

## Characterization of the complete mitochondrial genome of a stonefly species, *Kamimuria klapaleki* (Plecoptera: Pelidae)

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### ABSTRACT

We have sequenced and analyzed complete mitochondrial genome (mitogenomes) of the *Kamimuria klapaleki*, the third mitochondrial genome in the genus *Kamimuria*, which belongs to the family Pelidae in this paper. The mitogenome of *K. klapaleki* is circular with the length of 16,077 bp, which possessed 37 genes and a control region like other stonefly. The A+T content of the whole mitogenome was 67.1%. All PCGs were 11,217 bp in length, accounting for 65.3% of the content of A+T. The A+T content of lrRNA and srRNA were 72.3% and 66.4%. The highest A+T content was in the control region (76.2%). There are 15 gene overlaps and 9 gene intergenic spacers in this mitochondrial genome. In addition, we performed phylogenetic analysis by using the Bayesian (BI) and Maximum Likelihood (ML) methods based on the concatenated data set of PCGs from 11 species in Pelidae and two species in Styloperlidae (outgroups). The clade *K. chungnanshana* + *K. wangi* was a sister group to *K. klapaleki*, which is consistent with the traditional morphological classification.

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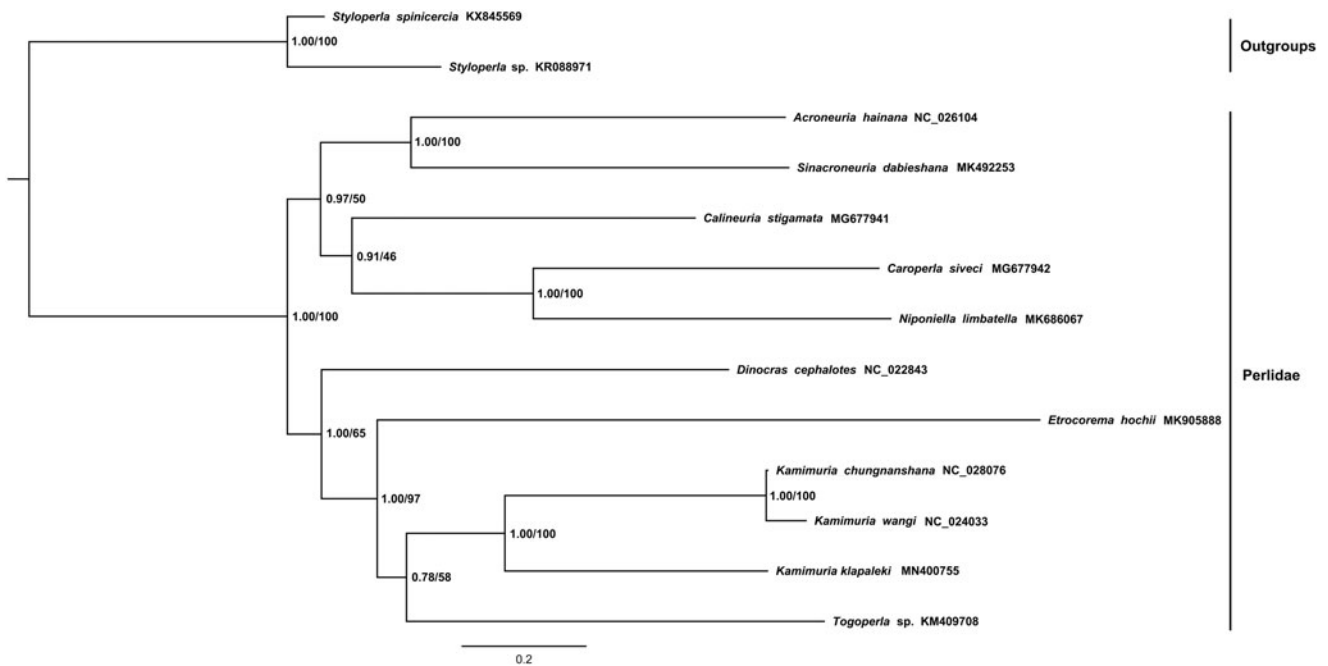
As far as we know, Pelidae is one of the biggest families in order Plecoptera. Most of the perlid are distributed in the north of the earth, while a few are distributed in southern Africa and South America (DeWalt et al. 2019). The genus *Kamimuria* was originally erected by Klapálek, which was treated as a subgenus of genus *Perla* and later elevated it to generic rank (Klapálek 1907, 1912). The mitochondrial genome is used as a useful model for various classification levels in comparative and evolutionary genomics, population genetics and phylogeny in recent years (Lin and Danforth 2004; Gissi et al. 2008; Cameron 2014; Song et al. 2016; Li et al. 2017). So far, there are approximately 80 species in the big genus *Kamimuria* over the whole world (DeWalt et al. 2019), but only two mitochondrial genomes of *K. wangi* and *K. chungnanshana* were reported. In this study, we sequenced *K. klapaleki* which was the third species endemic to China (distributed in Gansu, Sichuan and Xizang) in order to increase the molecular data for the genus *Kamimuria* (Qian et al. 2014; Wang et al. 2016).

The male specimen was collected by Weihai Li and Ying Wang from Longyuwan, Henan Province, China (33.699°N, 111.809°E) on 14 May 2016. The voucher specimen (No. VHL-0040) was preserved in 100% ethanol and stored in the Entomological Museum of the Henan institute of Science and Technology (HIST), Henan Province, China at -20°C till the DNA extraction. The genomic DNA was extracted from the

thorax muscle by using the QIAamp DNA Blood Mini Kit (Qiagen, Hilden, Germany).

The complete mt genome is circular in the length of 16,077 bp with the accession number MN400755, which possessed 37 genes and a control region. The gene arrangement was similar with other stoneflies (Wang et al. 2017, 2018; Wu et al. 2014). The A+T content of the whole mitogenome was 67.1% (A = 35.0%, T = 32.1%, C = 21.2%, G = 11.7%). All PCGs were 11,217 bp in length, accounting for 65.3% of the content of A+T. The length of lrRNA and srRNA was 1380 bp and 837 bp with the A+T content 72.3% and 66.4%, respectively. The highest A+T content was in the control region (76.2%). There are 15 gene overlaps with a total of 49 bp and genes overlapped from 1 to 8 bp. The gene intergenic spacers also existed (from 1 to 26 bp) in nine locations.

Maximum-likelihood (ML) and Bayesian inference (BI) phylogenetic analyses were performed on the concatenated data of PCGs from 11 species in Pelidae and two styloperlid (*Styloperla* sp. and *Styloperla spinicercia* as the outgroups) in Figure 1. The two methods provided the same tree topology which is consistent with the traditional morphological classification (Uchida and Isobe 1989; Zwick 2000). The result showed that the clade *K. chungnanshana* + *K. wangi* had a closer relationship with *K. klapaleki* and the monophyly of genus *Kamimuria* was recovered. We hope our data will be useful for further research.



**Figure 1.** Phylogenetic analyses of *Kamimuria klapaleki* based on the 13 protein-coding genes. The NCBI accession number for each species is indicated after the scientific name.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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