

Complete mitochondrial genome of nearly threatened freshwater ornamental fish, *Microphis deocata* and its phylogenetic relationship within Syngnathidae

Lakshman Sahoo^a, Ashoktaru Barat^a, Paramananda Das^a, Bismay Sahoo^a, Gargee Das^a, Jitendra. K. Sundaray^a, Sangram K. Sahoo^a, Saroj K. Swain^a, Khuntia Murmu^a and Dandadhar Sarma^b 

^aFish Genetics and Biotechnology Division, ICAR – Central Institute of Freshwater Aquaculture, Bhubaneswar, India; ^bDepartment of Zoology, Gauhati University, Guwahati, India

ABSTRACT

Microphis deocata (deocata pipefish), belonging to family Syngnathidae, is one of the important indigenous ornamental fish species listed as near threatened in the IUCN red list. Here, we first report the complete mitochondrial genome of deocata pipefish using Illumina next-generation sequencing platform. The total length of the mitogenome is 16,526 bp. It encompasses 13 protein coding genes, 2 ribosomal rRNAs, and 22 tRNAs. The WANCY region (a cluster of five tRNA genes) contains the 50 bp O_L light strand origin of replication. Phylogenetic analysis of Syngnathidae revealed *M. deocata* to cluster with *Oostethus manadensis*, forming a sister group with *Doryrhamphus japonicas* and *Dunckerocampus dactyliophorus*. The mitochondrial genome sequence data generated in the present study will play an important role in population genetic analysis and developing conservation strategies for this species.

ARTICLE HISTORY

Received 28 July 2020
Accepted 7 October 2020

KEYWORDS

Mitochondrial genome; Deocata; NGS; protein coding genes; phylogenetics; Syngnathidae

Introduction

Microphis deocata, popularly known as Indian royal green pipefish or rainbow belly pipefish or deocata pipefish, is a freshwater fish species belonging to the family Syngnathidae. The Syngnathids differ from other vertebrates by exhibiting 'male pregnancy' (Stölting and Wilson 2007). They have an extended body covered with armour of bony plates in place of scales, elongated snout and fused jaws (Wang et al. 2019). Due to specialized morphology, the fish is a popular aquarium fish with enormous demand. This has resulted in a decline in its population due to over exploitation. Now, the species is listed in the IUCN red list (<https://www.iucnredlist.org/species/168512/67623942>). Here, we first report the complete mitogenome of *M. deocata* and performed phylogenetic analysis among Syngnathidae species (27 species, 12 genera) available in the GenBank database. Fin sample of *M. deocata* (MD01) was collected from Narayanguri, Assam, India (GPS Coordinates: 90°59'43.2" E and 26°39'63.0" N) during September 2018 and kept in fish genomics laboratory of ICAR – Central Institute of Freshwater Aquaculture, Bhubaneswar, India. High molecular weight genomic DNA was isolated and the complete mitogenome of *M. deocata* was obtained by sequencing the DNA using Illumina Nextseq500 platform. A maximum likelihood (ML) tree based on the concatenated supergene consisting of 13 mitochondrial protein-coding genes was constructed using MEGAX.

The *M. deocata* mtDNA genome was 16,526 bp (Accession No. MT230531) in length and circular in shape. It contained 13

protein-coding genes (PCG), 22 tRNAs, 2 ribosomal RNAs and a putative control region. The arrangements of genes were identical to a typical vertebrate mitochondrial genome (Boore 1999; Bej et al. 2012; Sahoo et al. 2016). Like other vertebrate mitochondrial genome, the initiation codon for all 13 PCGs was ATG except *COI* where it was GTG. Most of the PCGs had TAA stop codon whereas ND2, COII, ND3, ND4, and Cytb had an incomplete stop codon T. In total, 11 intergenic regions with 21 bp were observed and 8 overlapping regions with 43 bp were observed as reported earlier (Yang et al. 2017).

Two non-protein coding ribosomal genes, 12s rDNA and 16s rDNA were of 942 bp and 1637 bp, respectively. Length of 22 tRNA genes ranged from 66 bp (tRNA-Cys) to 74 bp (tRNA-Leu). The WANCY region contained the 50 bp O_L light strand origin of replication, suggesting to play an important role in regulating light strand replication (Wong et al. 1983; Boore 1999). The control region (CR) or D-loop, the major non-coding region and commonly located between tRNA-Pro and tRNA-Phe genes, was 912 bp in length. As observed in other vertebrate mitogenomes, the CR of *M. deocata* contained similar conserved sequence blocks, including TAS, the central conserved sequence blocks (CSB-F, D, B and A) and conserved sequence blocks (CSB-2 and 3) (Wang et al. 2017).

Based on the concatenated supergene using 13 PCGs from 27 Syngnathidae species (12 genera), a maximum likelihood phylogenetic tree (Figure 1) was constructed by taking *Oryzias latipes* as an out group. In the present study, *M. deocata* clustered with *M. manadensis* (*Oostethus manadensis*),

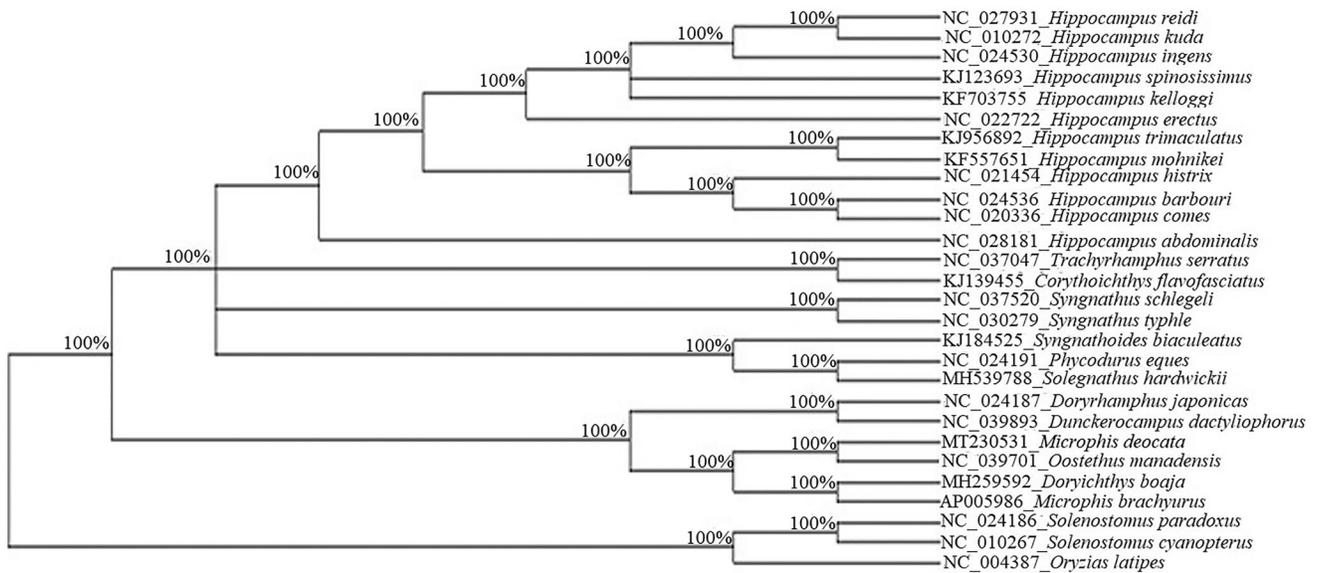


Figure 1. Phylogenetic tree of 27 Syngnathids based on 13 protein-coding genes.

forming a sister group with *Doryrhamphus japonicas* and *Dunckerocampus dactyliophorus*. As observed by Wang et al. (2019), *M. brachyurus* clustered with *Doryichthys boaja*. The sequence resource generated in the present study would play an important role in population genetics and developing conservation strategy of this species.

Acknowledgements

The authors are thankful to the Director ICAR-CIFA for providing laboratory facilities.

Disclosure statement

No potential conflict of interest was reported by the author(s).

ORCID

Dandadhar Sarma  <http://orcid.org/0000-0001-9094-7326>

Data availability statement

The data that support the findings of this study are openly available in the GenBank (Accession no. MT230531) at <https://www.ncbi.nlm.nih.gov/nucleotide/1866760761>.

References

- Bej D, Sahoo L, Das SP, Swain S, Jayasankar P, Das PC, Routray P, Swain SK, Jena JK, Das P. 2012. Complete mitochondrial genome sequence of *Catla catla* and its phylogenetic consideration. *Mol Biol Rep.* 39(12): 10347–10354.
- Boore JL. 1999. Animal mitochondrial genomes. *Nucleic Acids Res.* 27: 1767–1780.
- Sahoo L, Swain SK, Bej D, Das SP, Jayasankar P, Das P. 2016. Complete mitochondrial genome sequence of *Labeo fimbriatus* (Bloch, 1975). *mtDNA Part A.* 27(6):4019–4020.
- Stölting KN, Wilson AB. 2007. Male pregnancy in seahorses and pipefish: beyond the mammalian model. *BioEssays.* 29:884–896.
- Wang X, Zhang Y, Zhang H, Qin G, Lin Q. 2019. Complete mitochondrial genomes of eight seahorses and pipefishes (Syngnathiformes: Syngnathidae): insight into the adaptive radiation of syngnathid fishes. *BMC Evol Biol.* 19(1):119.
- Wang Z, Ge Y, Cheng R, Huang Z, Chen Z, Zhang G. 2017. Sequencing and analysis of the complete mitochondrial genome of *Hippocampus spinosissimus* Weber, 1913 (Gasterosteiformes: Syngnathidae). *mtDNA Part A.* 28(3):303–304.
- Wong JFH, Ma DP, Wilson RK, Roe BA. 1983. DNA sequence of the *Xenopus laevis* mitochondrial heavy and light strand replication origins and flanking tRNA genes. *Nucleic Acids Res.* 11(14):4977–4995.
- Yang QH, Lu Z, Zheng LY, Huang ZC, Lin Q, Wu JN, Zhou C. 2017. The complete mitochondrial genome of the Japanese seahorse, *Hippocampus mohnikei* (Syngnathiformes: Syngnathidae) and its phylogenetic implications. *Conserv Genet Resour.* 9(4):613–617.