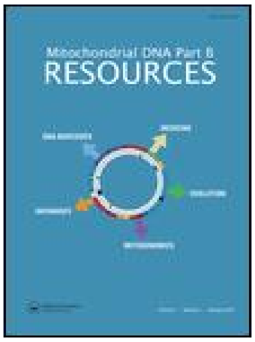

Mitochondrial DNA Part B
Resources

ISSN: (Print) 2380-2359 (Online) Journal homepage: http://www.tandfonline.com/loi/tmdn20

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

Hong Zou, Dong Zhang, WenXiang Li, Shun Zhou, ShanGong Wu & GuiTang Wang

To cite this article: Hong Zou, Dong Zhang, WenXiang Li, Shun Zhou, ShanGong Wu & GuiTang Wang (2016) The complete mitochondrial genome of Gyrodactylus gurleyi (Platyhelminthes: Monogenea), Mitochondrial DNA Part B, 1:1, 383-385, DOI: 10.1080/23802359.2016.1172042

To link to this article: http://dx.doi.org/10.1080/23802359.2016.1172042

MITOCHONDRIAL DNA PART B: RESOURCES, 2016
VOL. 1, NO. 1, 383–385
http://dx.doi.org/10.1080/23802359.2016.1172042

Taylor & Francis
Taylor & Francis Group

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]

[a]Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan, PR China; [b]University of Chinese Academy of Sciences, Beijing, PR China

ABSTRACT

Gyrodactylus gurleyi, was inhabited 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.

ARTICLE HISTORY
Received 2 March 2016
Revised 17 March 2016
Accepted 25 March 2016

KEYWORDS
Gyrodactylus gurleyi; Gyrodagtylidae; 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, 16.9% G, 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; Ye et al. 2014; Zhang et al. 2016).

The length of 12 PCGs was 9942 bp, accounting for 67.3% of the full length of the genome. As the four *Gyrodactylus* species (*G. salaris*, *G. thymalli*, *G. derjavinoides* and *G. kobayashii*), ATG was the unique start codon. The stop codon TAG was only found in three PCGs (*Nad3*, *Nad5* and *Nad6*), whereas TAA in the rest of the PCGs. The size of the 22 tRNA genes was 1374 bp, varying from 58 bp (*tRNA*$^{Ser(AGN)}$) to 71 bp (*tRNA*^{Glu}). Nineteen of them had conventional secondary structure, while *tRNA*$^{Ser(AGN)}$, *tRNA*$^{Ser(UCN)}$ and *tRNA*^{Cys} lacked DHU arms, which was similar to the other known Gyrodactylidae species. The *rrnL* and *rrnS* were 954 bp and 710 bp in size, respectively. They were adjacent to *tRNA*^{Thr} (upstream) and *Cox2* (downstream), and separated by *tRNA*^{Cys}, as described with other reported monopisthocotyleans (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%

CONTACT GuiTang gtwang@ihb.ac.cn Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan 430072, PR China

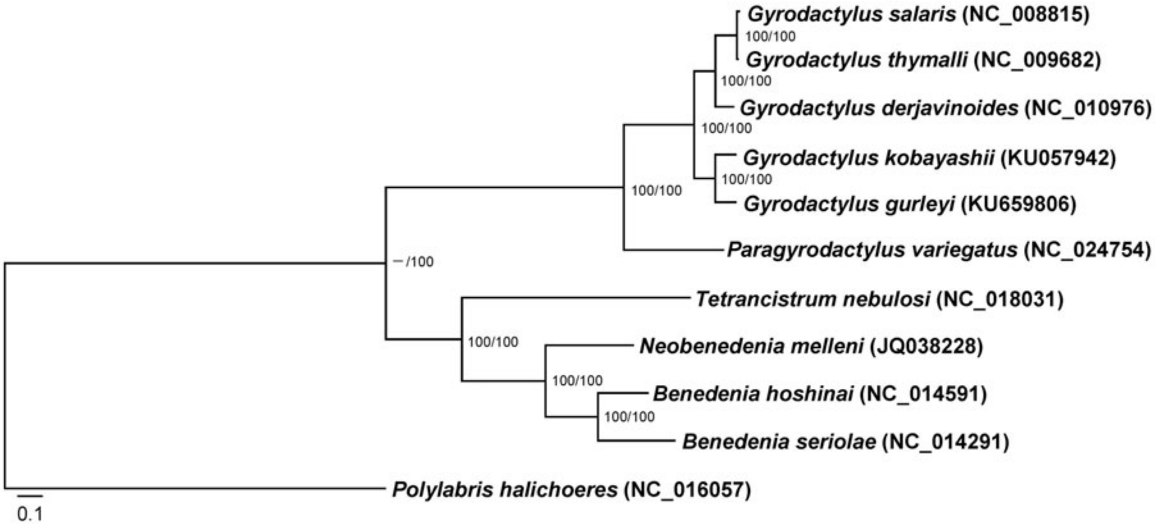

Figure 1. Phylogenetic relationships between *Gyrodactylus gurleyi* and other 9 monopisthocotyleans based on 3044 concatenated amino acid sequences representing 12 mitochondrial protein-coding genes, with *Polylabris halichoeres* used as an outgroup. The MtZoa model for maximum-likelihood analysis and MtREV 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.

identity. In contrast, *G. salaris* from Atlantic salmon and *G. thymalli* from grayling share 98% identity with 100% mitogenome alignment coverage.

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

	Position				Codon		
Gene/region	From	To	Size	Intergenic nucleotides	Start	Stop	Anti-codon
Cox3	1	639	639		ATG	TAA	
tRNA-His	643	707	65	3			GTG
Cytb	711	1784	1074	3	ATG	TAA	
Nad4l	1784	2032	249	−1	ATG	TAA	
Nad4	2005	3213	1209	−28	ATG	TAA	
tRNA-Phe	3216	3281	66	2			GAA
NC1	3282	4064	783				
Atp6	4065	4577	513		ATG	TAA	
Nad2	4587	5444	858	9	ATG	TAA	
tRNA-Val	5449	5513	65	4			TAC
tRNA-Ala	5514	5581	68				TGC
tRNA-Asp	5584	5648	65	2			GTC
Nad1	5649	6536	888		ATG	TAA	
tRNA-Asn	6538	6603	66	1			GTT
tRNA-Pro	6604	6667	64				TGG
tRNA-Ile	6663	6729	67	−5			GAT
tRNA-Lys	6730	6793	64				CTT
Nad3	6797	7144	348	3	ATG	TAG	
tRNA-Ser$^{(AGN)}$(S1)	7145	7203	59				GCT
tRNA-Trp	7207	7271	65	3			TCA
Cox1	7276	8823	1548	4	ATG	TAA	
tRNA-Thr	8836	8900	65	12			TGT
rrnL	8900	9853	954	−1			
tRNA-Cys	9854	9914	61				GCA
rrnS	9915	10,624	710				
Cox2	10,625	11,206	582		ATG	TAA	
tRNA-Glu	11,319	11,389	71	112			TTC
Nad6	11,393	11,875	483	3	ATG	TAG	
tRNA-Tyr	11,884	11,951	68	8			GTA
tRNA-Leu$^{(CUN)}$(L1)	11,954	12,019	66	2			TAG
tRNA-Gln	12,027	12,089	63	7			TTG
tRNA-Met	12,091	12,157	67	1			CAT
NC2	12,158	12,940	783				
tRNA-Ser$^{(UCN)}$(S2)	12,941	12,998	58				TGA
tRNA-Leu$^{(UUR)}$(L2)	12,999	13,066	68				TAA
tRNA-Arg	13,071	13,141	71	4			TCG
Nad5	13,140	14,690	1551	−2	ATG	TAG	
tRNA-Gly	14,702	14,768	67	11			TCC
	14,772	14,771		3			

Disclosure statement

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

Funding information

This work was supported by the Earmarked Fund for China Agriculture Research System (CARS-46-08), the National Natural Science Foundation of China (31272695, 31572658) and the major scientific and technological innovation project of Hubei Province (2015ABA045).

References

Huyse T, Buchmann K, Littlewood DTJ. 2008. The mitochondrial genome of *Gyrodactylus derjavinoides* (Platyhelminthes: Monogenea) – a mitogenomic approach for *Gyrodactylus* species and strain identification. Gene. 417:27–34.

Huyse T, Plaisance L, Webster BL, Mo TA, Bakke TA, Bachmann L, Littlewood DTJ. 2007. The mitochondrial genome of *Gyrodactylus salaris* (Platyhelminthes: Monogenea), a pathogen of Atlantic salmon (*Salmo salar*). Parasitology. 134:739–747.

Li RR, Li WX, Wu XD, Wang GT. 2013. Identification of *Gyrodactylus* species in goldfish (*Carassius auratus*) through morphological study and the analysis of the rDNA ITS sequence. Acta Hydrobiol Sin. 38:903–909.

Perkins EM, Donnellan SC, Bertozzi T, Whittington ID. 2010. Closing the mitochondrial circle on paraphyly of the Monogenea (Platyhelminthes) infers evolution in the diet of parasitic flatworms. Int J Parasitol. 40:1237–1245.

Plaisance L, Huyse T, Littlewood DTJ, Bakke TA, Bachmann L. 2007. The complete mitochondrial DNA sequence of the monogenean *Gyrodactylus thymalli* (Platyhelminthes: Monogenea), a parasite of grayling (*Thymallus thymallus*). Mol Biochem Parasitol. 154:190–194.

Ye F, King SD, Cone DK, You P. 2014. The mitochondrial genome of *Paragyrodactylus variegatus* (Platyhelminthes: Monogenea): differences in major non-coding region and gene order compared to *Gyrodactylus*. Parasit Vectors. 7:377.

Zhang D, Zou H, Zhou S, Wu SG, Li WX, Wang GT. 2016. The complete mitochondrial genome of *Gyrodactylus kobayashii* (Platyhelminthes: Monogenea). Mitochondrial DNA Part B: Resoureces. 1:154–155.

Zhang J, Wu X, Li Y, Xie M, Li A. 2014a. The complete mitochondrial genome of *Tetrancistrum nebulosi* (Monogenea: Ancyrocephalidae). Mitochondrial DNA. 1736:1–2.

Zhang J, Wu X, Li Y, Zhao M, Xie M, Li A. 2014b. The complete mitochondrial genome of *Neobenedenia melleni* (Platyhelminthes: Monogenea): mitochondrial gene content, arrangement and composition compared with two *Benedenia* species. Mol Biol Rep. 41:6583–6589.