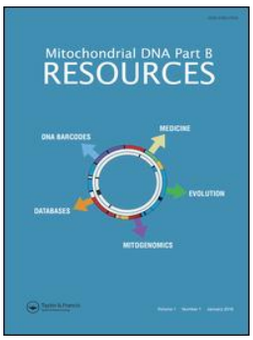

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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of *Artemia sinica* Cai, 1989 (Crustacea: Anostraca) using next-generation sequencing

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ABSTRACT

The complete mitochondrial genome of *Artemia sinica* was obtained using the next-generation sequencing (NGS) method. The mitochondrial genome is a circular molecule of 15,689 bp in length, with the typical structure of 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs) and 2 ribosomal RNA genes, and a non-coding control region (CR). The base composition is 31.53% A, 18.99% C, 16.50% G, and 32.98% T, with an A + T content of 64.51%. All tRNAs have a cloverleaf structure excepting *tRNA-Ser*$_1$, that represents the D-loop structure.

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KEYWORDS
Mitogenome; brine shrimp; *Artemia sinica*; protein-coding genes; transfer RNA genes; ribosomal RNA genes

The genus *Artemia* consists of seven bisexual species and a large number of parthenogenetic populations with different ploidy degrees (Asem et al. 2010). So far, the complete mitogenome of three bisexual species of *Artemia* (*Artemia franciscana*, *Artemia urmiana,* and *Artemia tibetiana*) have already been characterized(Valverde et al. 1994; Zhang et al. 2013). In this study, we sequenced and described the complete mitochondrial genome of *Artemia sinica* (GenBank: MK069595). The present study is a part of a more comprehensive project of characterizing the complete mitochondrial genome of genus *Artemia*.

The cysts of *A. sinica* (ARC: 1166) were collected from Ejinor Lake (Inner Mongolia, China) and stored in the *Artemia* Reference Center (Ghent University, Belgium). The total DNA was extracted from a cultured adult specimen. A genomic library was established followed by paired-end (2 × 150 bp) next-generation sequencing (10 Gb), using the Illumina HiSeq X-ten sequencing platform. Quality checks for sequencing reads were performed by FastQC (Andrews 2010) and the sequences were assembled and mapped to the reference *Artemia* mitochondrial genome (*A. franciscana*, X69067) with Spades v3.9.0 (Bankevich et al. 2012) and bowtie v2.2.9 (Langmead and Salzberg 2012). Putative tRNA genes were determined using the tRNAscan-SE2.0 (http://lowelab.ucsc.edu/tRNAscan-SE/) and ARWEN (http://130.235.46.10/ARWEN/) online software. All genes were annotated based on gene order on the reference mitochondrial map and using BLAST analysis (https://blast.ncbi.nlm.nih.gov). Additionally, to annotate PCGs and tRNAs, the position of start and stop codons, and secondary structures and the position of anticodons were re-considered, respectively.

The complete mitogenome of *A. sinica* was 15,689 bp in length, with 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), 2 ribosomal RNAs (rRNAs), and a control region (CR). The overall nucleotide composition of the major strand of the *A. sinica* mitogenome was as follows: 31.53% A, 18.99% C, 16.50% G, and 32.98% T, with a total A + T content of 64.51%.

Nine tRNAs (*tRNA-Ile*, *tRNA-Gln*, *tRNA-Cys*, *tRNA-Tyr*, *tRNA-Phe*, *tRNA-His*, *tRNA-Pro*, *tRNA-Leu*, and *tRNA-Val*) and four PCGs (*ND5, ND4, ND4L*, and *ND1*), as well as both rRNAs were encoded on the light strand. Just six PCGs (*ND2*, *COX1*, *ATP6*, *COX3*, *CYTB*, and *ND1*) began with the common ATG start codon. Stop codons included TAA (*ND2*, *ATP8*, *ATP6*, *ND3*, *ND4L*, *CYTB*, and *ND1*), TAG (*ND6*) and non-complete codons T (*COX1*, *COX2*, *COX3* and *ND5*, and *ND4*). The *12S rRNA* and *16S rRNA* were separated by the *tRNA-Val*.

Based on the results, the highest and lowest values of %GC tRNA composition belong to *tRNA-Lys* (46.9%) and *tRNA-Glu* (18.2%), respectively. Secondary structures of *tRNA-Ser*$_1$ showed the D-loop structure. The longest and shortest tRNAs were *tRNA-Ser*$_2$ (67 bp) and *tRNA-Ala* (59 bp), respectively.

CR was located between *12S rRNA* and *tRNA-Met*, with an A + T content of 67.58%. The longest gap and overlapping were determined between *tRNA-Gln/tRNA-Cys* (54 bp) and *tRNA-Phe/ND5* (13 bp), respectively.

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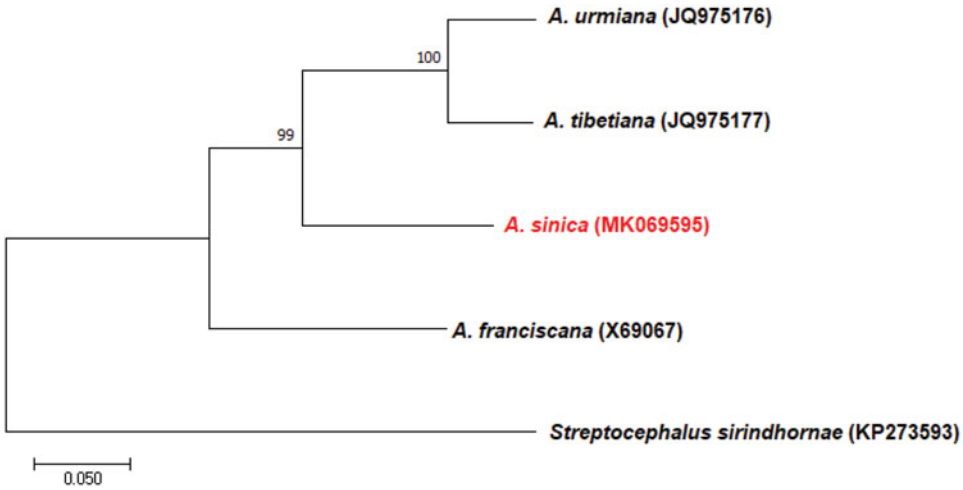

Figure 1. Phylogenetic tree showing the relationship among *A. sinica* and three other species from the *Artemia* based on maximum-likelihood (ML) approach. Numbers behind each node denote the bootstrap support values. The GenBank accession numbers are indicated on the right side of species names. *Streptocephalus sirindhornae* was used as an outgroup.

The phylogenetic relationship of *A. sinica* with members of the genus *Artemia* was determined from a concatenated dataset including the 13 PCGs and 2 rRNAs using the software MEGA 7.0.26 v. (Kumar et al. 2016) with 1000 bootstrap replicates and a GTR model (Figure 1). According to the result, *A. sinica* was placed as a clade sister to other Asian spp. All Asian species were clearly separated from American *A. franciscana*.

Disclosure statement

No potential conflict of interest was reported by the authors.

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