

MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of a deep-water Baikalian amphipoda *Brachyuropus grewingkii* (Dybowsky, 1874)Elena V. Romanova¹, Kirill V. Mikhailov^{2,3}, Maria D. Logacheva^{2,4}, Ravil M. Kamaltynov¹, Vladimir V. Aleoshin^{2,3}, and Dmitry Yu. Sherbakov^{1,5}¹Laboratory of Molecular Systematics, Limnological Institute, Siberian Branch of Russian Academy of Sciences, Irkutsk, Russia, ²Department of Evolutional Biochemistry, Belozersky Institute for Physicochemical Biology, Lomonosov Moscow State University, Moscow, Russia, ³Institute for Information Transmission Problems, Russian Academy of Sciences, Moscow, Russia, ⁴Faculty of Bioengineering and Bioinformatics, Lomonosov Moscow State University, Moscow, Russia, and ⁵Faculty of Biology and Soils, Irkutsk State University, Irkutsk, Russia

Abstract

In this study, we present a complete mitochondrial genome of a deep-water amphipoda *Brachyuropus grewingkii* (Dybowsky, 1874) from Lake Baikal. A circular mitochondrial DNA has 17,118 bp in length and contains 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNA genes, a putative control region, and five intergenic spacers. An extended control region and altered positions of some tRNA genes distinguish mitochondrial genome of *B. grewingkii* from the mitochondrial genomes described for other Baikalian amphipoda species.

Keywords

Amphipoda, Lake Baikal, mitochondrial genome

History

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Baikal (East Siberia) is the oldest and biggest lake which has very diverse endemic fauna originated from long period of adaptive radiation (Mats et al., 2011). Currently, there are more than 2600 animal species inhabiting Baikal described, and most of them are endemics (Timoshkin, 2010–2011). Amphipods (Crustacea) are the most numerous (about 350 species) and diverse invertebrates of the lake (Kamaltynov, 2001). These organisms can be a good model for studying mechanisms of adaptive radiation by analysis of their genomic sequences. A complete mitochondrial genome of amphipoda *Brachyuropus grewingkii* (Dybowsky, 1874) is presented.

Brachyuropus grewingkii is an endemic abyssal species from Lake Baikal. It usually occurs at the depths from 300 down to 1380 m (Kamaltynov, 2001). This polyphagous species has the largest body size (up to 90 mm) (Bazikalova, 1945, 1954) and possibly the longest lifespan in Baikalian amphipods (up to 10 years according to Bazikalova, 1954).

A specimen *B. grewingkii* was sampled by trawling with the beam trawl at the depth of 350–380 m not far from the estuary of Buguldeika river (Western coastline of the lake, 52°28'N, 106°06'E–52°28'N, 106°05'E) in August 2013. Total genomic DNA was extracted using Diatom DNA Prep 200 (Isogen, Russia). Generation of 6.4 M paired-end reads was performed by Illumina HiSeq2000 system (Illumina, San Diego, CA). The quality trimming and removing of adapters from reads was made by Trimmomatic-0.32 (Bolger et al., 2014). Processed reads were assembled de novo with SPAdes 3.0.0 (Bankevich et al., 2012).

The mitochondrial genome of Baikalian amphipoda *Eulimnogammarus verrucosus* (Rivarola-Duarte et al., 2014) was used to identify mitochondrial scaffold of *B. grewingkii* in the assembly using BLAST (Altschul et al., 1997). The complete sequence of mitochondrial genome of *B. grewingkii* (GenBank accession no. KP161875) was determined to be circular and had a length of 17,118 bp. The base composition of the heavy strand was A – 31.02%, T – 31.22%, C – 13.07%, and G – 24.68% and the GC content was 37.76%. A mitochondrial DNA sequence of *B. grewingkii* was annotated using MITOS pipeline (Bernt et al., 2013) with subsequent manual correction of gene boundaries. It had typical for metazoan gene content: 13 protein-coding genes, two ribosomal RNA genes, and 22 transfer RNA genes. *Brachyuropus grewingkii* mitochondrion also possesses a putative control region and five intergenic spacers ranging from 1 to 462 bp (Figure 1).

The order of protein coding genes and ribosomal genes in mitochondrial genome of *B. grewingkii* was found to be similar to the pancrustacean ground pattern (Kilpert & Podsiadlowski, 2006). In comparison with the available mitochondrial sequences of other Baikalian amphipod species *E. verrucosus* (Rivarola-Duarte et al., 2014) and *E. vittatus* (Romanova et al., 2014), the mitochondrial DNA of *B. grewingkii* is somewhat longer mainly due to greater length of putative control region.

The second feature of *B. grewingkii* mitochondrion is altered positions of some tRNA genes: *tRNA-Leu1*, *tRNA-Tyr*, and *tRNA-Asp*. The latter was identified in the middle of putative control region area. Further sequencing and analysis of mitochondrial genomes of other amphipod species will allow describing in more details the spectacular adaptive radiation in Baikalian endemic amphipods.

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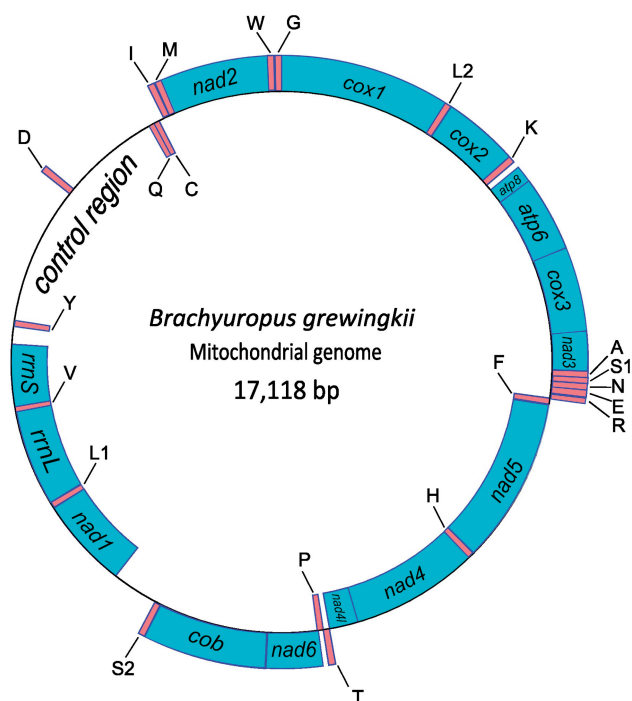


Figure 1. Map of the mitochondrial genome of *Brachyuropus grewingkii*. Protein-coding genes and ribosomal RNA genes are shown as sectors. Transfer RNAs are labeled by their single-letter amino acid code. The features located at the (–) strand are shown inside the circle.

Declaration of interest

The authors report that they have no conflicts of interest. The authors alone are responsible for the content and writing of the paper. The work was supported by the governmentally funded project No VI.61.1.3; Russian Foundation for Basic Research (Grants no. 13-04-90757-mol_rf_nr, 15-04-05841 A, 15-04-03848 A) and the Ministry of Education and Science of the Russian Federation (Grant no. 11.G34.31.0008 and the program “Scientific and scientific-pedagogical personnel of innovative Russia”).

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