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Complete mitochondrial genomes of the smooth tail nine-spined sticklebacks *Pungitius laevis* (Gasterosteiformes, Gasterosteidae)

Baocheng Guo, Takahito Shikano, Cui Wang and Juha Merilä

Department of Biosciences, Ecological Genetics Research Unit, University of Helsinki, Helsinki, Finland

ABSTRACT
The complete mitochondrial genome sequences of three divergent lineages of the smooth tail nine-spined stickleback (*Pungitius laevis*) were obtained with massive parallel sequencing of their genomic DNA. The genome sequences were 16,574–16,580 bp long, and the gene order and contents were identical to those of other sequenced *Pungitius* mitogenomes. Although the mitogenome sequences of all three *P. laevis* lineages clustered within the genus *Pungitius*, they were clearly distinct and showed divergence comparable to that seen between some *Pungitius* species.

The taxonomic status and phylogenetic positioning of the smooth tail nine-spined stickleback *Pungitius laevis* has been the subject of considerable debate over the past decades (Münzing 1969; Gross 1979; Keivany & Nelson 2000). While some treatments considered it to be a subspecies of the nine-spined stickleback *P. pungitius* (Keivany & Nelson 2000), others have classified it as a taxonomically valid and independent species (Kottelat & Freyhof 2007). A recent study based on partial mitochondrial DNA (mtDNA) fragments revealed the existence of three highly distinct mtDNA lineages within *P. laevis* and suggested that they have diverged 1.4–2.0 Mya (Wang et al. 2015). Access to full mtDNA should help to further clarify the evolutionary history and phylogenetic affinities of these *P. laevis* lineages.

**CONTACT**
Juha Merilä juha.merila@helsinki.fi Department of Biosciences, University of Helsinki, P.O. Box 65, FI-00014, Helsinki, Finland

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Figure 1. A maximum-likelihood tree of 11 Gasterosteidae fishes, including three *P. laevis* lineages, and an outgroup species (*Aulorhynchus flavidas*) based on 37 mitochondrial genes. Bootstrap support is indicated at nodes. GenBank accession numbers are indicated in brackets.
We sequenced genomic DNA of three *P. laevis* specimens, each belonging to a different lineage (cf. Wang et al. 2015; lineage I, 47°25′N, 03°13′E; lineage II, 45°40′N, 00°14′E; lineage III, 47°32′N, 03°38′E). The Illumina HiSeq2000 platform was used with 100 paired-end strategy. Depending on the lineage, between 5.4 and 7.7 million reads were produced and aligned against the *P. sinensis* mitogenome (Hwang et al. 2012a) with bwa-0.5.10 (Li & Durbin 2009). In each individual, 100% of the reference genome had onefold coverage; 18.61–99.08% had ≥ 20-fold coverage, with a mean coverage of 14.58–75.02-fold. The complete mitochondrial genomes of *P. laevis* lineages I, II and III are 16 576, 16 574 and 16 580 bp in length, respectively (GenBank Accession Nos. KT989567-69). Each contained 37 genes (13 protein-coding, 22 transfer RNA (tRNA), two ribosomal RNA (rRNA)) and a control region. The position and direction of these genes were identical to those of other Gasterosteidae mitochondrial genomes (Miya et al. 2001; Kawahara et al. 2009; Hwang et al. 2012a,b). Most of the protein-coding genes, except ND2, COII, ND4 and Cytb, end with a stop codon in all lineages. The overall base composition of the entire genome in each lineage is 27.6–27.7% for A, 26.9–27.0% for T, 17.3% for G and 28.0–28.3% for C. A maximum likelihood tree of 11 Gasterosteidae fishes, including the three *P. laevis* lineages and the tube-snout (*Aulorhynchus flavidus*) as an outgroup species, was constructed based on the 37 genes using RAxML v.8.0 (Stamatakis 2014) under the GTR + GAMMA model with 37 gene partitions and 100 thorough bootstrap replicates. All *Pungitius* fish formed a single cluster, with the three *P. laevis* lineages exhibiting high levels of divergence from each other (Figure 1). The 37 gene regions (15 584 bp) showed 93.2–98.7% nucleotide identity between the *P. laevis* lineages and other *Pungitius* species (i.e. *P. pungitius*, *P. sinensis* and *P. kaibarae*). Nucleotide identity among the three *P. laevis* lineages was 96.2–97.8%.

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**Disclosure statement**

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

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**References**


