

The 18S rDNA sequences support polyphyly of the Hypsibiidae (Eutardigrada)

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ABSTRACT

To extend data on 18S rDNA gene phylogeny within the Eutardigrada and to provide additional information on unclear taxonomic status of a glacier tardigrade *Hypsibius klebelsbergi*, gene sequences from seven tardigrade species of the family Hypsibiidae (*Hypsibius klebelsbergi*, *Hypsibius cf. convergens 1*, *Hypsibius cf. convergens 2*, *Hypsibius scabropygus*, *Hebesuncus conjungens*, *Isohypsibius cambrensis*, *Isohypsibius granulifer*) were analysed together with previously published sequences from ten further eutardigrade species or species groups. Three distinctly separated clades within the Hypsibiidae, 1) the Ramazzottius - Hebesuncus clade, 2) the Isohypsibius clade (*Isohypsibius*, *Halobiotus*, *Thulinus*), and 3) the Hypsibius clade (*Hypsibius spp.*) have been obtained in each of four phylogenetic trees recovered by Maximum Parsimony, Neighbour Joining, Minimum Evolution and UPGMA. *Hypsibius klebelsbergi* has been located always within the Hypsibius clade. The detailed sister group relationship was not resolved adequately, but there is robust support for a sister group relationship between the Hypsibius clade and the remaining clades. We cannot exclude that the Ramazzottius - Hebesuncus clade is a sister group of the Macrobiotus clade. Our findings suggest polyphyly of the Hypsibiidae, and thus multiple evolutions of some structures currently applied as diagnostic characters (e.g., claws, buccal apophyses).

Key words: Tardigrada, Hypsibiidae, polyphyly, 18S rRNA, morphological characters
