



The systematics of Holarctic bosminids and a revision that reconciles molecular and morphological evolution

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ABSTRACT: Bosminids are ubiquitous and abundant crustacean herbivores in freshwater ecosystems. They are among the best preserved zooplankters in limnological sediments, making them ideal paleolimnological indicators of ecosystem change. Moreover, their egg banks make possible the study of paleogenetics and resurrection ecology. A major limitation to these comparative disciplines is that the relatedness and identities of compared bosminid specimens or subfossils is often uncertain. We aimed to remedy this by developing the first robust molecular phylogeny of the group and inferring patterns of morphological evolution. We used sequence alignments of five nuclear rDNA genes (partial 18S rDNA, internal transcribed spacer 1 [ITS-1], 5.8S, ITS-2, and partial 28S rDNA) and one mitochondrial gene (partial 16S rDNA) from representative Holarctic species from all of the proposed subgenera and genera. No evidence of within-individual sequence variation in the gene regions analyzed was found for the genus *Bosmina* and the genus *Eubosmina*. Our nuclear and mitochondrial genetic results revealed a robust phylogeny and were congruent with morphological changes. Competing morphological schemes of bosminid systematics were reconciled by reassigning several species to different subgenera, resurrecting the genus *Eubosmina*, erecting a new subgenus, and revising the character coding systems that created paraphyletic groups. The results provide an evolutionary framework with diagnostic genetic and morphologic characters for studies of bosminid paleolimnology and paleogenetics.

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