Abstract

Water mites (Acariformes, Hydrachnidia) of Siberia: DNA-based species identification for global climate change monitoring programs*

PAVEL B. KLIMOV[1,2*], VITALY A. STOLBOV[2], DENIS V. KAZAKOV[2], MARIA O. FILIMONOVA[2,3], SERGEY D. SHEYKIN[2] & ANDREY V. TOLSTIKOV[2]

[1]*Department of Biological Sciences, Purdue University, 915 W State St., #G-225, West Lafayette, Indiana, 47907, USA*
 pklimov@purdue.edu; *https://orcid.org/0000-0002-9966-969X*
[2]*X-BIO Institute, Tyumen State University, Tyumen, 625003, Russia*
 vitusstgu@mail.ru; *kazakov.denis.95@mail.ru;* *tunguz@inbox.ru;* *atolus@yahoo.com*
[3]*Tyumen Scientific Centre SB RAS, Institute of the Problems of Northern Development, 86 Malygina str., Tyumen, 625026, Russia*
 mashaofilimonova@yandex.ru
*Corresponding author

Water mites (Hydrachnidia) are good model organisms for the assessment and long-term monitoring of the biological impacts of natural and human-induced environmental changes in freshwater ecosystems, including those related to global climate change. There are approximately 7,500 species, 485 genera and 56 families. Water mite communities can be affected by pollution and variations in temperature, dissolved oxygen level, conductivity and carbonate concentrations. Due to the complex interactions of water mites with other members of the macroinvertebrate fauna and their habitats, water mite assemblages can rapidly respond to perturbations in the interconnected ecological networks of aquatic communities, and therefore are particularly suitable for early warning systems that monitor water quality. However, monitoring programs using water mites as bioindicators may be impeded by difficulties associated with species identification. Siberia is a crucial region for biodiversity conservation and climatic research by being a major carbon sink due to the large amounts of carbon preserved in permafrost and sequestered by vast boreal forests and peatbogs, and is also a key region for climate change research. There are several reference sites in the Arctic tundra, forest and grassland areas allocated for long-term monitoring of climatically active gases, as well as assessment of the impact of climate change on animal and plant communities.

Here we address the current constraints on water mite taxonomy by integrating conventional morphology, DNA sequence data (using the COX1 barcoding locus) and extensive voucher photo documentation to create and validate a tool for accurate species identification of water mites in Western Siberia. A significant portion of sampling was done at a dedicated climate monitoring and biodiversity research site. We identified a total of 95 species, of which, one was a conventional new species and 15 taxa were cryptic species having large among-species COX1 K2P distances but lacking any apparent morphological differences. Our a priori species delimitation was successfully validated a posteriori. An automatic species delimitation algorithm (ASAP) identified exactly the same set of 95 species, with a species delimitation threshold of 6.1%. This result agrees with previous works suggesting a large threshold of 5.6–6.0% for water mites, but contrasts with the BOLD approach which uses a much lower threshold to identify BINs (1%).

Furthermore, by comparing our identified sequences with GenBank data, we expanded the known geographic ranges of several water mite species. Using extensive GenBank data on mites in Canadian waters, three species were detected to be Holarctic rather than Palaearctic as thought previously (*Limnesia undulatoides*, *Oxus nodigerus* and *Arrenurus papillator*). Three other species, *Torrenticola brevirostris*, *Hygrobates limnocrenicus* and *Unionicola parvipora*, were recorded for the first time in Russia. In addition, we provide an annotated species checklist that reports the distribution, ecology and bioindication potential, and COX1 barcode sequence data, along with high-resolution photographs of each DNA voucher specimen.

Future ecological and biodiversity studies will benefit from using molecular tools for accurate identification of useful mesofaunal bioindicator organisms, such as water mites. Our system will provide a large morphological and molecular reference dataset for further research in ecology and biodiversity and will allow reliable species identification by non-specialists; this will help identify changes in patterns in diversity, abundance and distribution of water mite species due to climate change through long-term monitoring programs.