**File S1**  **Detailed methods for the phylogenetic analysis, and the results of the analysis**

**Methods**

The 18S dataset for phylogenetic analysis included one sequence we determined from a specimen collected from MS, the type locality (ICHUM-8610; accession number LC789200), and 32 sequences from 31 cypridoidean species and one outgroup taxon (*Pontocypris* *mytiloides*, Pontocypridoidea) taken from the INSD (Table S2). Methods for sequence alignment (1583 positions in the aligned dataset; Files S2, S3), selection of the optimal substitution model (GTR + G + I), maximum likelihood (ML) analysis, and drawing the tree were as described by Munakata et al. (2022).

**Result**

In our 18S-based ML tree (Figure below), *L. fonticola* forms a weakly supported clade (59% ultrafast bootstrap support, or uBS) as the sister taxon to a well-supported clade (96% uBS) containing the three taxa in Cypricericinae included in the analysis. Among the five other subfamilies represented by two or more genera in our analysis, Cyclocypridinae, Candoninae, and Paracypridinae were well-supported clades.



**Figure** Maximum-likelihood (ML) tree for cypridoidean ostracods based on 18S sequences (1583 positions). Numbers near nodes are ultrafast bootstrap support (uBS) values, as percentages. Scale at bottom indicates branch length in substitutions per site.

**REFERENCE**

Munakata M, Tanaka H, Kakui K. 2022. Taxonomy and natural history of *Cavernocypris hokkaiensis* sp. nov., the first ostracod reported from alpine streams in Japan. Zoosyst Evol **98(1):**117–127. doi: 10.3897/zse.98.80442.