

The complete mitochondrial DNA sequence of *Pectenocypris* sp. (Actinopterygii: Cyprinidae) from Serkap River, Sumatra, Indonesia

Dwi Atminarso^{a,b}, Arif Wibowo^{a,b}, Wahyu Endra Kusuma^c, Eko Prianto^d, Harald Ahnelt^e, Anti Vasemägi^{f,g} and Yoshinori Kumazawa^h

^aResearch Institute for Inland Fisheries, Agency for Research and Human Resource Development, Ministry of Marine Affairs and Fisheries, Palembang, Indonesia; ^bInland Fishery Resources Development and Management Department, Southeast Asian Fisheries Development Center, Palembang, Indonesia; ^cDepartment of Aquaculture, Faculty of Fisheries and Marine Science, University of Brawijaya, Malang, Indonesia; ^dResearch Center for Fisheries, Agency for Research and Human Resource Development, Ministry of Marine Affairs and Fisheries, Jakarta, Indonesia; ^eDepartment of Theoretical Biology, University of Vienna, Vienna, Austria; ^fDepartment of Biology, Division of Genetics and Physiology, University of Turku, Turku, Finland; ^gInstitute of Veterinary Medicine and Animal Sciences, Estonian University of Life Sciences, Tartu, Estonia; ^hDepartment of Information and Basic Science and Research Center for Biological Diversity, Graduate School of Natural Sciences, Nagoya City University, Nagoya, Japan

ABSTRACT

The whole mitochondrial genome of a small cyprinid freshwater fish *Pectenocypris* sp. collected from Serkap River, Central Sumatra, Indonesia was sequenced. This mitochondrial genome consisted of 16,589 bp and included 37 genes in the same order as in many other vertebrates including the human. Phylogenetic analysis suggested that this taxon clusters with *Boraras maculatus* among several *Rasbora* species.

ARTICLE HISTORY

Received 1 January 2018
Accepted 3 January 2018

KEYWORDS





Phylogenetic tree;
mitochondrial genome;
freshwater fish; Cyprinidae;
Pectenocypris

Pectenocypris (Actinopterygii: Cyprinidae) consists of four known freshwater fish species which are distributed in Sumatra and Borneo Islands: *P. balaena*, *P. korthausae*, *P. micromysticetus* and *P. nigra*. They are phytoplankton filter feeders (Rainboth 1991) but also feed on zooplankton (Kottelat 1982; Roberts 1989). All the species are small in size (<45 mm in standard length) and typically occur in acidic freshwaters. They have slender body, numerous and extraordinary extended gill rakers and a unique shaped lower pharyngeal jaw (Kottelat 1982; Roberts 1989; Tan and Kottelat 2009; Wibowo et al. 2016).

We conducted field survey at freshwaters in Central Sumatra and found possibly new species assignable to *Pectenocypris*. An adult individual of the undescribed *Pectenocypris* species with a standard length 31.1 mm was collected in peat waters of the Serkap River system in the Riau Province near Pelalawan, Central Sumatra (geographic coordinate: 00°34'42"N, 102°39'17"E) in 2013. The whole body specimen was deposited to the Museum Zoologicum Bogoriense (MZB), Bogor under the catalogue number MZB 22148. A small portion of muscle tissue was excised under the dorsal fin and preserved in ethanol for subsequent

DNA extraction by Genomic DNA Mini Kit (Geneaid/ New Taipei City). Mitochondrial DNA was purified by digesting the linear nuclear DNA with the exonuclease V under the Mseek protocol (Jayaprakash et al. 2015) and then sequenced using the NEXTFlex™ Rapid DNA-Seq kit (Bioo Scientific/ Texas) with the Illumina NextSeq platform. This resulted in a single, circular DNA sequence which was then blasted against the Mitofish database (Iwasaki et al. 2013) for the confirmation of a fish mitochondrial DNA.

The complete mitochondrial DNA sequence of *Pectenocypris* sp. thus determined (16,589 bp; INSD database accession number LC337232) consisted of 37 genes for 13 protein subunits, 22 tRNAs, and two rRNAs together with a major non-coding region in the same order as in human (Anderson et al. 1981) and many other vertebrates. All protein genes had an ATG start codon except for the cytochrome oxidase subunit 1, and NADH dehydrogenase subunits 4L and 5 genes, which started with GTG, GTG and ATA, respectively. Seven protein genes were terminated with the TAA stop codon and the remaining six genes required polyadenylation for the establishment of stop codons in mRNAs. All tRNA genes can be folded into the

CONTACT Arif Wibowo  wibowo@daad-alumni.de  Research Institute for Inland Fisheries, Agency for Research and Human Resource Development, Ministry of Marine Affairs and Fisheries and Inland Fishery Resources Development and Management Department/Southeast Asian Fisheries Development Center, Jl. Gubernur H.A Bastari No 08, Palembang 30252, South Sumatera, Indonesia; Yoshinori Kumazawa  kuma@nsc.nagoya-cu.ac.jp  Department of Information and Basic Science and Research Center for Biological Diversity, Graduate School of Natural Sciences, Nagoya City University, Nagoya, Japan

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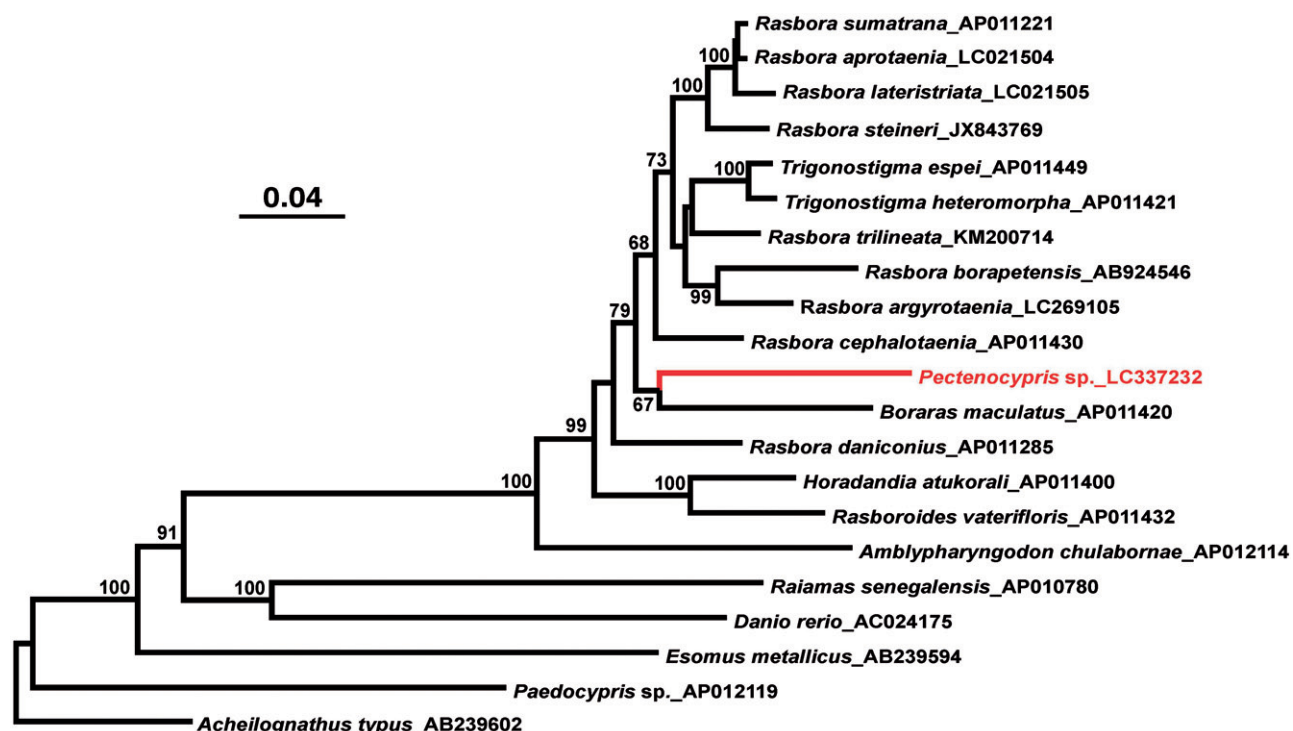


Figure 1. A maximum likelihood tree illustrating the phylogenetic position of *Pectenocypris* sp. among other rasborine cyprinids. The maximum likelihood analysis was conducted using concatenated amino acid sequences of 13 mitochondrial protein genes (3,813 sites) and Garli v2.0 (Zwickl 2017) under the mtREV + IG substitution model. Numbers at each node are bootstrap probabilities by 500 replications shown only when they are 50% or larger. INSD accession numbers of mitogenomic sequences for each taxon are shown along with the taxon name.

standard cloverleaf secondary structures (Kumazawa and Nishida 1993).

This is the first complete mitochondrial genome sequence from genus *Pectenocypris*. The phylogenetic tree (Figure 1) suggested that *Rasbora* is not monophyletic in relation to genera *Trigonostigma*, *Pectenocypris*, and *Boraras*, which is in agreement with earlier molecular studies (Rüber et al. 2007; Britz et al. 2009; Tang et al. 2010). It was also suggested that contrary to the earlier work (e.g. Tang et al. 2010) *Pectenocypris* sp. is more closely related to *Boraras maculatus* (dwarf rasbora) than to other rasborine cyprinids examined although the bootstrap probability for this relationship was not very high (67%; Figure 1).

Acknowledgements

We thank Drs. Satoshi Honda and Kaoru Ishii of Inland Fisheries Resources Development and Management Department (IFRDMD) and Southeast Asian Fisheries Development Center (SEAFDEC), and Mr. Atsushi Saga and Ms. Yo Soma of Marino Forum 21 for providing and arranging the SEAFDEC short-term training for DA at Nagoya City University. Our gratitude is extended to the Laboratory of Molecular Ecology of Research Institute for Inland fisheries where a part of our molecular analysis was done.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

Funding

This work was supported by the Research Institute for Inland Fisheries through DIPA 2013.

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