



## Article

### ***Haemoproteus nucleocondensus* n. sp. (Haemosporida, Haemoproteidae) from a Eurasian songbird, the Great Reed Warbler *Acrocephalus arundinaceus***

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#### Abstract

*Haemoproteus* (*Parahaemoproteus*) *nucleocondensus* n. sp. (Haemosporida, Haemoproteidae) is described from a Eurasian songbird, the Great Reed Warbler *Acrocephalus arundinaceus* based on the morphology of its blood stages and partial sequences of the mitochondrial cytochrome *b* gene. Transmission of this haemoproteid occurs in Africa, where the Great Reed Warblers are infected. Due to unclear reasons, its transmission does not occur at European breeding grounds of this bird, resulting in absence of the parasites in juvenile birds before and during seasonal migration. *Haemoproteus nucleocondensus* can be readily distinguished from other avian haemoproteids by tiny, compact microgametocyte nuclei that are significantly smaller than macrogametocyte nuclei, a rare character of haemosporidian parasites. By this morphological feature, the new species is similar to *Haemoproteus payevskyi*, *Haemoproteus micronuclearis*, and *Haemoproteus nucleofascialis*. *Haemoproteus nucleocondensus* can be readily distinguished from both *H. payevskyi* and *H. micronuclearis*, primarily due to its numerous growing gametocytes (size greater than erythrocyte nuclei), which do not touch the envelope of erythrocytes along their entire margin; such gametocytes do not develop in *Haemoproteus payevskyi* and *H. micronuclearis*, but present in *H. nucleofascialis*. However, microgametocyte nuclei are band-like in shape in the latter parasite; that is not a case in *H. nucleocondensus*. Illustrations of blood stages of the new species are given, and morphological and phylogenetic analyses identify the DNA lineages that are associated with these parasites. Genetic distance between *cyt b* gene sequences of the new species and *H. payevskyi*, *H. micronuclearis*, and *H. nucleofascialis* is 4.4%, 5.9%, and 8.1%, respectively. Cytochrome *b* gene sequences (GenBank no. JX026901) can be used for bar-coding in studies of *H. nucleocondensus*.

**Key words:** avian haemosporidians, *Haemoproteus*, new species, *Acrocephalus arundinaceus*, microscopy, PCR, barcoding

#### Introduction

Haemoproteids (Haemosporida: Haemoproteidae) are widespread in birds all over the world and are transmitted by blood-sucking dipteran insects belonging to the Ceratopogonidae and Hippoboscidae (Greiner *et al.* 1975; McClure *et al.* 1978; Atkinson & van Riper, 1991; Bishop & Bennett, 1992). Over 140 species of avian *Haemoproteus* have been described mainly based on the morphological features of their blood stages and the limited information about vertebrate host specificity (Bishop & Bennett, 1992; Valkiūnas, 2005; Iezhova *et al.* 2011). Characterization of the diversity and distribution of avian haemoproteids is important to better understand the challenges facing wildlife health because some species of these parasites cause pathology in birds (Miltgen *et al.* 1981; Atkinson *et al.* 1988; Cardona *et al.* 2002), are sometimes lethal (Ferrell *et al.* 2007; Olias *et al.* 2011), and can affect host fitness (Nordling *et al.* 1998; Marzal *et al.* 2005; Valkiūnas, 2005; Møller & Nielsen, 2007). Heavy haemoproteid infections are also pathogenic to and may kill biting midges (Valkiūnas & Iezhova, 2004) although this phenomenon has not been sufficiently investigated.