

## Evolution of mitochondrial genomes in Baikalian amphipods

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### Abstract

© 2016 The Author(s). Background: Amphipods (Crustacea) of Lake Baikal are a very numerous and diverse group of invertebrates generally believed to have originated by adaptive radiation. The evolutionary history and phylogenetic relationships in Baikalian amphipods still remain poorly understood. Sequencing of mitochondrial genomes is a relatively feasible way for obtaining a set of gene sequences suitable for robust phylogenetic inferences. The architecture of mitochondrial genomes also may provide additional information on the mechanisms of evolution of amphipods in Lake Baikal. Results: Three complete and four nearly complete mitochondrial genomes of Baikalian amphipods were obtained by high-throughput sequencing using the Illumina platform. A phylogenetic inference based on the nucleotide sequences of all mitochondrial protein coding genes revealed the Baikalian species to be a monophyletic group relative to the nearest non-Baikalian species with a completely sequenced mitochondrial genome - *Gammarus duebeni*. The phylogeny of Baikalian amphipods also suggests that the shallow-water species *Eulimnogammarus* has likely evolved from a deep-water ancestor, however many other species have to be added to the analysis to test this hypothesis. The gene order in all mitochondrial genomes of studied Baikalian amphipods differs from the pancrustacean ground pattern. Mitochondrial genomes of four species possess 23 tRNA genes, and in three genomes the extra tRNA gene copies have likely undergone remodeling. Widely varying lengths of putative control regions and other intergenic spacers are typical for the mitochondrial genomes of Baikalian amphipods. Conclusions: The mitochondrial genomes of Baikalian amphipods display varying organization suggesting an intense rearrangement process during their evolution. Comparison of complete mitochondrial genomes is a potent approach for studying the amphipod evolution in Lake Baikal.

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