

Keywords

Hard ticks, *Midichloria*,
Hyalomma marginatum,
Migratory birds.

CORRESPONDING AUTHOR**Valentina Serra**

valentina.serra@unimi.it

JOURNAL HOME PAGEriviste.unimi.it/index.php/haf

UNIVERSITÀ DEGLI STUDI DI MILANO
DIPARTIMENTO DI SCIENZE VETERINARIE
PER LA SALUTE, LA PRODUZIONE ANIMALE
E LA SICUREZZA ALIMENTARE



Detection of a novel bacterium of the genus *Midichloria* (family *Midichloriaceae*) in avian-borne *Hyalomma marginatum* ticks and their trans-Saharan migratory hosts.

V. Serra^{1,*}, C. Bazzocchi¹, I. Di Lecce²

¹ Department of Veterinary Medicine, University of Milan, Via Celoria 10, 20133 Milan, Italy.

² Wild Urban Evolution and Ecology Lab, Centre of New Technologies, University of Warsaw, Banacha 2C, 02-097 Warsaw, Poland.

Ticks are haematophagous ectoparasites of vertebrates habitually parasitizing avian species, which may contribute to tick dispersal across continents during migrations (Hasle 2013; Altizer et al., 2011). *Midichloria* bacteria can be transmitted to the vertebrate host during the tick bite (Bazzocchi et al., 2013; Serra et al., 2018). Although many avian species are common hosts of ticks harbouring *Midichloria* (e.g. *Ixodes*, *Hyalomma*), the circulation of this bacterium in birds has never been investigated. The aims of this study are: 1) evaluate the presence of *Midichloria* DNA in *H. marginatum* ticks and blood collected from trans-Saharan migratory birds; 2) quantify *Midichloria* bacteria in ticks through a novel quantitative PCR (qPCR).

A total of 256 *H. marginatum* ticks and 97 blood samples were collected from three different migratory species (*Phoenicurus phoenicurus*, *Saxicola rubetra* and *Sylvia communis*) on Ventotene Island (Central Italy) and DNAs were extracted. A nested-PCR targeting the 16S rRNA gene of *Midichloria* was used to detect bacterial presence. Subsequently, primers targeting the *gyrB* gene of *Midichloria* and the *cal* gene of *H. marginatum* were designed and used in a qPCR for *Midichloria* quantification. Results were expressed as *gyrB/cal* copy numbers ratio.

94% of *Hyalomma* ticks harbored DNA of *Midichloria* belonging to the monophylum associated with ticks, while the bacterial DNA was detected in 44.3% of blood samples. Furthermore, engorged ticks showed significantly higher bacteria load than unengorged ticks (Table 1; Wilcoxon sum-rank test: $z=3.14$; $p=0.0017$), similarly to what has been observed for *M. mitochondrii* in *I. ricinus* ticks.

This work provides evidence for the presence of circulating *Midichloria* DNA in long-distance migratory birds, suggesting an enhanced worldwide spread of these bacteria across haematophagous ectoparasite populations. Future studies are necessary to increase the knowledge of *Midichloria* role in the biology of this tick species.

Table 1: Range values of *gyrB* and *cal* copy numbers and of *gyrB/cal* ratios obtained in *H. marginatum* ticks through qPCR analysis.

	<i>gyrB</i> copy number range	<i>cal</i> copy number range	<i>gyrB/cal</i> range
Unengorged ticks	$6.8 \times 10^2 - 1.5 \times 10^5$	$7.2 \times 10 - 5.8 \times 10^3$	$7.7 - 5.2 \times 10^2$
Engorged ticks	$2.2 \times 10^2 - 1.8 \times 10^5$	$6.6 \times 10 - 6.2 \times 10^2$	$1.5 \times 10 - 8.2 \times 10^3$

References

- Altizer, S., Bartel, R., Han BA., 2011. Animal migration and infectious disease risk. *Science*. 331, 296-302.
- Bazzocchi, C., Mariconti, M., Sassera, D., Rinaldi, L., Martin, E., Cringoli, G., Urbanelli, S., Genchi, C., Bandi, C., Epis, S., 2013. Molecular and serological evidence for the circulation of the tick symbiont *Midichloria* (Rickettsiales: Midichloriaceae) in different mammalian species. *Parasites & Vectors*. 6, 350-56.
- Hasle, G., 2013. Transport of ixodid ticks and tick-borne pathogens by migratory birds. *Frontiers in Cellular and Infection Microbiology*. 3, 1-6.
- Serra, V., Cafiso, A., Formenti, N., Verheyden, H., Plantard, O., Bazzocchi, C., Sassera, D., 2018. Molecular and Serological Evidence of the Presence of *Midichloria* mitochondrii in Roe Deer (*Capreolus capreolus*) in France. *Journal of Wildlife Diseases*. doi: 10.7589/2017-09-241.