

through the two consecutive mass extinctions on Pangaea and subsequent radiations during the Jurassic through early Cretaceous shaped the modern familial diversity of otophysans.

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**The Mitogenomic Supermatrices to Resolve Cypriniformes Tree of Life: An Empirical Approach Based on 472 Complete and 2171 Partial mtDNA Sequences**

Fishes of the order Cypriniformes are almost completely restricted to freshwaters and comprise over 4,000 species placed in 6+ families, each with poorly defined subfamilies and/or tribes. This study attempts comprehensive resolution of the cypriniform phylogenies by combining a mitogenomic tree as a backbone constraint for the robust higher-level relationships and numerous partial sequences downloaded from GenBank for the reconstruction of lower-level relationships within the constrained clades. The mitogenomic tree is based on 472 sequences (including 6 outgroups) and the resulting best-scoring ML tree is congruent with the previous molecular phylogenies based on both mitogenomes and nuclear genes. A total of 17,057 partial sequences from cypriniforms were available from GenBank and they were sorted into 9 mitochondrial genes from 1138 species, of which 1039 species were those from the *cyt b* gene alone. Thus we constructed two matrices comprising 1) *cyt b* gene only (CB dataset: 1134 bp from 1511 spp.; missing data 2.53%) and 2) all 9 genes (ALL dataset: 9784 bp from 1610 spp.; missing data 57.6%) and the two matrices were subjected to partitioned ML analyses with the mitogenomic tree as a backbone constraint. The best-scoring ML tree based on the CB dataset derived from 24 runs using a fast bootstrap (BS) option in RAxML places all species from the partial sequences (1039 spp.) in reasonable positions, with 62.2% of the internal branches being supported by  $\geq 80\%$  BS probabilities. The ALL dataset is currently analyzed in a similar manner and the preliminary results will be presented.

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