Concordance between molecular and morphology-based phylogenies of Korean *Enhydrosoma* (Copepoda: Harpacticoida: Cletodidae) highlights important synapomorphies and homoplasies in this genus globally

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Abstract

Three new species of *Enhydrosoma* Boeck, 1873 are described from Korea, all found in muddy sediments in the sublittoral zone. They also all have a bifurcate rostrum, just like the type species of this genus, *E. curticauda* Boeck, 1872, and one recently described Korean representative, *E. coreana* Kim, Trebukova, Lee & Karanovic, 2014. These five species share a number of other morphological features, and mostly differ in details of integumental relief, caudal rami shape, and ornamentation of the male antennula. We aim to compare molecular and morphology-based phylogenies obtained for four Korean species of *Enhydrosoma* and two other members of the family Cletodidae: *Geenhydrosoma intermedia* (Chislenko, 1978) from Korea and Russia and *Stylicletodes* sp. from Korea. Similar studies in other animal groups have helped to re-evaluate the suitability of morphological characters for reconstructing phylogenetic relationships and taxonomic revisions, and the genus *Enhydrosoma* is considered to be polyphyletic and in urgent need of revision. We use partial sequences of the mtCOI gene for our molecular phylogeny and 32 non-additive characters for our morphology-based phylogeny. High congruence between all cladograms suggests that reconstructing phylogenetic relationships in this group of harpacticoids may be straightforward, but highlights as homoplastic some morphological characters previously considered important for defining superspecific taxa in this family. On the other hand, some characters previously overlooked in species descriptions show a significant phylogenetic signal. Even though there is no doubt about the monophyly of the Korean *Enhydrosoma*, their high average pairwise maximum likelihood distances suggest only a remote relationship, and explain their sympatry and/or parapatry. Weak bootstrap support for our basal nodes in molecular phylogenies shows limitations of a single-gene approach, and probably cannot be resolved without a wider taxon and character sampling. Wider taxon sampling will also be necessary to improve bootstrap values of basal nodes in morphology-based cladograms.

Key words: Cladistics, East Asia, mtCOI, phylogeny, sublittoral, taxonomy