



## 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: *Geehydrosoma 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 straight-forward, but highlights as homoplastic some morphological characters previously considered important for defining supraspecific 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