The complete mitochondrial genome of *Microphysogobio elongatus* (Teleostei, Cyprinidae) and its phylogenetic implications

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Abstract

Mitochondria are important organelles with independent genetic material of eukaryotic organisms. In this study, we sequenced and analyzed the complete mitogenome of a small cyprinid fish, *Microphysogobio elongatus* (Yao & Yang, 1977). The mitogenome of *M. elongatus* is a typical circular molecule of 16,612 bp in length containing 13 protein-coding genes (PCGs), 22 transfer RNA genes, two ribosomal RNA genes, and a 930 bp control region. The base composition of the *M. elongatus* mitogenome is 30.8% A, 26.1% T, 16.7% G, and 26.4% C. All PCGs used the standard ATG start codon with the exception of COI. Six PCGs terminate with complete stop codons, whereas seven PCGs (*ND2*, *COII*, *ATPase 6*, *COIII*, *ND3*, *ND4*, and *Cyt b*) terminate with incomplete (T or TA) stop codons. All tRNA genes exhibited typical cloverleaf secondary structures with the exception of tRNA^{Ser(AGY)}, for which the dihydrouridine arm forms a simple loop. The phylogenetic analysis divided the subfamily Gobioninae in three clades with relatively robust support, and that *Microphysogobio* is not a monophyletic group. The complete mitogenome of *M. elongatus* provides a valuable resource for future studies about molecular phylogeny and/or population genetics of *Microphysogobio*.

Keywords

Gobioninae, mitogenome, paraphyly

* These authors contributed equally to this work.
Introduction

The genus *Microphysogobio* Mori, 1934, small gudgeons of the subfamily Gobioninae, was originally established by Mori (1934) for *M. hsinglungshanensis* Mori, 1934 (Sun et al. 2021). Currently, this genus comprises approximately 30 species that are widely distributed in East Asia, including China, Vietnam, Mongolia, Laos, and the Korean Peninsula (Jiang et al. 2012; Huang et al. 2016; Huang et al. 2017). The prominent feature of the lip papillae was considered a diagnostic character for defining the genus *Microphysogobio* and distinguishing it from other genera in the subfamily Gobioninae (Yue 1998). Molecular phylogenetic studies of the subfamily Gobioninae has confirmed the monophyletic nature of the Gobioninae (Tang et al. 2011; Zhao et al. 2016). However, the phylogenetic relationships of *Microphysogobio* and related genera have not been fully resolved, and it is a long-standing issue in the classification of Gobioninae.

The typical vertebrate mitogenome is approximately 15–18 kb in length, consisting of 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, two ribosomal RNA (rRNA) genes, and one non-coding control (*D-loop*) region (Wolstenholme 1992; Boore 1999). Mitochondrial genomic DNA has the following characteristics: small size, multiple copies, maternal inheritance, conservative gene products, no introns, fast evolutionary rate, and rare recombination (Boore 1999; Xiao and Zhang 2000). Therefore, it is widely used in species identification, molecular evolution, and phylogenetic studies (Imoto et al. 2013; Sharma et al. 2020). Historically, several genes on the mitochondrial genome, such as *Cyt b* gene and *D-loop* (Wang et al. 2002; He and Chen 2006) were used to study the evolutionary relationships. More recently, with advances in sequencing technology and data analysis methods, information on fish mitochondrial genomes has been accumulating in public databases (Miya and Nishida 2000; Miya et al. 2003; Saitoh et al. 2006; Yamanoue et al. 2007; Kim et al. 2009).

*Microphysogobio elongatus* (Yao & Yang, 1977) is a small, benthic, freshwater fish which is widely distributed in China (Yue 1998; Wang 2019). However, little is known regarding *M. elongatus*, with previous studies focusing on resources investigation and taxonomy (Li et al. 2012; Liu et al. 2013; Zhang et al. 2018). In this study, we sequenced, annotated, and characterized the complete mitochondrial genome of *M. elongatus*. Additionally, we reconstructed the mitogenomic phylogeny of Gobioninae, involving 103 species and subspecies based on 13 PCGs to confirm the taxonomic status of *M. elongatus* and its relationships within Gobioninae.

Materials and methods

Ethics statements

For field collection, no specific permissions are required for the collection of gobionine fishes from public areas. The field collections did not involve endangered or protected species, and the collection site is not a protected area.
Sample collection and DNA extraction

Individuals of *M. elongatus* were collected from Jiangkou County, Guizhou Province, China (27°46'12"N, 108°46'56"E), in August 2019. The specimens were preserved in 95% ethanol and stored at –20 °C until DNA extraction. Genomic DNA was extracted using a standard high-salt method (Sambrook et al. 1989). The integrity of the genomic DNA was measured by 1% agarose gel electrophoresis, and the concentration and purity of DNA were determined using an Epoch 2 Microplate Spectrophotometer (BioTek Instruments, Inc., Vermont, USA).

PCR amplification and sequencing

The entire mitogenome of *M. elongatus* was amplified in overlapping PCR fragments by 14 primer pairs designed from the mitogenome of *M. kiatingensis* (GenBank accession number NC_037402) by Primer Premier v. 5.0 software (Lalitha 2000). The primers used in this study are provided in Suppl. material 1: Table S1. Each PCR reaction was carried out in 35 μL total volume, containing 17.5 μL of 2×Taq Plus Master-Mix (CoWin Biosciences, Beijing, China), 1 μL of each primer (10 μM) and 1.0 μL of template DNA (100 ng). The PCR reactions were performed under the following conditions: an initial pre-denaturation at 95 °C for 5 min, 35 cycles of 95 °C for 30 s, 42–55 °C for 30 s, 72 °C for 1–2 min, and a final extension at 72 °C for 10 min. Amplification products were fractionated by electrophoresis through 1% agarose gels. The lengths of fragments were determined by comparison with the DL2000 DNA marker (TaKaRa, Japan). The PCR products were sequenced by ABI PRISM 3730 (Sangon Biotech. Co., Ltd, China).

Mitogenome annotation and sequence analysis

The mitogenome was initially assembled by the SeqMan software of DNASTar (DNASTAR Inc., Madison, WI, USA), then manually proofread based on sequencing peak figures. The assembled mitogenome sequence was subsequently annotated using MitoAnnotator on the MitoFish homepage (Iwasaki et al. 2013). All tRNA genes were identified with tRNAscan-SE search server (Lowe and Chan 2016) and MITOS WebServer (Bernt et al. 2013). The base composition, codon usage, and relative synonymous codon usage (RSCU) of all PCGs were calculated using MEGA v. 6.0 (Tamura et al. 2013). Strand asymmetry was calculated using the following formulae: AT-skew = (A – T) / (A + T) and GC-skew = (G – C) / (G + C) (Perna and Kocher 1995).

Phylogenetic analysis

For phylogenetic analysis, 103 gobionine fishes were downloaded from GenBank. Additionally, *Acheilognathus omeiensis* (NC_037404.1), *Rhodeus ocellatus* (NC_011211.1), and *R. sinensis* (NC_022721.1) were used as outgroups. Species
Results and discussion

Genome organization and nucleotide composition

The complete mitochondrial genome of *M. elongatus* was first reported and analyzed in this study. The full length of the *M. elongatus* mitochondrial genome sequence had 16,612 bp. The complete mitochondrial genome of *M. elongatus* was annotated and submitted to GenBank (GenBank accession number MN832777). It consisted of 13 PCGs, 22 tRNA genes, two rRNA genes, and one control region (Fig. 1; Table 1). All mitochondrial genes were encoded on the heavy strand (H strand), except the ND6 gene and eight tRNAs (Table 1). The arrangement and content of these genes were conserved and typical of *Microphysogobio* mitochondrial genomes (Hwang et al. 2014; Lin et al. 2014; Cheng et al. 2015). The *M. elongatus* mitogenome contained a total of 21 bp overlapping regions which were in six pairs of neighboring genes, ranging from 1 to 7 bp in length. The longest overlapping region (7 bp) was located between ATP8 and ATP6, ND4L and ND4. A total of 65 bp intergenic nucleotides (IGN) were dispersed in 13 locations, ranging from 1 to 31 bp in length (Table 1). The longest intergenic spacer was located between tRNA^Asn^ and tRNA^Cys^; these overlapping and intergenic regions are very common in fish mitochondrial genomes (Zhang and Wang 2018; Wang et al. 2020).

The nucleotide composition of the *M. elongatus* mitogenome was as follows: 30.8% A, 26.1% T, 16.7% G, and 26.4% C, and were slightly (56.9%) A+T rich (Table 2). In addition, the A+T contents of PCGs, rRNAs, and tRNAs were also slightly A+T rich (Table 2). Compared to the entire mitogenome, the control region, known as an A+T
Table 1. Mitochondrial genome organization of Microphysogobio elongatus.

| Gene         | Strand | Position | Length (bp) | Intergenic nucleotide | Anticodon | Codon Start | Codon Stop |
|--------------|--------|----------|-------------|-----------------------|-----------|-------------|------------|
| tRNA-Phe     | H      | 1-69     | 69          | 0                     | GAA       | ATG         | TAG        |
| tRNA-Ile     | H      | 70-1029  | 960         | 0                     | TCP       | ATG         | TA-        |
| tRNA-Val     | H      | 1030-1101| 72          | 0                     | TAC       | ATG         | TA-        |
| tRNA-Leu(UUR)| H      | 1102-2793| 1692        | 0                     | TAA       | ATG         | TAG        |
| ND1          | H      | 2794-2869| 76          | 1                     | TAA       | ATG         | TAG        |
| tRNA-Trp     | H      | 2871-3845| 975         | 4                     | ATG       | ATG         | TAG        |
| tRNA-Asn     | L      | 3850-3921| 72          | -2                    | GAT       | ATG         | TA-        |
| tRNA-Gln     | L      | 3920-3990| 71          | 1                     | TTG       | ATG         | TAG        |
| tRNA-Met     | H      | 3992-4060| 69          | 0                     | CAT       | ATG         | TAG        |
| ND2          | H      | 4061-5106| 1046        | 0                     | ATG       | ATG         | TAG        |
| tRNA-Trp     | H      | 5107-5177| 71          | 2                     | TCA       | ATG         | TA-        |
| tRNA-Asn     | L      | 5180-5248| 69          | 1                     | TGC       | ATG         | TA-        |
| tRNA-Gln     | L      | 5250-5322| 73          | 31                    | GTT       | ATG         | TA-        |
| tRNA-Cys     | L      | 5354-5421| 68          | 2                     | GCA       | ATG         | TA-        |
| tRNA-Tyr     | L      | 5424-5493| 70          | 1                     | GTA       | ATG         | TAG        |
| COI          | H      | 5495-7045| 1551        | 0                     | GTG       | ATG         | TAG        |
| tRNA-Ser(UCN)| L      | 7046-7116| 71          | 3                     | TGA       | ATG         | T-         |
| tRNA-Asp     | H      | 7120-7191| 72          | 13                    | GTC       | ATG         | TA-        |
| COII         | H      | 7205-7895| 691         | 0                     | ATG       | ATG         | T—         |
| tRNA-Lys     | H      | 7896-9791| 76          | 1                     | TTT       | ATG         | T—         |
| ATPase 8     | H      | 7973-8137| 165         | -7                    | ATG       | ATP         | T—         |
| ATPase 6     | H      | 8131-8313| 683         | 0                     | ATP       | ATP         | T—         |
| COIII        | H      | 8814-9597| 784         | 0                     | ATG       | ATP         | T—         |
| tRNA-Gly     | H      | 9598-9669| 72          | 0                     | TCC       | ATG         | TA-        |
| ND3          | H      | 9670-10019| 350       | 0                     | ATG       | ATG         | TA-        |
| tRNA-Arg     | H      | 10020-10088| 69      | 0                     | TCG       | ATG         | TA-        |
| ND4L         | H      | 10089-10385| 297     | -7                    | ATG       | ATG         | TA-        |
| ND4          | H      | 10379-11760| 1381    | 0                     | ATG       | ATG         | TA-        |
| tRNA-His     | H      | 11761-11829| 69      | 0                     | GTG       | ATG         | TA-        |
| tRNA-Ser(AGY)| H      | 11830-11898| 69       | 1                     | GCT       | ATG         | T—         |
| tRNA-Leu(CUN)| H      | 11900-11972| 73       | 0                     | TAG       | ATG         | T—         |
| ND5          | H      | 11973-13808| 1836    | -4                    | ATG       | ATG         | TAG        |
| ND6          | L      | 13805-14326| 522     | 0                     | ATG       | ATG         | TAG        |
| tRNA-Glu     | L      | 14327-14395| 69       | 5                     | TTC       | ATG         | TA-        |
| Cyt b        | H      | 14401-15541| 1141    | 0                     | ATG       | ATG         | T—         |
| tRNA-Thr     | H      | 15542-15613| 72      | -1                    | TGT       | ATG         | T—         |
| tRNA-Pro     | L      | 15613-15682| 70      | 0                     | TGG       | ATG         | T—         |
| D-loop       | H      | 15683-16612| 930    | 0                     | ATG       | ATG         | T—         |

rich region, contained the highest A+T content (68.1%) (Table 2). The skew statistics revealed a positive AT-skew and a negative GC-skew across the whole mitogenome (Table 2), indicating a bias toward As and Cs.

**Protein-coding genes and codon usage**

The 13 PCGs were 11,423 bp in total length. The longest PCG was 1836 bp (ND5), and the shortest was 165 bp (ATP8) (Table 1). The average base composition of the 13 PCGs were as follows: 28.7% A, 28.2% T, 16.2% G, and 26.9% C (Table 2). All PCGs were initiated with the typical ATG codon except COI with GTG as its initiator codon. Six PCGs (ND1, COI, ATPase 8, ND4L, ND5, and ND6) terminated with a
complete stop codon. The others terminated with an incomplete stop codon TA- or T—, which would be completed as TAA by post-transcriptional polyadenylation at the 3′ end of the mRNA (Ojala et al. 1981).

The relative synonymous codon usage (RSCU) values of the 13 PCGs were analyzed and shown in Suppl. material 5: Fig. S5 and Suppl. material 3: Table S3. The total number of codons, excluding termination codons, in the 13 PCGs was 3808 (Suppl. material 3: Table S3). Among them, CUA, AUU, and UUA were most frequent. Seven codons (AAG, UCG, AGG, AGA, CGC, CGU, and GCG) were rarely represented. Furthermore, the three most frequent amino acids were Leu, Ser, and Ile (Suppl. material 6: Fig. S6).

### Transfer and ribosomal RNAs

The mitogenome of *M. elongatus* contains 22 tRNAs, which were interspersed across the circular genome, ranging from 68 bp (tRNA\textsubscript{Cys}) to 76 bp (tRNA\textsubscript{Leu(UUR)} and tRNA\textsubscript{Lys}) in length (Table 1). The secondary structure of all tRNA sequences were predicted and the results showed they are capable of folding into typical cloverleaf secondary structures except for tRNA\textsubscript{Ser(AGY)}, in which the dihydrouridine (DHU) arm did not form a stable structure (Suppl. material 7: Fig. S7). This unique secondary structure has been commonly witnessed in many other fishes (Zhang and Wang 2018; Zhong et al. 2018). The average base composition of the tRNAs was 28.4% A, 26.9% T, 23.5% G, and 21.2% C (Table 2).

The 12S rRNA and 16S rRNA were the only two ribosomal genes in the mitogenome of *M. elongatus*. They were 960 bp and 1692 bp in length, respectively (Table 1). Similar to other fishes (Broughton et al. 2001; Zhang and Wang 2018), the 12S rRNA and 16S rRNA were located between tRNA\textsubscript{Phe} and tRNA\textsubscript{Val}, and between tRNA\textsubscript{Val} and tRNA\textsubscript{Leu(UUR)}, respectively (Table 1). Their average base composition was as follows: 34.2% A, 20.0% T, 21.2% G, and 24.6% C. The average A + T content of both rRNAs was 54.2% (Table 2). The lengths and A + T content of these two rRNAs were well within the ranges observed in other *Microphysogobio* mitogenomes (Lin et al. 2014; Hwang et al. 2014; Cheng et al. 2015).

### Mitochondrial control region

The mitochondrial control region (CR), or *D-loop*, is responsible for replication and transcription of the mitogenome (Boore 1999). The CR of *M. elongatus* was 930 bp

### Table 2. Nucleotide composition of the *Microphysogobio elongatus* mitochondrial genome.

|                     | Length(bp) | A%  | T%  | G%  | C%  | A+T% | AT-skew | GC-skew |
|---------------------|------------|-----|-----|-----|-----|------|---------|---------|
| Genome              | 16612      | 30.8 | 26.1 | 16.7 | 26.4 | 56.9 | 0.081   | -0.226  |
| PCGs                | 11423      | 28.7 | 28.2 | 16.2 | 26.9 | 56.9 | 0.009   | -0.249  |
| 1\textsuperscript{st} codon position | 3808      | 27.7 | 29.6 | 16.0 | 26.7 | 57.3 | -0.032  | -0.251  |
| 2\textsuperscript{nd} codon position | 3808      | 30.1 | 27.5 | 14.5 | 27.9 | 57.6 | 0.045   | -0.318  |
| 3\textsuperscript{rd} codon position | 3807      | 28.3 | 27.4 | 18.2 | 26.1 | 55.7 | 0.016   | -0.179  |
| rRNA                | 2652       | 34.2 | 20.0 | 21.2 | 24.6 | 54.2 | 0.261   | -0.073  |
| tRNA                | 1562       | 28.4 | 26.9 | 23.5 | 21.2 | 55.3 | 0.028   | 0.052   |
| \textit{D-loop} region | 930       | 34.2 | 33.9 | 13.3 | 18.6 | 68.1 | 0.005   | -0.165  |
The mitochondrial genome of *Microphysogobio elongatus*

in length and located between tRNA$_{\text{Phe}}$ and tRNA$_{\text{Pro}}$. Multiple homologous sequence alignment revealed three conserved structures (termination-associated sequence (TAS), central conserved sequence blocks (CSB-F, CSB-E, and CSB-D) and conserved sequence blocks (CSB-1, CSB-2, and CSB-3)) within the CR (Suppl. material 8: Fig. S8), as seen in most fish mitogenomes (Broughton et al. 2001; Zhang and Wang 2018).

**Figure 1.** Circular map of the M. elongatus mitogenome.

**Mitochondrial phylogeny within Gobioninae**

We reconstructed the phylogenetic tree of gobionine fishes based on the 13 concatenated protein-coding genes. The optimal partitioning scheme for the dataset and the best-fitting substitution model for each partition were provided in Suppl. material 4: Table S4. The trees resulting from the BI and ML analyses showed a consensus topology, and
the only differences were the Bayesian posterior probabilities and ML bootstrap values (Fig. 2, Suppl. material 9: Fig. S9). The phylogenetic analysis revealed that Gobioninae could be separated into three clades (Tribe Sarcocheilichthyini, Tribe Gobionini and Hemibarbus-Squalidus group) with Squalidus gracilis majimae excluded (Fig. 2), which was consistent with previous phylogenetic studies (Tang et al. 2011; Zhao et al. 2016).

The Hemibarbus-Squalidus group includes Belligobio, Hemibarbus, and Squalidus (BS = 99%, PP = 100%). The Hemibarbus-Squalidus group was located at the basal position Gobioninae in the phylogenetic tree. This confirmed morphology-based hypothesis that Hemibarbus and Belligobio might represent the primitive group of Gobioninae (Bănărescu 1992). Hemibarbus and Belligobio were similar in morphological, and therefore, Bănărescu and Nalbant (1973) assigned Belligobio as a subgenus of Hemibarbus. The phylogenetic tree of Gobioninae subfamily based on single gene confirmed the close relationship of Squalidus to Hemibarbus (Yang et al. 2006; Liu et al. 2010; Tang et al. 2011). Nonetheless, the phylogenetic tree suggests that the classification of S. g. majimae should be further revised.

The tribe Gobioninae includes Gobiobotia, Xenophysogobio, Saurogobio, Pseudogobio, Platysmacheilus, Biwia, Microphysogobio, Romanogobio, Abbottina, Acanthogobio, Gobio, and Ladislavia (BS = 85%, PP = 97%). Within the group, Ladislavia taczanowskii was at the basal position. The phylogenetic tree from mtDNA supported Ladislavia should be included in the Gobioninae group (Tang et al. 2011). Bănărescu and Nalbant (1973) highlighted that Acanthogobio seemed to be a morphologically derived species of Gobio, as confirmed in our study. Microphysogobio is not monophyletic because of the placement of Biwia, Romanogobio, and Platysmacheilus which are found nested within Microphysogobio; this is in accordance with previous studies based on mitochondrial and nuclear genes (Yang et al. 2006; Tang et al. 2011). In morphology, P. exiguous and Microphysogobio showed similar characteristics that were a single row of dentition, with indicated that the evolutionary process was the decreasing number of teeth rows (Yu and Liu 2011). The taxonomic status of Microphysogobio remains uncertain because its putative member species were found to be broadly polyphyletic.

The tribe Sarcocheilichthyini includes Coreius, Coreoleuciscus, Gnathopogon, Paracanthobrama, Gobiocypris, Pungtungia, Pseudopungtungia, Pseudorasbora, Rhinogobio, and Sarcocheilichthys (BS = 86%, PP = 100%). Based on our trees, Pungtungia herzi was assigned to Pseudopungtungia, and a grouping like this has been proposed in an earlier study (Kim et al. 2013). Our results and a previous study by Kim et al. (2013) suggested an unstable taxonomic status of the Pseudopungtungia genus, which is polyphyletic. The placement of Gobiocypris within the Gnathopogon gives support to Gobiocypris as a subgenus of Gnathopogon (Tang et al. 2011). Moreover, we found that Paraleucogobio was also included in Gnathopogon, so we speculated that Paraleucogobio might also be a subgenus of Gnathopogon. Surprisingly, the phylogenetic tree showed that Sarcocheilichthys biwaensis and S. variegatus microculus had almost non-existent branch lengths. Komiya (2014) et al. suggested multiple colonization events of Lake Biwa by S. biwaensis and S. v. microculus and confirmed the rapid speciation of S. biwaensis from an ancestral S. v. microculus form. Therefore, we surmise that S. biwaensis
and *S. v. microoculus* probably have mitochondrial introgression. Introgressive hybridization was not rare between closely related species (Yang et al. 2006).

Several monophyletic clades of *Coreius*, *Coreoleuciscus*, *Pseudorasbora*, *Rhinogobio*, *Sarcocheilichthys*, *Gobiobotia*, *Xenophysogobio*, *Saurogobio*, *Pseudogobio*, *Abbottina*, and *Squalidus* were supported (Fig. 2). The monophyletic of *Sarcocheilichthys*, *Rhinogobio*, *Coreius*, *Gobiobotia*, *Saurogobio*, *Pseudogobio*, and *Squalidus* are consistent with the phylogenetic results of Yang et al. (2006) on 44 species of Gobioninae using the mitochondrial *Cyt b*. Our results showed that phylogenetic analyses utilizing mitogenome sequences partially resolved genus- and species-level relationships within Gobioninae. However, extensive taxon sampling is required to completely resolve the relationships within the subfamily Gobioninae.

**Conclusions**

In the present study, we sequenced and described the complete *M. elongatus* mitogenome (16,612 bp) that contains 37 genes and one control region as typical for vertebrate mitogenomes. The characteristics of the newly sequenced mitogenome are mostly consistent with those reported in other *Microphysogobio* mitogenomes. The subfamily Gobioninae was composed of three major lineages, and the phylogenetic trees strongly supported the non-monophyly of *Microphysogobio*. The results of the present study will be useful for further investigation of the evolutionary relationships within Gobioninae.
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**Supplementary material 1**

**Table S1. Primers used for PCR**  
Authors: Renyi Zhang, Qian Tang, Lei Deng  
Data type: molecula data  
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Link: https://doi.org/10.3897/zookeys.1061.70176.suppl1

**Supplementary material 2**

**Table S2. List of species used to construct the phylogenetic tree in the present study**  
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Data type: molecula data  
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Link: https://doi.org/10.3897/zookeys.1061.70176.suppl2

**Supplementary material 3**

**Table S3. Codon usage in the PCGs of the *Microphysogobio elongatus* mitogenome**  
Authors: Renyi Zhang, Qian Tang, Lei Deng  
Data type: molecula data  
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Link: https://doi.org/10.3897/zookeys.1061.70176.suppl3
Supplementary material 4

Table S4. PartitionFinder results
Authors: Renyi Zhang, Qian Tang, Lei Deng
Data type: molecular data
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Supplementary material 5

Figure S1. Relative synonymous codon usage (RSCU) in the M. elongatus mitogenome
Authors: Renyi Zhang, Qian Tang, Lei Deng
Data type: molecular data
Explanation note: Codon families are provided on the X-axis and the RSCU values on the Y-axis.
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Link: https://doi.org/10.3897/zookeys.1061.70176.suppl5

Supplementary material 6

Figure S2. Codon distribution in the M. elongatus mitogenome
Authors: Renyi Zhang, Qian Tang, Lei Deng
Data type: molecular data
Explanation note: CDspT, codons per thousand codons. Codon families are provided on the X-axis.
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Link: https://doi.org/10.3897/zookeys.1061.70176.suppl6
**Supplementary material 7**

**Figure S3. Putative secondary structures of the 22 tRNA genes identified in the mitochondrial genome of *M. elongatus***

Authors: Renyi Zhang, Qian Tang, Lei Deng  
Data type: molecular data  
Explanation note: All tRNA genes are shown in the order of occurrence in the mitochondrial genome starting from tRNA\(^{Phe}\). The tRNAs are labelled with abbreviations of their corresponding amino acid. Dashed lines (-) indicate Watson-Crick base pairings.  
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Link: https://doi.org/10.3897/zookeys.1061.70176.suppl7

**Supplementary material 8**

**Figure S4. Control region of the *M. elongatus* mitochondrial genome**

Authors: Renyi Zhang, Qian Tang, Lei Deng  
Data type: molecular data  
Explanation note: The termination associated sequence domain (TAS), the central conserved domains (CSB-F, CSB-E, CSB-D) and the conserved sequence block domains (CSB-1, CSB-2, CSB-3) are shown in red font, and the conserved sequences are marked by black font and underlined.  
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Link: https://doi.org/10.3897/zookeys.1061.70176.suppl8
Supplementary material 9

Figure S5. Phylogenetic relationships of Gobioninae based on complete mitochondrial genomes using Bayesian analyses
Authors: Renyi Zhang, Qian Tang, Lei Deng
Data type: phylogenetic data
Explanation note: Bayesian posterior probabilities are shown at the nodes.
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Link: https://doi.org/10.3897/zookeys.1061.70176.suppl9