Dear Drs. Dries Bonte and Silke Bauer

Editors of *Oikos*

We are submitting a **revised version** of manuscript **OIK-08199**, in which we have made changes in response to the comments received from the reviewer. We are grateful for the opportunity to revise and send you a new version of our manuscript.

Below we have pasted the reviewer’ comments, and inserted our RESPONSES after each comment, as well as indicated where in the text the relevant changes have been made.

We hope the manuscript is now acceptable for publication.

Sincerely,

Daniela de Angeli Dutra and co-authors

Reviewer: 1  
  
Summary: This study uses an impressive dataset to determine whether migratory bird species play roles in influencing the prevalence, diversity and geographical spread of avian haemosporidian parasites in South America. The overall topic of the study is relevant to the journal’s scope and the analyses are structured in a way that could give important insights.

We appreciate the reviewer’s positive comment regarding our manuscript.

However there are some issues that need to be addressed. The Abstract and Introduction are used to introduce far too many unlinked concepts and do not give the reader a sense of what the study is about, what it aims to achieve or why it is necessary. Please see below for specific comments.

We have partially addressed this issue and modified the introduction aiming to maintain as well modifications suggested by previous reviewers and editor Silke Bauer in our first submission to Oikos.

In addition, the transparency of the methods needs to be improved and some technical issues must be dealt with, such as inspection of model diagnostics and testing for residual autocorrelation.

We have performed most of reviewer’s suggestions. Besides, we annexed to the supplementary material a copy of our R scripts to increase methods transparency.  
  
Abstract: Is this study about the transmission or about the biogeography of parasites? These are very different aspects of disease ecology / epidemiology, yet both are introduced here. As below, some refinement of the study’s primary aims and objectives will be necessary before editing the text to remove irrelevant background information.

Our objective in this study was to evaluate the potential impact of migrants in parasite transmission to new areas and the impact of this transmission to the bird communities whom migrant birds are a part of during their migration route. We have added a phrase in the abstract to introduce better our ideas L6-7.   
   
Lines 27 – 51: I find this passage to be very jumbled and difficult to follow. There seem to be many different ideas being introduced here but they are not cohesive nor are they supported well. Impacts of migration and/or introduction of species on transmission, evolution, prevalence, host richness, host diversity, biogeography and disease ecology, as well as the potential use of parasites as geographical markers, are all introduced very briefly. The result is that none of these ideas is developed with adequate support from the literature and the reader has no real sense of what this study is really about or aims to achieve. I suggest some major edits of this text so that the background that is most relevant to the present study is fully introduced and developed using strong support from the literature. The hypothesis-driven predictions that are listed at the end of the Intro are good and should be used to guide the structure of the introductory text.

We understand and agree with reviewer’s point and this passage have been restructured.  
  
Line 51: Most readers of this generalist journal will not know what avian haemosporidian parasites are, how they are transmitted or why they are useful models for testing predictions from disease ecology hypotheses. Please take a few lines to properly introduce the study system, with adequate reference to the literature.

We understand the reviewer’s concern and added a short explanation about avian haemoporidians parasites. L5X-5Y

Line 76: This section would be better focused on why it is important to understand the impacts of migratory species on the geographical spread of these parasites in the chosen study system. The authors have not invested much space in this Introduction on explaining why this research is needed or how its findings can be used.

A phrase was added to make more explicit the importance of this study. L8X-8Y  
  
Line 88: This second prediction seems plausible but the authors have already introduced another concept that contrasts with this prediction: that migrants can move away from high prevalence areas and so regions with more migratory routes should have lower prevalence. Please consider using more balance based on the literature when stating these predictions.

We understand the reviewer’s concern and acknowledge we presented both concepts in our manuscript. However, in our previous review it was suggested by the editor to present the mechanism by which migration can have a protective effect in our introduction and we agree it is important to highlight both possibilities in our paper.

Line 93: Wouldn’t some resident birds occupy very large geographical ranges as well, potentially leading to large ranges for resident-only parasites in some cases? And wouldn’t some migrants only migrate over small distances rather than large distances?

We appreciate this comment. However, we do not agree with the reviewer’s point since migrants can enhance a pathogen geographical range due to its ability to transport biomass and associated organisms (such as parasites) through their migratory route, what do not occur for parasites present only in resident species.   
  
Line 128: There has been no introduction on effects of spatial or phylogenetic autocorrelation on parasite prevalence or richness. Please add some relevant background introduction material so that readers are more familiar with how these mechanisms can influence inferences

We appreciate this suggestion and added a few lines in the introduction (L5X to 5Y) to address this issue.

Line 133: It is unclear whether inclusion of random site effects would adequately control for spatial clustering. Given the large number of specific sites, with some being quite close to one another, it seems like a more appropriate spatial autocorrelation term might be needed to ensure more precise parameter estimates. Please run a Moran’s I on the residuals of the model to more adequately quantify the amount of residual spatial variation left. If this number is still substantial, the authors will need to use more appropriate spatial effects (such as a Markov Random Field).

Residual Moran’s I values were calculated as well for the last two models, which we could account for geographical coordinates in the data. We obtained no significant value.  
  
Model descriptions: The sections that describe the models would benefit greatly from mathematical equations to formally illustrate the models. This would help to identify which parameters were being estimated and would allow the authors to give a more complete description of the prior distributions that were used for each parameter. For example in line 168 the authors state: “we applied the Gamma distribution family” but it is not clear for which parameter this distribution was used as a prior.

We understand the reviewer’s concern and decided to provide a copy of our R scripts in the supplementary material. In addition, we have also added more information regarding the models through the methods section.   
  
Line 159: It is understandable to try and use a higher resolution when classifying lineages based on the types of hosts they infect, but the incredibly low sample sizes for some of these categories (as shown in Supp Figures) suggests that the categories are not that meaningful for inference.

We thank the reviewer for this comment and decided to remove these results due to the low number of lineages in some variables. We agree with the reviewer’s point of view and recognize some categories might not be meaningful for inference.  
  
Line 195: The negative binomial is a discrete probability distribution, which models counts. It seems fine to model prevalence using this distribution, but only if the total number of sampled birds was used as an offset. There is no description of this offset, so please include one and ensure you correctly state what prior was used for the overdispersion parameter.

We agree with the reviewer and indeed we used the total number of birds as offset. We added this information in the manuscript (L18X).  
  
Line 208: Why was this model not also run using Bayesian inference? It seems strange to mix Bayesian and frequentist methods throughout the study, and means that parameter inferences have slightly different meanings.

We modified our analyses and now all three models are performed using Bayesian analyses.   
  
Results: Some more scrutiny of the models is needed to describe whether adequate mixing and convergence was achieved and whether the models gave reasonable representations of the underlying data generating processes. For example, it could be useful to generate posterior simulations for the datapoints that were used to generate Supplementary Figure 1 and then add these to the figure, just to visualize whether the model comes anywhere close to depicting patterns seen in the observed data. This sort of scrutiny is necessary to determine whether the parameter estimates from the models have any real utility.

We have checked all models for chain convergence and have added that information to the paper in the method and result sections(LXXX and LXXX). In all our models, chains were well converged. Our results were generated using the model’s posterior simulations by using the function “conditional\_effects” from “brms” package. This function allow us to visualize our results based on simulations obtained from our models, therefore, it doesn’t reflect our raw dataset.   
  
Line 277: Doesn’t this result only apply for Plasmodium parasites and not for the entire dataset?

As demonstrated in our result section, the present result is true when analysning both haemosporidian genera together. Therefore, we refer to both genera (*Plasmodium* and *Haemoproteus*). We modified the text to make it clearer (L28X).

We thank the reviewer for all his comments on our manuscript.