The complete mitochondrial genome of a Chinese endemic stonefly species, *Sinacroneuria dabieshana* (Plecoptera: Perlidae)

Jinjun Cao\textsuperscript{a,b}, Weihai Li\textsuperscript{a} and Ying Wang\textsuperscript{a}

\textsuperscript{a}Department of Plant Protection, Henan Institute of Science and Technology, Xinxiang, China; \textsuperscript{b}Postdoctoral Research Base, Henan Institute of Science and Technology, Xinxiang, China

**ABSTRACT**

The complete mitochondrial genome of *Sinacroneuria dabieshana* Li & Murányi, the first representative of the genus *Sinacroneuria*, was sequenced and annotated. This mitogenome was 15,752 bp long and encoded 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), two ribosomal RNA genes (rRNAs) and a control region. The *S. dabieshana* mitogenome with an A + T content of 67.3% presented a positive AT-skew (0.058) and a negative GC-skew (−0.303). Ten PCGs started with a typical ATN codon, except ATP8, COI and ND1 initiated with GTG, CCG and TTG, respectively. Eleven PCGs use the typical stop codon TAA/TAG, except COI and ND5 gene terminated with a single T. The Bayesian (BI) and maximum-likelihood (ML) trees both showed that *S. dabieshana* and *Acroneuria hainana* are the sister group. Phylogenetic relationships among six genera within Perlidae were recovered as (*Caroperla + (Acroneuria + Sinacroneuria) + (Dinocras + (Togoperla + Kamimuria))).

Yang and Yang (1995) established the genus *Sinacroneuria* in the subfamily Acroneurinae. The genus *Sinacroneuria* contains 11 species and is primarily distributed in China (DeWalt et al. 2019). Li et al. (2014) described the species of *S. dabieshana* from Henan and Hubei Province of central China, which represents the northernmost distribution of the genus in China. As far as we know, no mitochondrial genome (mitogenome) sequences belonging to genus *Sinacroneuria* has been published. In this paper, the complete mitogenome sequence of *S. dabieshana* (GenBank accession no. MK492253) was reported at the first time.

The specimen of *S. dabieshana* was collected by Weihai Li at Dabie Mountains, Henan Province, China in 2015. Samples and voucher specimens were deposited in Henan institute of Science and Technology (HIST), China. The total genomic DNA was extracted from adult’s thorax muscle using the QIAamp DNA Mini Kit (QIAGEN, Hilden, Germany) and sequenced by high-throughput sequencing method. Annotation of the complete mitogenome was amplified and sequenced as described in published studies (Li et al. 2017; Wang et al. 2017, 2018; Liu et al. 2018; Cao et al. 2019). We assembled the sequence reads into contigs using the BioEdit version 7.0.5.3 (Hall 1999).

The mitogenome of *S. dabieshana* was 15,752 bp in length, which contained 22 transfer RNA genes (tRNAs), 13 protein-coding genes (PCGs), two ribosomal RNA genes (rRNAs) and a putative control region. The gene order and organization of *S. dabieshana* are consistent with those of putative ancestors of insects (Boore 1999). The nucleotide composition of *S. dabieshana* mitogenome was 35.6% of A, 31.7% of T, 21.3% of C, 11.4% of G, 67.3% of A + T content. The A + T content of PCGs, tRNAs and rRNAs was 65.7%, 68.8% and 71.3%, respectively. The control region was located between *rrnS* and *tRNA^Lys* genes with a length of 851 bp, and the A + T content was 77.5%. The initial codons for ten PCGs of *S. dabieshana* were the canonical putative start codons ATN, while ATP8 used GTG, COI used CCG and ND1 used TTG as start codon. The typical termination codon (TAA/TAG) occurs in 11 PCGs, and the remaining two PCGs (COII and ND5) were stopped with a single T. All tRNAs had the typical cloverleaf secondary structures except for the *tRNA^Ser(AGN)* lack of the stem-loop structure of the dihydrouridine (DHU) arm.

The concatenated nucleotide sequences of 13 PCGs and 2 rRNAs from seven Perlidae species and two species (*Pteronarccys princeps* and *Pteronarcella badia* as outgroups) were used in phylogenetic analysis to better understand the relationship among Perlidae species. The Bayesian (BI) and maximum-likelihood (ML) analyses generated the phylogenetic trees with the same topologies (Figure 1). Result shows *S. dabieshana* and *Acroneuria hainana* are the sister group. Phylogenetic relationships among six genera within Perlidae were recovered as (*Caroperla + (Acroneuria + Sinacroneuria) + (Dinocras + (Togoperla + Kamimuria))). Our result was inconsistent with the traditional morphological classification.
Additional taxon sampling will be required to resolve this problem.

Disclosure statement
No potential conflict of interest was reported by the authors.

Funding
This work was supported by the initial Project of Henan Institute of Science and Technology [Nos. 2014028 and 2015026] and the National Natural Science Foundation of China [No. 31801999].

References
Boore JL. 1999. Animal mitochondrial genomes. Nucleic Acids Res. 27:1767–1780.
Cao JJ, Wang Y, Li N, Li WH, Chen X. 2019. Characterization of the nearly complete mitochondrial genome of a Chinese endemic stonefly species, Caroperla siveci (Plecoptera: Perlidae). Mitochondrial DNA: Part B. 4:553–554.
DeWalt RE, Maehr MD, Neu-Becker U, Stueber G. 2019. Plecoptera species file online. [accessed 7 Feb 2019]. http://Plecoptera.SpeciesFile.org.
Hall TA. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp Ser. 41:95–98.
Li H, Leavengood JJM, Chapman EG, Burkhardt D, Song F, Jiang P, Liu J, Zhou XG, Cai WZ. 2017. Mitochondrial phylogenomics of Hemiptera reveals adaptive innovations driving the diversification of true bugs. Proc R Soc B. 284:1862.
Li WH, Murányi D, Wang RF. 2014. A new species of Sinacronoeuria (Plecoptera: Perlidae) from China with a provisional key to species. Zootaxa. 3895:285–291.
Liu YQ, Song F, Jiang P, Wilson JJ, Cai WZ, Li H. 2018. Compositional heterogeneity in true bug mitochondrial phylogenomics. Mol Phylogenet Evol. 118:135–144.
Sivec I, Stark BP, Uchida S. 1988. Synopsis of the world genera of Perlinae (Plecoptera: Perlidae). Scopolia. 16:1–66.
Wang Y, Cao JJ, Li WH. 2017. The complete mitochondrial genome of the styloperlid stonefly species Stylonypha spinicercia (Insecta: Plecoptera) with family-level phylogenetic analyses of the Pteronarcyoidae. Zootaxa. 4243:125–138.
Wang Y, Cao JJ, Murányi D, Li WH. 2018. Comparison of two complete mitochondrial genomes from Perlodidae (Plecoptera: Perlidae) and the family-level phylogenetic implications of Perlidae. Gene. 675:254–264.
Yang C, Yang D. 1995. A new genus and new species of Plecoptera from east China (Perlidae: Acronoeurinae). Entomol J East China. 4:1–2.