

MITOGENOME ANNOUNCEMENT

**The complete mitochondrial genome of Baikalian amphipoda
Eulimnogammarus vittatus Dybowsky, 1874**

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Abstract

A complete mitochondrial genome sequence of amphipoda *Eulimnogammarus vittatus* Dybowsky, 1874 from Lake Baikal was obtained using next-generation sequencing approach. Mitochondrial DNA with the length of 15,534 bp contains 13 protein-coding genes, 2 ribosomal RNA, 23 transfer RNA and non-coding sequences: a putative control region and 7 intergenic spacers. A brief comparative analysis of mitochondrial genomes of *E. vittatus* and its sister species *Eulimnogammarus verrucosus* was performed.

Keywords

Amphipoda, genome annotation, mitochondrial genome, next-generation sequencing

History

Received 4 September 2014
Accepted 7 September 2014
Published online 29 September 2014

Amphipods (Crustacea) are the most diverse animals in Lake Baikal (East Siberia). This group of invertebrates is known to originate in course of long endemic adaptive radiation, the beginning of which dates back to more than 20 myr (Mats et al., 2011). According to the most modern taxonomic system, there are

more than 347 amphipod species from 71 genera inhabiting the lake (Kamaltynov, 2001). Still the phylogenetic relationships of Baikalian amphipods remain poorly understood mostly due to low resolution of the molecular markers used (McDonald et al., 2005).

Table 1. Organization of the mitochondrial genome of *E. vittatus*.

Feature	Strand	From	To	Size (bp)	Start	Stop
<i>COI</i>	+	1	1537	1537	ATT	T(AA)
<i>tRNA-Leu2</i>	+	1538	1598	61		
<i>CO2</i>	+	1599	2280	682	TTG	T(AA)
<i>tRNA-Lyz</i>	+	2281	2340	60		
<i>tRNA-Asp</i>	+	2341	2401	61		
<i>ATP8</i>	+	2402	2557	156	GTG	TAA
<i>ATP6</i>	+	2551	3219	669	ATG	TAA
<i>CO3</i>	+	3219	4004	786	ATG	TAA
Intergenic spacer-1	n.a.	4005	4006	2		
<i>ND3</i>	+	4007	4360	354	ATG	TAG
<i>tRNA-Ala</i>	+	4359	4417	59		
<i>tRNA-Ser1</i>	+	4416	4467	52		
Intergenic spacer-2	n.a.	4468	4470	3		
<i>tRNA-Asn</i>	+	4471	4531	61		
<i>tRNA-Glu</i>	+	4529	4591	63		
<i>tRNA-Arg</i>	+	4586	4645	60		

(continued)

Table 1. Continued

Feature	Strand	From	To	Size (bp)	Start	Stop
<i>tRNA-Phe</i>	–	4644	4703	60		
<i>ND5</i>	–	4703	6415	1713	TTG	TAA
<i>tRNA-His</i>	–	6416	6477	62		
<i>ND4</i>	–	6478	7786	1309	ATG	T(AA)
<i>ND4L</i>	–	7780	8073	294	ATG	TAA
Intergenic spacer-3	n.a.	8074	8076	3		
<i>tRNA-Thr</i>	+	8077	8136	60		
<i>tRNA-Pro</i>	–	8136	8197	62		
Intergenic spacer-4	n.a.	8198	8202	5		
<i>ND6</i>	+	8203	8700	498	ATG	TAA
<i>Cyt b</i>	+	8700	9836	1137	ATG	TAA
<i>tRNA-Ser2</i>	+	9835	9895	61		
Intergenic spacer-5	n.a.	9896	10,218	323		
<i>tRNA-Leu1</i>	–	10,219	10,278	60		
Intergenic spacer-6	n.a.	10,279	10,374	96		
<i>ND1</i>	–	10,375	11,307	933	TTG	TAG
<i>tRNA-Pro</i>	–	11,308	11,368	61		
<i>16S rRNA</i>	–	11,369	12,352	984		
<i>tRNA-Val</i>	–	12,353	12,406	54		
<i>12S rRNA</i>	–	12,405	13,026	622		
Control region		13,027	14,079	1053		
<i>tRNA-Tyr</i>	–	14,080	14,140	61		
<i>tRNA-Gln</i>	–	14,138	14,193	56		
<i>tRNA-Cys</i>	–	14,194	14,250	57		
Intergenic spacer-7	n.a.	14,251	14,309	59		
<i>tRNA-Ile</i>	+	14,310	14,370	61		
<i>tRNA-Met</i>	+	14,372	14,432	61		
<i>ND2</i>	+	14,433	15,414	982	TTG	T(AA)
<i>tRNA-Trp</i>	+	15,415	15,474	60		
<i>tRNA-Gly</i>	+	15,475	15,534	60		

The incomplete stop codons are labeled in the table with parentheses.

Eulimnogammarus vittatus is an endemic species which widely distributed in Baikal at the depth range of 0 to 2 meters (sometimes down to 30 meters) (Kamaltynov, 2001). A specimen for this study was collected at the water's edge near the village Sukhoi Ruchey (51° 38' 48" N, 103° 45' 14" E) in November 2012.

Exactly 4.6 million paired-end reads were obtained from the total genomic DNA of *E. vittatus* using HiSeq 2000 system (Illumina, San Diego, CA). The reads were cleaned from the adapter sequences with Trimmomatic-0.32 (Bolger et al., 2014) and assembled de novo using Velvet 1.2.10 (Zerbino & Birney, 2008). Mitochondrial scaffold of *E. vittatus* was identified in the assembly using BLAST (Altschul et al., 1997) and the reference sequence of *Gammarus duebeni* (Genbank NC_017760, Krebs & Bastrop, 2012). The mitochondrial scaffold of *E. vittatus* had mean coverage of 21 and contained a single gap, which was subsequently closed by Sanger sequencing. By mapping reads on both ends of the scaffold, the assembled mitochondrial DNA sequence of amphipod *E. vittatus* was determined as circular with the length of 15,534 bp. The GC content of the heavy strand was 32.58% with the following base composition: A – 34.20%, T – 33.22%, C – 12.68% and G – 19.90%. Sequence annotation was performed using the MITOS pipeline (Bernt et al., 2013), and the gene boundaries were revised and corrected manually. The annotation found 13 protein-coding genes, 2 ribosomal RNA genes and 23 transfer RNA genes in the mitochondrial DNA of *E. vittatus*. The sequence also contains 1053 bp long putative control region and 7 intergenic spacers ranging from 2 to 323 bp (Table 1). Annotated mitochondrion of *E. vittatus* is available in GenBank (KM287572).

The genes order of *E. vittatus* mitochondrial genome was almost identical with the one of its sister species *E. verrucosus* described earlier (Rivarola-Duarte et al., 2014). However

E. vittatus had two copies of *tRNA-Pro* and an altered position of *tRNA-Leu1*. These two species possess different start codons in *ND1*, *ND4*, *ND4L* and *ND5* genes and different stop codons in *ND1* and *ND4* genes.

Utilization of complete mitochondrial genome sequences can allow resolving contradictions in systematics of Baikalian amphipods as well as discovering mechanisms of rapid adaptive radiation which take place in ancient lakes.

Declaration of interest

The authors report 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 (grant No 13-04-90757-mol_rf_nr) 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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