



Sequencing and characterization of complete mitogenome DNA for *Rasbora myersi* (Cypriniformes: Cyprinidae: Rasbora) and its evolutionary significance

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ARTICLE INFO

Keywords:

Rasbora myersi
Mitogenome
Gene arrangement
Light strand origin
Phylogeny

ABSTRACT

The Seluang fish (*Rasbora myersi*) is a small ray-finned fish categorized under the genus *Rasbora* in the Cyprinidae family. In this study, the complete mitogenome sequence of *R. myersi* was sequenced using two primer pairs targeting overlapping regions. The mitogenome is 16,581 bp in length, encompassing 22 transfer RNA genes, 13 protein-coding genes, two ribosomal RNA genes and a putative control region. Identical gene organisation was observed between this species and other genus counterparts. The heavy strand accommodates 28 genes while the light strand houses the other nine genes. Most protein-coding genes utilize ATG as start codon, excluding COI gene, which employs GTG instead. The central conserved sequence blocks (CSB-F, CSB-E and CSB-D), variable sequence blocks (CSB-3, CSB-2 and CSB-1) as well as the terminal associated sequence (TAS) are conserved within the control region. The *R. myersi* formed a trio with *R. borapetensis* and *R. argyrotaenia* in a moderately strong clade with bootstrap value of 86. This work acts as essential gateway towards further molecular evolution and population genetics studies of the *Rasbora* genus in future.

1. Introduction

The *Rasbora myersi* or Seluang fish is one of the members of the genus *Rasbora* under the Cyprinidae family, and it was first described by Brittan (1954). This ray-finned fish species is silvery in colour across both body scales and fins, unlike the bright coloration as seen in other *Rasbora* genus members (Brittan, 1954). *R. myersi* can grow up to full length of 7.3 cm upon adulthood, benthopelagic in nature and inhabiting tropical freshwater streams and peat swamp (Brittan, 1954; Sule et al., 2018). The distribution of this fish species is across South-east Asia including Malaysia and Indonesia (Brittan, 1954).

The *Rasbora* genus where the Seluang fish reside has large heterogeneous freshwater fish variety, earning this genus the title of most species-enriched genus under the family Cyprinidae (Eschmeyer, 2015). The very close morphological characteristics that this *Rasbora* genus members shared are deemed as one of the daunting challenges in taxonomical classifications, and there is no qualms that this group was given a term, the “catch-all” group (Brittan, 1954; Kottelat and Vidthayanon, 1993; Siebert and Guiry, 1996; Kottelat, 2005; Liao et al.,

2010; Tang et al., 2010). Several efforts of classifications in the past (Kottelat and Vidthayanon, 1993; Siebert and Guiry, 1996; Kottelat, 2005; Liao et al., 2010) have been attempted but majority of the researchers in this field still adopt the *Rasbora sensu lato* concept proposed by Brittan (1954) in which eight *Rasbora* species complexes are used. Thus far, the resolution in terms of cryptic diversity of the *Rasbora* genus is still poor due to the lack of research focus onto this genus, both morphologically (Liao et al., 2010) and molecularly (Kusuma et al., 2016).

As mentioned earlier, the advancement of the research onto this *Rasbora* genus is very much on its baby steps with some notable research emerged from the recent years establishing these fishes as ecotoxicological indicators of water pollutions (Wijeyaratne and Pathiratne, 2006; Lim et al., 2018). Furthermore, the mitogenome deposited in the GenBank database only amounted to 16 to date with the inclusion of *R. borapetensis*, *R. aprotaenia*, *R. argyrotaenia*, *R. trilineata*, *R. cephalotaenia*, *R. pauciperforata*, *R. vaterifloris*, *R. sumatrana*, *R. espei*, *R. heteromorpha*, *R. maculata*, *R. steineri*, *R. sarawakensis*, *R. lateristriata*, *R. daniconius* and *R. hobelmami* (Miya, 2009; Tang et al., 2010; Chang

Abbreviations: PCR, polymerase chain reaction; L-strand, light strand; H-strand, heavy strand

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<https://doi.org/10.1016/j.genrep.2019.100499>

Received 24 May 2019; Received in revised form 12 August 2019; Accepted 2 September 2019

Available online 03 September 2019

2452-0144/ © 2019 Published by Elsevier Inc.