The complete mitochondrial genome of Gyrodactylus gurleyi (Platyhelminthes: Monogenea)

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**MITOGENOME ANNOUNCEMENT**

**The complete mitochondrial genome of *Gyrodactylus gurleyi* (Platyhelminthes: Monogenea)**

Hong Zou\(^a\), Dong Zhang\(^a\)\(^b\), WenXiang Li\(^a\), Shun Zhou\(^a\)\(^b\), ShanGong Wu\(^a\) and GuiTang Wang\(^a\)

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**ABSTRACT**

*Gyrodactylus gurleyi* was collected on the fins and gills of goldfish (*Carassius auratus*), which belonged to the family Gyrodactylidae. In this study, we sequenced the complete mitochondrial genome of *G. gurleyi* with the total length of 14 771 bp. The mitogenome contained 12 protein-coding genes (PCGs), 22 tRNA genes, two rRNA genes and two major non-coding regions (NC1 and NC2). The overall AT content was 72.1%. In phylogenetic analysis, *G. gurleyi* and *G. kobayashii* clustered together and then united with the clade of other three *Gyrodactylus* species (*G. salaris, G. thymalli* and *G. derjavinoides*) with high nodal support.

**KEYWORDS**

Gyrodactylus gurleyi; Gyrodactyliidae; mitochondrial genome; phylogenetics

*Gyrodactylus gurleyi* was collected on the fins and gills of goldfish (*Carassius auratus*) from Wuhan (30°31’23”N, 114°23’01”E), China. It was identified by morphology and ITS molecular marker (Li et al. 2013). The specimen (accession no. IHB20150315006) was stored in the Museum of Aquatic Organisms, Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan, China. The sequences of total mt genomic DNA of *G. gurleyi* were retrieved using long PCR and Sanger method of DNA sequencing.

The complete mt genome of *G. gurleyi* was circular and 14 771 bp in size (GenBank accession no. KU659806). It contained 12 protein-coding genes (PCGs, lacking Atp8), 22 tRNA genes, two rRNA genes and two major non-coding regions (NC1 and NC2) (Table 1). All the genes were transcribed from the same strand. The nucleotide composition was computed at 29.2%A, 42.9% T and 11.1% C. The AT content of 72.1% was lower than that of *Paragyrodactylus variegatus* (76.3%), but higher than that of other four *Gyrodactylus* species (*G. salaris*, 62.3%; *G. thymalli*, 62.8%; *G. derjavinoides*, 68.2%; *G. kobayashii*, 71.6%) (Huyse et al. 2007; Plaisance et al. 2007; Huyse et al. 2008; Perkins et al. 2010; Ye et al. 2014; Zhang et al. 2014a, 2014b, 2016). In addition, there were 37 bp overlapping sequences and 1763 space sequences, among which the biggest were NC1 (783 bp) and NC2 (783 bp).

Phylogenetic relationships between *G. gurleyi* and other nine monopisthocotyleans were inferred by using concatenated amino acid sequences of the 12 PCGs. The same tree topology was obtained by two different computational algorithms: Bayesian inference (BI) and maximum likelihood (ML), in which *G. gurleyi* and *G. kobayashii* clustered together and then united with the clade of 3 *Gyrodactylus* species (*G. salaris, G. thymalli* and *G. derjavinoides*) with high nodal support (Figure 1). In addition, although *G. gurleyi* and *G. kobayashii* generally parasitized on the same host, sequence alignments showed that 99% (14 623 bp) mitogenome sequence of *G. gurleyi* was covered by that of *G. kobayashii* with only 80%
In contrast, *G. salaris* from Atlantic salmon and *G. thymalli* from grayling share 98% identity with 100% mitogenome alignment coverage.

**Disclosure statement**

The authors report no conflict of interest. The authors alone are responsible for the content and writing of the manuscript.

**Funding information**

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**References**


**Figure 1.** Phylogenetic relationships between *Gyrodactylus gurleyi* and other 9 monopisthocotyleans based on 3044 concatenated amino acid sequences representing 12 mitochondrial protein-coding genes, with *Polyplabris halichoeres* used as an outgroup. The MZhox model for maximum-likelihood analysis and MREV model for Bayes analysis are selected. Scale bar corresponds to the estimated number of substitutions per site. Bootstrap support values in percent units above nodes are displayed as follows: maximum likelihood bootstrap/Bayesian posterior probabilities.

**Table 1.** Organization of the mitochondrial genome of *Gyrodactylus gurleyi*.

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<th>Gene/region</th>
<th>Position</th>
<th>Intergenic codon</th>
<th>Codon</th>
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<th>Stop</th>
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