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Complete mitochondrial genome of the nine-spined stickleback *Pungitius pungitius* (Gasterosteiformes, Gasterosteidae)

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**ABSTRACT**

The complete mitochondrial genome of the nine-spined stickleback *Pungitius pungitius* was obtained with Illumina sequencing of genomic DNA. The assembled mitogenome sequence was 16582 bp long, and the gene number, order and contents were identical to those of other sequenced *Pungitius* mitogenomes. The complete mitogenome of *P. pungitius* from its European range can provide an important template for further phylogenetic and population genetic studies of the *Pungitius* species complex.

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Gasterosteidae; genome; mtDNA; nine-spined stickleback; *Pungitius pungitius*

The nine-spined stickleback *Pungitius pungitius* is the most geographically widespread member of the genus *Pungitius*, with a circumpolar distribution (Wootton 1976). It is an important model species in evolutionary biology, genetics and behavioural research (Östlund-Nilsson et al. 2007; Merilä 2013). *Pungitius pungitius* has been the focus of many population genetic and phylogeographic studies using mitochondrial gene fragments (e.g., Aldenhoven et al. 2010; Shikano et al. 2010; Bae & Suk 2015; Wang et al. 2015), but until now, only a partial assembly of the whole mitochondrial genome has been available from one individual originating from Hokkaido, Japan (Kawahara et al. 2009).

We sequenced the genomic DNA of one *P. pungitius* individual collected from Montagny-lès-Seurre, France (47°01’ N, 05°15’E) on the Illumina HiSeq2000 platform with 100 paired-end strategy, and aligned 7.5 million reads against the *Pungitius sinensis* mitogenome (Hwang et al. 2012a) with bwa-0.5.10 (Li & Durbin 2009). The mean coverage of the

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Figure 1. A maximum-likelihood tree inferred from 37 mitochondrial genes among nine Gasterosteidae fishes and an out-group species. Bootstrap support is indicated at nodes. GenBank accession numbers are indicated in brackets.
alignment was 56.89-fold, and 100% of the genome has 1-fold coverage (99.35% with ≥20-fold coverage). The consensus sequence of the *P. pungitius* mitochondrial genome was exported with SAMtools 1.2 (Li et al. 2009) and manually checked. The complete mitochondrial genome of *P. pungitius* was 16 582 bp (GenBank Accession No. KT989571) and consisted of 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes and a control region. The order and direction of these genes are identical to those of other Gasterosteidae species including *Pungitius* fishes (Miya et al. 2001; Kawahara et al. 2009; Hwang et al. 2012a,2012b). Of the 13 protein-coding genes, 4 (ND2, COII, ND4 and Cytb) showed an incomplete stop codon. The base composition of the entire genome was 27.5% for A, 28.0% for T, 17.3% for G and 28.2% for C. The phylogenetic position of *P. pungitius* among Gasterosteidae fishes was confirmed based on a maximum-likelihood tree constructed with the 37 genes (15 583 bp in total) using RAxML v.8.0 (Stamatakis 2014; GTR + GAMMA model, 37 gene partitions and 100 thorough bootstrap replicates). *P. pungitius* clustered with other *Pungitius* fishes, including Japanese *P. pungitius*, Korean *P. sinensis* and Korean *P. kaibarae* (Figure 1). Nucleotide identity in the 37 gene regions of *P. pungitius* was 98.7%, 98.6% and 93.9% in comparisons with those of Japanese *P. pungitius* (AB445130), Korean *P. sinensis* (EU332748) and Korean *P. kaibarae* (EU332749), respectively.

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**Declaration of interest**

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