




Peer Community In Infections

A four-year study reveals the potential role of the soft tick *Ornithodoros maritimus* in the transmission and circulation of *Babesia* sp. YLG in Yellow-legged gull colonies.

Thomas Pollet based on peer reviews by **Hélène Jourdan-Pineau**  and **Tahar Kernif**

Claire Bonsergent, Marion Vittecoq, Carole Leray, Maggy Jouglin, Marie Buysse, Karen D. McCoy, Laurence Malandrin (2023) A soft tick vector of *Babesia* sp. YLG in Yellow-legged gull (*Larus michahellis*) nests. bioRxiv, ver. 3, peer-reviewed and recommended by Peer Community in Infections. <https://doi.org/10.1101/2023.03.24.534071>

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Worldwide, ticks and tick-borne diseases are a persistent example of problems at the One Health interface between humans, wildlife, and environment (1, 2). The management and prevention of ticks and tick-borne diseases require a better understanding of host, tick and pathogen interactions and thus get a better view of the tick-borne pathosystems.

In this study (3), the tick-borne pathosystem included three component species: first a seabird host, the Yellow-legged gull (YLG - *Larus michahellis*, Laridae), second a soft nidicolous tick (*Ornithodoros maritimus*, Argasidae, syn. *Alectorobius maritimus*) known to infest this host and third a blood parasite (*Babesia* sp. YLG, Piroplasmidae). In this pathosystem, authors investigated the role of the soft tick, *Ornithodoros maritimus*, as a potential vector of *Babesia* sp. YLG. They analyzed the transmission of *Babesia* sp. YLG by collecting different tick life stages from YLG nests during 4 consecutive years on the islet of Carteau (Gulf of Fos, Camargue, France). Ticks were dissected and organs were analyzed separately to detect the presence of *Babesia* sp DNA and to evaluate different transmission pathways.

While the authors detected *Babesia sp.* YLG DNA in the salivary glands of nymphs, females and males, this result reveals a strong suspicion of transmission of the parasite by the soft tick. *Babesia sp.* YLG DNA was also found in tick ovaries, which could indicate possible transovarial transmission. Finally, the authors detected *Babesia sp.* YLG DNA in several male testes and in endospermatophores, and notably in a parasite-free female (uninfected ovaries and salivary glands). These last results raise the interesting possibility of sexual transmission from infected males to uninfected females.

As pointed out by both reviewers, this is a nice study, well written and easy to read. All the results are new and allow to better understand the role of the soft tick, *Ornithodoros maritimus*, as a potential vector of *Babesia sp.* YLG. They finally question about the degree to which the parasite can be maintained locally by ticks and the epidemiological consequences of infection for both *O. maritimus* and its avian host. For all these reasons, I chose to recommend this article for Peer Community In Infections.

References:

- Dantas-Torres et al (2012). Ticks and tick-borne diseases: a One Health perspective. *Trends Parasitol.* 28:437. <https://doi.org/10.1016/j.pt.2012.07.003>
- Johnson N et al (2022). One Health Approach to Tick and Tick-Borne Disease Surveillance in the United Kingdom. *Int J Environ Res Public Health.* 19:5833. <https://doi.org/10.3390/ijerph19105833>
- Bonsergent C, Vittecoq M, Leray C, Jouglin M, Buysse M, McCoy KD, Malandrin L. A soft tick vector of *Babesia sp.* YLG in Yellow-legged gull (*Larus michahellis*) nests. bioRxiv, 2023.03.24.534071, ver. 3 peer-reviewed and recommended by Peer Community in Infections. <https://doi.org/10.1101/2023.03.24.534071>

Reviews

Evaluation round #1

DOI or URL of the preprint: <https://doi.org/10.1101/2023.03.24.534071>

Version of the preprint: 1

Authors' reply, 07 July 2023

Dear Peer Community,

We are pleased to bring to your attention the revision of the manuscript entitled « A soft tick vector of *Babesia sp.* YLG in Yellow-legged gull (*Larus michahellis*) nests ».

We propose to modify the title to replace *Ornithodoros maritimus* by soft tick not only to make the title more generalist but mainly because the name of this tick genus is being subjected to changes.

We've addressed all the remarks and comments pointed by the reviewers, especially we added statistical analysis. We now submit both a revised version of our manuscript (we posted the final version on bioarxiv) and a response letter to each reviewer.

We wish to thank both reviewers for their time and valuable input to this manuscript.

We hope that our article is now ready to be recommended.

Yours sincerely,

On behalf of co-authors,

Claire Bonsergent

[Download tracked changes file](#)

Decision by **Thomas Pollet**, posted 13 June 2023, validated 13 June 2023

Dear authors,

Thank you for submitting your preprint in PCI Infections. Your manuscript has been evaluated by two reviewers. Both highlighted the relevance of the questions addressed and the good quality of your study and results. However, before being recommended in PCI Infections, you should consider several remarks and comments pointed out by the reviewers.

Please address these points and submit both a revised version of your manuscript and a response letter. I look forward to receiving your revised manuscript.

Yours sincerely

Thomas Pollet

Reviewed by **Hélène Jourdan-Pineau** , 22 May 2023

Please find attached my review for this manuscript.

[Download the review](#)

Reviewed by **Tahar Kernif**, 06 June 2023

Title: *Ornithodoros maritimus* as a vector of *Babesia* sp. YLG in Yellow-legged gull (*Larus michahellis*) nests

Comments of Reviewer :

The present manuscript reports an interesting study conducted on *Ornithodoros maritimus* isolated from the Yellow-legged gull in order to estimate the epidemiological action and the propagation of *Babesia* sp. which is considered as the unique blood parasite species previously detected in gull chicks in the colony.

it is really a very complete study because several parameters concerning the infection of ticks by this endoparasite (*Babesia* sp.) were studied, including dissection of fresh ticks to isolate different organs and test for the presence of the parasite using molecular assays. The main results raise the interesting possibility of sexual transmission of *Babesia* sp. from infected males to uninfected females and also the transovarial transmission of the parasite.

The paper is very well written, however certain technical details are needed to make the work more rewarding in terms of data.

Line 100. In the study location section, it would be interesting to add the climatographic conditions of the study area

Line 128-177. the presentation of this part needs to be completely reviewed

- Line 129. In the molecular study section, replace 18S r RNA by 18S r DNA
- Line 131; 134; 146; 158; 171. put all primers in a table not in supplementary Material.
- Line 133. I think it is better to detail the composition of the 30 µL PCR reaction mix and nested PCR cycling than to refer to a reference, especially since this is the first part of the molecular detection and characterization of piroplasms.
- Line 140. Controls !!! a title to change or remove

- Line 141-144. the purpose of this alignment is unclear
- Line 142. The access number "OP542291" doesn't match with *O. maritimus*! <https://www.ncbi.nlm.nih.gov/nuccore/OP542291>
- Line 145. why an 18S rRNA gene for the molecular identification of *O. maritimus* not 16S or 12S mitochondrial gens?

Line 181. In Ticks collections results I don't understand the meaning of (Bonsergent, 2023)

Line 193. it is always necessary to support the results with statistical tests to estimate the significance of the data obtained. even more, do not forget to cite figures and tables in the text

Line 198. proceed with the same way 'percentage and ratio with positive ticks coming from

Line 232. The study of variability of the *cox1* gene lacks precision concerning the haplotyping method used (manual, or with bioinformatics tools such as DnaSP)

Table 1. What does the ? mean? as well as the Y's and the R's

The best way to present haplotyping result would be the phylogenetic construction which allows to visualize the clusters relating to each haplotype

It would be also interesting to specify Haplotype (gene) diversity (Hd), Nucleotide diversity (Pi) and Estimate the Evolutionary Divergence between Sequences