

Publication

Hidden biodiversity revealed by integrated morphology and genetic species delimitation of spring dwelling water mite species (Acari, Parasitengona: Hydrachnidia)

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Background: Water mites are among the most diverse organisms inhabiting freshwater habitats and are considered as substantial part of the species communities in springs. As parasites, Hydrachnidia influence other invertebrates and play an important role in aquatic ecosystems. In Europe, 137 species are known to appear solely in or near spring- heads. New species are described frequently, especially with the help of molecular species identification and delimitation methods. The aim of this study was to verify the mainly morphology-based taxonomic knowledge of spring- inhabiting water mites of central Europe and to build a genetic species identification library. Methods: We sampled 65 crenobiontic species across the central Alps and tested the suitability of mitochondrial (cox 1) and nuclear (28S) markers for species delimitation and identification purposes. To investigate both markers, distance- and phylogeny-based approaches were applied. The presence of a barcoding gap was tested by using the automated barcoding gap discovery tool and intra- and interspecific genetic distances were investigated. Furthermore, we analyzed phylogenetic relationships between different taxonomic levels. Results: A high degree of hidden diversity was observed. Seven taxa, morphologically identified as *Bandakia con- creta* Thor, 1913, *Hygrobates norvegicus* (Thor, 1897), *Ljania bipapillata* Thor, 1898, *Partnunia steinmanni* Walter, 1906, *Wandesia racovitzai* Gledhill, 1970, *Wandesia thori* Schechtel, 1912 and *Zschokkea oblonga* Koenike, 1892, showed high intraspecific cox 1 distances and each consisted of more than one phylogenetic clade. A clear intraspecific threshold between 5.6-6.0% K2P distance is suitable for species identification purposes. The monophyly of Hydrachnidia and the main superfamilies is evident with different species clearly separated into distinct clades. cox 1 separates water mite species but is unsuitable for resolving higher taxonomic levels. Conclusions: Water mite species richness in springs is higher than has been suggested based on morphological species identification alone and further research is needed to evaluate the true diversity. The standard molecular species identification marker cox 1 can be used to identify species but should be complemented by a nuclear marker, e.g. 28S, to resolve taxonomic relationships. Our results contribute to the taxonomical knowledge on spring inhabiting Hydrachnidia, which is indispensable for the development and implementation of modern environment assessment methods, e.g. metabarcoding, in spring ecology.

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