

The complete mitochondrial genome of a stonefly species, *Etrocorema hochii* (Plecoptera: Perlidae)

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ABSTRACT

The mitochondrial genome of *Etrocorema hochii* (Wu, 1938), the first representative of *Etrocorema*, was sequenced and annotated in this study. The complete circular mitochondrial genome (mitogenome) was 15,854 bp in length using Illumina sequencing and harboured 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNA), two ribosomal RNA genes (rRNA), and one control region in the typical stonefly gene order. The nucleotide composition of this genome is A (36.0%), T (31.4%), C (20.9%), and G (11.7%). All PCGs use the typical start codon ATN, except *ND1*, *ND2*, and *COI*, which start with TTG, GTG, and ACC, respectively. Only the *ND5* genes terminated with single T—, and the rest use the stop codon TAA/TAG. We used this new nucleotide information under Bayesian and maximum-likelihood analyses to explore the relationships of Perlidae. Phylogenetic analyses showed that *E. hochii* is closely related to the clade (*Togoperla* + *Kamimuria*), which is widely accepted view.

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As we know, about 400 species of Perlidae in the world, most species are widely distributed in the northern part of the earth, and a few are extended to the southern part of Africa and South America (DeWalt et al. 2019). But, there are only three species have been reported in the genus *Etrocorema* of the family Perlidae in the world. The earliest discovered species *E. ahenobarba* was found in Southeast Asian mainland, Sumatra, Borneo in 1909 (Sivec et al. 1988). Subsequently, the second species *E. Hochii* was reported but the species was originally named in genus *Tetropina* by Wu (1938) but tentatively placed in genus *Etrocorema* by Zwick (1984). And, the *E. Hochii* was a special species which only distribute in Hainan, China. The last species *E. belumensis* was discovered in Malaya and presented by Wan Nur Asiah and Che Salmah (Wan Nur Asiah 2009). Although eight species in Perlidae have been sequenced and published, the genus *Etrocorema* has not yet been involved (Qian et al. 2014; Elbrecht et al. 2015; Huang et al. 2015; Wang, Ding, et al. 2016; Wang, Wang, et al. 2016; Cao, Li, et al. 2019; Cao, Wang, et al. 2019; Li et al. 2019). In this paper, the complete mitochondrial genome sequences of *E. Hochii* were determined using Illumina sequencing for the first time which representative the genus *Etrocorema* to facilitate future studies on the identification, population genetics, and evolution of the Perlidae. The specimens of *E. hochii* was collected in Yinggeling National Nature Reserve (19.06°N, 109.57°E), Hainan Province, China in April 2016.

Samples and voucher specimens (No. Voh-0068) were deposited in the museum of Henan Institute of Technology, Henan Province, China.

The complete mitogenome of *E. Hochii* is 15,854 bp in length with the GenBank accession number MK905888, which contains 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, two ribosomal RNA (rRNA) genes, and one control region.

In general, the *E. hochii* mitogenome was clearly biased towards A/T nucleotides (A = 36.0%, T = 31.4%, G = 11.7%, and C = 20.9%) which is similar to the range reported from Plecopteran mitogenomes. All PCGs started with codon ATN, except *ND1*, *ND2*, and *COI*, which initiate with TTG, GTG, and ACC, respectively. Only the *ND5* genes terminated with single T, and the rest 12 genes use the stop codon TAA/TAG. The total length of 13 PCGs was 11,211 bp with 65.1% A + T content. The A + T content of tRNAs and rRNAs was 70.6% and 71.7%, respectively. The length of 12S rRNA and 16S rRNA was 881 bp and 1,435 bp with A + T content as 70.5% and 73.4%, respectively.

The phylogenetic relationships of *E. Hochii* were inferred by Bayesian (BI) and Maximum-Likelihood (ML) analysis based on the sequences of the 13 PCGs from two Pteronarcyid species (*Pteronarcys princeps* and *Pteronarcella badia* as out-group) and eight published Perlid species (Figure 1). Phylogenetic tree confirms that *E. hochii* is clustered with the two genera (*Togoperla* + *Kamimuria*) into a clade, which is

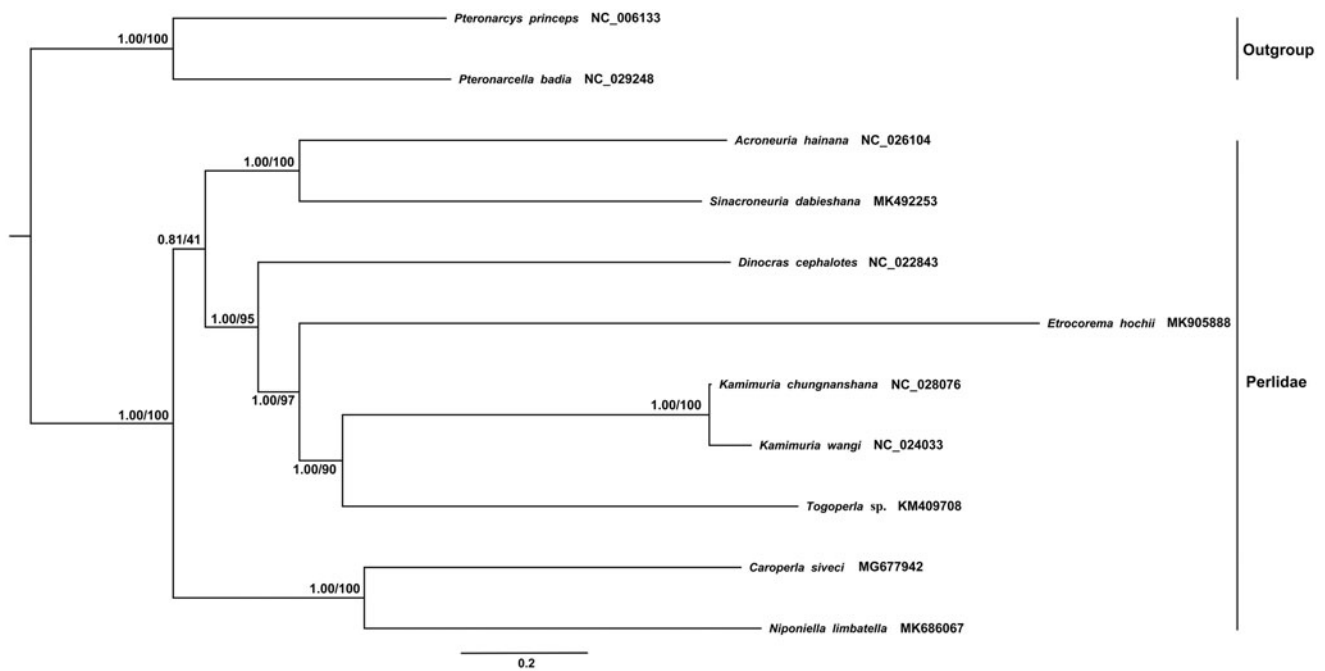


Figure 1. Bayesian inference (BI) and maximum-likelihood (ML) phylogenetic trees from 11 species based on the mitogenomic sequence data of 13 PCGs.

widely accepted view. We hope our data will be useful for further study.

Disclosure statement

No potential conflict of interest was reported by the authors.

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