



Congruent co-evolution of the feather mite genus *Trouessartia* (Acariformes: Trouessartiidae) and endemic Malagasy warblers (Passeriformes: Bernieridae)*

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The feather mite genus *Trouessartia* (Analgoidea: Trouessartiidae), with 145 known species, is the second most species-rich genus of feather mites. Species of *Trouessartia* are mostly associated with passerines (oscines and suboscines), with a few associations with woodpeckers. On hosts, the mites inhabit flight feathers, most commonly occurring on the secondaries and rectrices.

Here, we report *Trouessartia* feather mites on Malagasy warblers (Sylvoidea: Bernieridae), reconstruct their phylogenetic relationships and analyze their host associations. Bernieridae is a small, endemic passerine family from Madagascar with 12 species in 8 genera. Mites were collected from live birds using the powder dusting method. Using morphological and DNA sequence data (COX1), we analyzed mites from 8 species (7 genera) of Malagasy warblers and identified 9 mite species. A maximum likelihood tree was inferred in IQ-TREE v1.6.12 and genetic K2P distances (Kimura 2-parameter) were calculated in PAUP v4.0a.

All recognized species were new to science and formed a monophyletic clade, the *bernieriae* species group. This group is characterized by the fusion of epimerites I (a rare character state in *Trouessartia*) and the well-developed hysteronotal sclerotized rings. Based on the shape of the idiosoma, mites were grouped in the “wide” (six species) and “narrow” (three species) morphotypes. The interspecific K2P and intraspecific distances were 4.2–19.8% and 0.2–1.3%, respectively.

Seven species were monoxenous and two species were stenoxenous (one species on two *Xanthomixis* spp., and another—on *Bernieria madagascariensis* and *Oxylabes madagascariensis*). Most host species harbor only one mite species, while *B. madagascariensis*, *Cryptosylvicola andrianasoloi* and *Xanthomixis zosterops*, each bears two co-existing species, belonging to “wide” and “narrow” morphotypes. Our maximum likelihood tree vs known host phylogeny show nearly perfect pattern of host-parasite co-diversification. The origin of the “narrow” grouping of mites was however uncertain (either via a duplication on the subclade of large-sized warblers *Oxylabes*–*Bernieria*, or via an ancestral transfer from the *Hartertula*–*Randia* subclade).

The ancestor of the *bernieriae* species group apparently co-dispersed to Madagascar on the common ancestor of Malagasy warblers and then co-specified with these hosts, with a few duplication events. This pattern of nearly perfect coevolution contrasts with that usually observed in continental and migratory birds, which usually exhibit higher levels of multi-host mite species and host shifts.

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