinsimpson.github.io/gratia/>

Sorci, G., & Faivre, B. (2009). Inflammation and oxidative stress in vertebrate host–parasite systems. *Philos. Trans. R. Soc. B: Biol. Sci., 364*(1513), 71-83. doi:<https://doi.org/10.1098/rstb.2008.0151>

Stager, M., Eddy, D. K., Cheviron, Z. A., & Carling, M. D. (2021). Haemosporidian infection does not alter aerobic performance in the pink-sided junco (*Junco hyemalis mearnsi*). *bioRxiv*. doi:<https://doi.org/10.1101/2021.09.20.460914>

Sun, N. W., Goodwin, S. E., Griego, M. S., Gerson, A. R., & Clotfelter, E. D. (2020). Does blood loss explain higher resting metabolic rates in nestling birds with hematophagous ectoparasites? *J. Avian Biol., 51*(2). doi:<https://doi.org/10.1111/jav.02264>

Thompson, L. J., Brown, M., & Downs, C. T. (2015). The effects of long-term captivity on the metabolic parameters of a small Afrotropical bird. *J. Comp. Physiol. B, 185*, 343-354. doi:<https://doi.org/10.1007/s00360-015-0888-6>

Valkiūnas, G. (2005). *Avian malaria parasites and other haemosporidia*. Boca Raton, USA: CRC press.

Valkiūnas, G., Ilgūnas, M., Bukauskaitė, D., Fragner, K., Weissenböck, H., Atkinson, C. T., & Iezhova, T. A. (2018). Characterization of *Plasmodium relictum*, a cosmopolitan agent of avian malaria. *Malar. J., 17*(1), 1-21. doi:<https://doi.org/10.1186/s12936-018-2325-2>

Valkiūnas, G., Zehtindjiev, P., Dimitrov, D., Križanauskienė, A., Iezhova, T. A., & Bensch, S. (2008). Polymerase chain reaction-based identification of *Plasmodium* (*Huffia*) *elongatum*, with remarks on species identity of haemosporidian lineages deposited in GenBank. *Parasitol. Res., 102*, 1185-1193. doi:<https://doi.org/10.1007/s00436-008-0892-9>

Van Riper III, C., Van Riper, S. G., Goff, M. L., & Laird, M. (1986). The epizootiology and ecological significance of malaria in Hawaiian land birds. *Ecol. Monogr., 56*(4), 327-344. doi:<https://doi.org/10.2307/1942550>

Videvall, E., Cornwallis, C. K., Ahrén, D., Palinauskas, V., Valkiūnas, G., & Hellgren, O. (2017). The transcriptome of the avian malaria parasite *Plasmodium ashfordi* displays host‐specific gene expression. *Mol. Ecol., 26*(11), 2939-2958.

Videvall, E., Cornwallis, C. K., Palinauskas, V., Valkiūnas, G., & Hellgren, O. (2015). The avian transcriptome response to malaria infection. *Mol. Biol. Evol., 32*(5), 1255-1267. doi:<https://doi.org/10.1093/molbev/msv016>

Videvall, E., Palinauskas, V., Valkiūnas, G., & Hellgren, O. (2020). Host transcriptional responses to high-and low-virulent avian malaria parasites. *Am. Nat., 195*(6), 1070-1084. doi:<https://doi.org/10.1086/708530>

Wilairatana, P., Mala, W., Milanez, G. D. J., Masangkay, F. R., Kotepui, K. U., & Kotepui, M. (2022). Increased interleukin-6 levels associated with malaria infection and disease severity: a systematic review and meta-analysis. *Sci. Rep., 12*(1), 5982. doi:<https://doi.org/10.1038/s41598-022-09848-9>

Williams, R. (2005). Avian malaria: clinical and chemical pathology of *Plasmodium gallinaceum* in the domesticated fowl *Gallus gallus*. *Avian Pathol., 34*(1), 29-47. doi:<https://doi.org/10.1080/03079450400025430>

Wood, S. N. (2017). *Generalized additive models: an introduction with R*. Boca Raton, USA: CRC press.

Wunderlich, C. M., Delić, D., Behnke, K., Meryk, A., Ströhle, P., Chaurasia, B., . . . Wunderlich, F. T. (2012). Cutting edge: Inhibition of IL-6 trans-signaling protects from malaria-induced lethality in mice. *J. Immunol., 188*(9), 4141-4144. doi:<https://doi.org/10.4049/jimmunol.1102137>

Zuk, M., & Stoehr, A. M. (2002). Immune defense and host life history. *Am. Nat., 160*(S4), S9-S22. doi:<https://doi.org/10.1086/342131>

Figure captions

Figure 1. Parasitemia (%) on different days post inoculation (DPI) of two Plasmodium species. Panel A represents the observed level of parasitemia (given in %) (dots) and predicted GAMM (lines, gray areas around the lines represent 95% CI). Panel B represents the difference between smoothers. Time periods when the difference between smoothers is significantly different from zero are marked by black rectangles.

Figure 2. RMR at different days post inoculation (DPI) in different birds’ groups. Panel A represents the observed RMR level (dots) and GAMM predictions (lines and 95% CI). Panel B represents the difference between smoothers. Time periods when the difference between smoothers is significantly different from zero are marked by black rectangles. The red shading reflects the level of parasitemia.

Figure 3. IL-6 at different days post inoculation (DPI) in different birds’ groups. Panel A represents the observed IL-6 concentration (dots) and GAMM predictions (lines and 95% CI). Panel B represents the difference between smoothers. Time periods when the difference between smoothers is significantly different from zero are marked by black rectangles. The red shading reflects the level of parasitemia.

Table 1. GAMM parameters characterizing the course of parasitemia after parasite inoculation.

| Parametric terms | | | | |
| --- | --- | --- | --- | --- |
| Term | Value | Std.Error | t | p |
| (Intercept) | 0.260 | 0.365 | 0.714 | 0.475 |
| Lineage (GRW2) | -0.221 | 0.564 | -0.391 | 0.695 |
| Smooth terms | | | |
| Term | edf | F | p |
| s(DPI): SGS1 | 6.939 | 234.997 | 0.000 |
| s(DPI): GRW2 | 6.286 | 119.558 | 0.000 |
| Random factor | 25.379 | 109.395 | 0.000 |

Table 2. GAMM parameters characterizing the course of RMR after parasite inoculation.

| Parametric terms | | | | |
| --- | --- | --- | --- | --- |
| Term | Value | Std.Error | t | p |
| (Intercept) | 0.867 | 0.108 | 8.000 | <0.001 |
| Lineage (SGS1) | -0.021 | 0.011 | -1.951 | 0.053 |
| Lineage (GRW2) | 0.007 | 0.011 | 0.635 | 0.526 |
| log10(Mass) | 0.446 | 0.097 | 4.581 | <0.001 |
| Smooth terms | | | |
| Term | edf | F | p |
| s(DPI): Control | 3.353 | 3.050 | 0.019 |
| s(DPI): SGS1 | 3.479 | 12.959 | <0.001 |
| s(DPI): GRW2 | 4.746 | 5.796 | <0.001 |
| Random factor | 32.231 | 2.134 | <0.001 |

Table 3. GAMM parameters characterizing the course of IL-6 concentration after parasite inoculation.

| Parametric terms | | | | |
| --- | --- | --- | --- | --- |
| Term | Value | Std.Error | t | p |
| (Intercept) | 1.102 | 0.018 | 61.611 | <0.001 |
| Lineage (SGS1) | 0.029 | 0.025 | 1.140 | 0.255 |
| Lineage (GRW2) | -0.081 | 0.026 | -3.118 | 0.002 |
| Smooth terms | | | |
| Term | edf | F | p |
| s(DPI): Control | 3.836 | 25.138 | <0.001 |
| s(DPI): SGS1 | 3.480 | 23.977 | <0.001 |
| s(DPI): GRW2 | 3.900 | 15.019 | <0.001 |
| Random factor | 25.264 | 0.929 | <0.001 |