



***Picobia dziabaszewskii* sp. nov. (Acari, Syringophilidae)—combined description (morphology with DNA barcode data) of a new quill mite species parasitizing *Garrulax formosus* (Passeriformes: Leiothrichidae)**

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Abstract

A new species of quill mites *Picobia dziabaszewskii* sp. nov. (Acari, Syringophilidae) parasitizing *Garrulax formosus* (Verreaux) (Passeriformes: Leiothrichidae) is described using combined data sources: standard morphological information extended by mitochondrial cytochrome oxidase I sequence (COI) and domene D2 of the nuclear gene 28S rDNA data (DNA barcode). Additionally, the case of polymorphism within domene D2 region of 28 rDNA is registered for the first time in syringophilid mites.

Key words: quill mites, *Picobia*, ectoparasites, *Garrulax formosus*, DNA barcoding, systematics

Introduction

Mites of the family Syringophilidae (Acari, Prostigmata, Cheyletoidea) are permanent parasites inhabiting the quills of feathers in many groups of birds. Up to now, quill mites have been represented by 269 species grouped in 53 genera (Skoracki, pers. comm). Traditionally, the family is divided into two subfamilies: Syringophilinae Lavoipierre and Picobiinae Johnston and Kethley (including *Picobia* Haller), however, recently the two-subfamilial structure of syringophilids has been questioned by phylogenetic reconstructions based on DNA sequences (Głowska *et al.* unpublished data). There are 22 known species of the genus *Picobia*, associated with 14 host families belonging to three bird orders: Passeriformes (12), Piciformes (1) and Coraciiformes (1) (Skoracki 2011). Although syringophilids have been studied intensively for several years in the regard of taxonomy, all descriptions made so far, have been rested solely on external morphology. Since the DNA barcoding system, based mainly on COI (cytochrome oxidase I DNA sequences) and D1-D2 region of nuclear gene 28S rDNA was proposed as a standard tool for effective determination of most metazoan species (Hebert *et al.* 2003, Sonnenberg *et al.* 2007) and the procedure of nondestructive DNA isolation (leaving the undamaged mites exoskeleton for comparative morphological analysis) was described (Dabert *et al.* 2008), it seems reasonable to extend the previous descriptive norms in this group of mites by information concerning the DNA barcode. Applying this approach in the basic taxonomic studies might be a good starting point for further more detailed studies on this field, e.g. detection of cryptic species (Skoracka 2009) or verification of species status among mites from different habitats and having different life cycles (Martin *et al.* 2010).

In this paper we present a taxonomic description of a new species combining the standard morphological analysis with the DNA barcode data. The new quill mite species *Picobia dziabaszewskii* sp. nov. parasitizes the Red-winged Laughingthrush *Garrulax formosus* (Verreaux) (Passeriformes: Leiothrichidae), that is a first record of *Picobia* from hosts of this family. Additionally, we register the case of intragenomic substantial differentiation (polymorphism) within domene D2 of the nuclear gene 28S rDNA in syringophilids for the first time.