Zootaxa 2537: 47–57 (2010)
www.mapress.com/zootaxa/

Article

ISSN 1175-5326 (print edition)
ZOOTAXA
ISSN 1175-5334 (online edition)

Phylogenetic relationships among *Unionicola* (Acari: Unionicolidae) mussel-mites of North America based on mitochondrial cytochrome oxidase I sequences

DALE D. EDWARDS[1,3], MALCOLM F. VIDRINE[2] & BRIAN R. ERNSTING[1]

[1]*Department of Biology, University of Evansville, Evansville, IN 47722, USA.*
[2]*Division of Sciences, Louisiana State University at Eunice, Eunice, LA 70535*
[3]*Corresponding author. E-mail: de3@evansville.edu*

Abstract

Water mites of the genus *Unionicola* Haldeman, 1842 are common symbionts of molluscs, living on the gills or mantle and foot of their hosts and using these tissues as sites of oviposition. Phylogenetic relationships among species that comprise the genus are poorly understood and what is known has been based on a limited number of morphological and life history characters or molecular sequence data using closely-related taxa. The present study uses sequence data from the cytochrome oxidase subunit I (*cox1*) gene (664 bp) to reconstruct evolutionary relationships among representative species of North American *Unionicola* from eight subgenera that occur in symbiotic association with freshwater mussels. Maximum parsimony and maximum likelihood analysis yielded trees with similar topologies, and most of the branches have moderate to high bootstrap support. The topologies of these gene trees are mostly congruent with a previously published morphologically-derived tree. Specifically, the gene trees support monophyly among mites from subgenera that occur in association with the gill tissues of host mussels. The molecular trees of *Unionicola* mites generated by this study must, however, be interpreted with caution, given that the analysis is based exclusively on *Unionicola* subgenera from North America. A more robust phylogeny of *Unionicola* mussel-mites will require the addition of molecular sequence data from taxa outside of North America.

Key words: *Unionicola*, North America, *cox1* gene, phylogeny

Introduction

Water mites (Hydrachnidia) of the genus *Unionicola* Haldeman 1842 (Acari: Unionicolidae) are a cosmopolitan and diverse collection of Acariformes with more than 238 named species in 57 subgenera occurring in freshwater habitats on all continents except Antarctica (Smit 2008; Wen *et al.* 2008). Members of the genus commonly occur in symbiotic association with sponges or molluscs during one or more stages of their life cycle. More than half of the described species of *Unionicola* are symbionts of freshwater mussels, living on the gills or mantle and foot of their hosts and using these tissues as sites of oviposition (Vidrine 1996a).

Our understanding of the evolutionary relationships among *Unionicola* water mites is rather limited and most of what is known has been derived from taxonomic studies. For example, Vidrine (1996b) suggested, without providing quantitative evidence, that species of sponge-associated mites of the subgenus *Hexatax* Thor 1926 (formerly *Unionicola*[1] Haldeman 1842) represented the least-derived taxon within the genus and subsequently identified twenty groups of *Unionicola* subgenera based on the sets of morphological characters that they shared. More recently, Edwards and Vidrine (2006) published a phylogenetic hypothesis for North American mussel-mites based on morphological and life history characters. The topology of the tree generated by this analysis indicated two major clades, with subgenera that occur in association with a host's mantle tissues (*Pentatax* Thor 1922, *Anodontinatax* Vidrine 1986, *Neoatax* Lundblad 1941, *Causeyatax*

Accepted by T. Goldschmidt: 14 Jun. 2010; published: 15 Jul. 2010