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Molecular characterization of *Haemoproteus sacharovi* (Haemosporida, Haemoproteidae), a common parasite of columbiform birds, with remarks on classification of haemoproteids of doves and pigeons

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Abstract

Haemoproteus (Haemosporida, Haemoproteidae) is the largest genus of avian haemosporidian parasites, some species of which cause lethal diseases in birds. Subgenera *Parahaemoproteus* and *Haemoproteus* are usually accepted in this genus; these parasites are transmitted by biting midges (Ceratopogonidae) and hippoboscids (Hippoboscidae), respectively. As of yet, species of *Parahaemoproteus* have not been reported to infect doves and pigeons (Columbiformes), parasites of these birds have not been reported to be transmitted by biting midges (Ceratopogonidae). Applying microscopy and PCR based methods, we identified mitochondrial cytochrome *b* (*cyt b*) sequences of *Haemoproteus sacharovi*, a widespread parasite of doves and pigeons. Phylogenetic relationships of dove haemoproteids, which traditionally have been classified in the subgenus *Haemoproteus*, showed that *H. sacharovi* and *H. turtur*, common parasites of doves, branch in the clade with *Parahaemoproteus* species, indicating that these haemoproteids may belong to this subgenus and are likely transmitted by biting midges. This study provides barcodes for *H. sacharovi*, clarifies the taxonomic positions of *H. sacharovi* and *H. turtur*, and indicates directions for development of classification of avian haemoproteid species. Our analysis shows that the current subgeneric classification of avian haemoproteids is generally effective, but the position of some species may need to be revised.

Key words: *Haemoproteus*, *Parahaemoproteus*, haemosporidians, Columbidae, Hippoboscidae, Ceratopogonidae, barcoding

Introduction

Avian haemosporidians (Protista, Haemosporida) are a phylogenetically distinct and evolutionarily successful group of heteroxenous protists exclusively transmitted by blood-sucking dipterans (Levine, 1988). These protists parasitize many birds throughout the world (Greiner *et al.* 1975; McClure *et al.* 1978; Bishop & Bennett, 1992; Valkiūnas 2005) and have been the subject of extensive research for over 120 years. In some bird populations, between 50–100% of the individuals are infected with these blood parasites (Valkiūnas *et al.* 2003; Fernandez *et al.* 2010; Belo *et al.* 2011). Lethal cases of haemosporidian infections occur both in domestic and wild birds (Garnham 1966; Ferrell *et al.* 2007; Atkinson & LaPointe 2009) emphasizing the importance of the extended investigations of these parasites, particularly in light of emerging highly virulent haemoproteosis recently documented among captive parrots in Europe (Olias *et al.* 2011).

According to current taxonomy (Valkiūnas 2005), *Haemoproteus* is the largest genus of avian haemosporidian parasites; over 140 morphologically distinct parasites have been described and are categorized into subgenera *Haemoproteus* and *Parahaemoproteus*. Species of these subgenera are transmitted by hippoboscids