



<http://dx.doi.org/10.11646/zootaxa.3630.2.8>

<http://zoobank.org/urn:lsid:zoobank.org:pub:CADA4E33-70E5-4268-ADAC-790FB7065A48>

Phylogenetics of the tribe Phalacroscylini (Siphonaptera: Ctenophthalmidae: Neopscyllinae) based on molecular and morphological evidence

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Abstract

Six genera of the tribe Phalacroscylini were analysed based on molecular (18S rDNA and 28S rDNA) and morphological characters, using maximum parsimony analyses and Bayesian inference. The results support the paraphyly of the tribe Phalacroscylini, as shown in a previous study based only on molecular characters. Three main clades were identified: one includes the genera *Neopscylla*, *Epitedia*, *Catallagia*, and *Delotelis*; another includes *Phalacroscylla* and *Strepsylla*; and a third one includes only *Meringis*. In order to propose a phylogenetic classification we recognize three tribes, transferring *Epitedia*, *Catallagia* and *Delotelis* to Neopscyllini; keeping Phalacroscylini only for *Phalacroscylla* and *Strepsylla*; and proposing the new tribe Meringini for *Meringis*.

Key word: Fleas, Holarctic, *Neopscylla*, Neopscyllini, Phalacroscylini, phylogenetic relationships

Introduction

More than 3,000 publications related to fleas (Siphonaptera) have been published (Lewis & Lewis 1985), consisting mostly of species level studies or dealing with the medical implications of fleas to humans and domestic animals. From a phylogenetic point of view there are many gaps in the knowledge about fleas, and some authors have suggested that the reconstruction of their phylogenetic history is difficult because of their highly specialized morphological adaptations associated with their ectoparasitic habits, which promote character convergence and make it difficult to postulate homologies (Whiting 2002; Medvedev 2006a). Most of the characters used for diagnoses of fleas are selected from their extraordinarily complex genitalia, or the presence and distribution of stout spines (Whiting *et al.* 2008).

The monophyly of the order Siphonaptera is well supported (Whiting 2002; Whiting *et al.* 2008) and most flea genera and many tribes represent natural groups; however, there are many cases where the assignment of a flea genus to a particular family is uncertain, with some families (e.g., Ctenophthalmidae) almost certainly constituting paraphyletic assemblages of a wide array of genera (Whiting *et al.* 2008; Medvedev 2010). There are only a few studies dealing with higher phylogenetic relationships. Hopkins and Rothschild (1953) presented an intuitive evolutionary hypothesis for the families based on Karl Jordan's extensive work. Smit (1982) formulated a phylogenetic hypothesis, where he recognized five superfamilies, although the relationships within each group were completely unresolved. Medvedev (1994, 1998) presented the most comprehensive attempt to reconstruct Siphonapteran phylogeny based on morphological evidence, distinguishing four infraorders. Whiting *et al.* (2008) provided the first formal cladistic analysis of Siphonaptera, based on molecular evidence, finding that Hystrichopsyllidae and Ctenophthalmidae are paraphyletic. There are some phylogenetic analyses at lower taxonomic levels, namely Pulicoidea (Cheetham 1988), Rhopalopsyllidae (Linardi & Guimaraes 1993), *Ctenophthalmus* (Morrone *et al.* 2000), *Neopscylla* and *Geusibia* (Lu and Wu 2003, 2005), *Hystrichopsylla* (Acosta and Morrone 2005), *Hectopsylla* (Blank *et al.*, 2007), *Nycteridiopsylla* (Hastriter *et al.*, 2009), and *Strepsylla* (Acosta 2010).