

PHYLOGENETIC RELATIONSHIPS AMONG SPECIES OF THE SUBGENUS *PARASITATAX* (ACARI: UNIONICOLIDAE: *UNIONICOLA*) BASED ON DNA SEQUENCE OF THE MITOCHONDRIAL CYTOCHROME OXIDASE I GENE

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ABSTRACT - Morphological differences among species of parasitic water mites in subgenus *Parasitatax* (Unionicolidae: *Unionicola*) are comparatively minor, with taxonomic distinctions among most members of the taxon based on subtle differences in one or two morphological characters. Two species of the subgenus, *Unionicola formosa* Dana and Whelpley, 1836 and *U. foili* Edwards and Vidrine, 1994 are morphologically indistinguishable and have been designated separate species on the basis of host specificity and allozyme analysis. The present study examines heterogeneity in sequence data of the mitochondrial cytochrome oxidase subunit I (COI) gene among four putative species of the subgenus *Parasitatax*: *U. dimocki* Vidrine, 1986, *U. foili*, *U. formosa*, and *U. ypsilophora* Bonz, 1783. Because populations of *U. formosa* from different species of host mussels are genetically divergent, intraspecific diversity of the COI gene among host-associated populations of *U. formosa* was also examined. DNA sequence data was used to construct a phylogenetic hypothesis for the group and assess the degree to which a phylogeny based on molecular data is consistent with traditional taxonomy. Maximum parsimony and maximum likelihood analysis each yielded a single tree with the same topology and high bootstrap support. The gene tree indicates two major clades, with *U. dimocki* and *U. ypsilophora* forming one clade and *U. foili* along with host-associated populations of *U. formosa* forming the other. The latter clade resolved into two branches and indicated that one host-associated population of *U. formosa* is more closely related to *U. foili* than it is to other host-associated populations of *U. formosa*.

Key words - Unionicolidae, *Unionicola*, *Parasitatax*, COI gene, phylogeny, mussel mites, water mites.

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