

Integrative taxonomy and phylogeny of the damselfly genus *Forcepsioneura* Lencioni, 1999 (Odonata: Coenagrionidae: Protoneurinae) with description of two new species from the Brazilian Atlantic Forest

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Abstract. *Forcepsioneura* Lencioni, 1999 is a small genus of eight forest-dependent damselfly species endemic to the Brazilian Atlantic Forest domain. Some of its species are difficult to identify due to their strong morphological similarities. Thus, the use of DNA sequences for taxonomic purposes is warranted. This study examined the diversity among mitochondrial COI and 16S and nuclear PRMT markers in *Forcepsioneura*, identified discrete evolutionary units based on morphological and molecular characters, and described two new species using an integrative approach to propose species-level hypotheses. The first molecular phylogeny of *Forcepsioneura* species, including seven of the 10 valid species, is presented. *Forcepsioneura gabriela* sp.n. and *Forcepsioneura janeae* sp.n. are described and illustrated based on males. *Forcepsioneura gabriela* sp.n. is closely related to *F. garrisoni* Lencioni, 1999 and *F. regua* Pinto & Kompier, 2018 and was included in the light blue group, but was recovered with high K2P COI divergence values relative to *F. garrisoni*. PRMT and ribosomal 16S rDNA sequences were too conservative to distinguish this new species from others of the light blue group. Nevertheless, *F. gabriela* sp.n. can be distinguished from other *Forcepsioneura* by its coloration and shape and length of the ventrobasal process of cercus and MP vein. On the other hand, we were unable to get COI sequences for *F. janeae* sp.n., but morphological diagnostic characters, such as, coloration and shape of the posterior lobe of the prothorax and ventrobasal process of cercus supported its proposal as a new species. A concatenated Bayesian analysis of all markers supported the monophyly of both *Forcepsioneura* and the light blue group of species. This study affirmed the value of COI sequence variation for species-level studies but did not support the use of PRMT and 16S for this group of damselflies, as there was very little interspecific variation between some closely related species.

Key words. DNA-barcoding, dragonfly, molecular phylogeny, Protoneuridae, Zygoptera.

1. Introduction

Recent studies on Odonata phylogeny based on morphological and molecular characters have resulted in a comprehensive family-level phylogenetic hypothesis for the suborder Zygoptera (damselflies) (DIJKSTRA et al. 2014) and suggested Protoneuridae as a polyphyletic group (BYBEE et al. 2008; CARLE et al. 2008; PESSACQ 2008; DIJKSTRA et al. 2014). These studies, however, recognize all protoneurid species occurring in the New World, including the type-genus *Protoneura* Selys, 1857, as a

monophyletic group. This group is currently treated as a subfamily of Coenagrionidae, with Protoneurinae damselflies comprising 123 species distributed in 15 genera (GARRISON & VON ELLENRIEDER 2016).

Forcepsioneura Lencioni, 1999 is a small genus of forest-dependent damselflies endemic to the Brazilian Atlantic Forest domain, except for *F. sancta* (Hagen in Selys, 1860), also recorded from the Cerrado of the Central Brazilian plateau. Species in the genus occur in