

MITOGENOME ANNOUNCEMENT

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

Baocheng Guo^a, Elisavet-Aspasia Toli^{a,b} and Juha Merilä^a

^aDepartment of Biosciences, Ecological Genetics Research Unit, University of Helsinki, Helsinki, Finland; ^bDepartment of Biological Application & Technology, University of Ioannina, Greece

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 16 582 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.

ARTICLE HISTORY

Received 8 December 2015
Accepted 22 December 2015

KEYWORDS

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

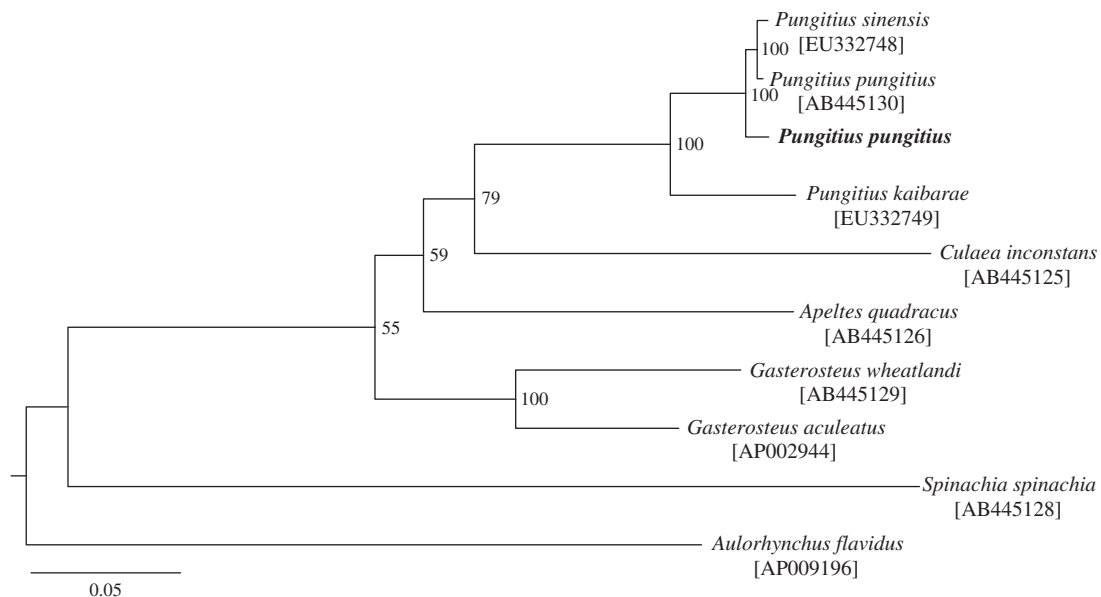


Figure 1. A maximum-likelihood tree inferred from 37 mitochondrial genes among nine Gasterosteidae fishes and an out-group species. Bootstrap support is indicated at nodes. GenBank accession numbers are indicated in brackets.

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.

Acknowledgements

We thank Pekka Ellonen, Laura Häkkinen, Tiina Hannunen and Sami Karja for help with laboratory and bioinformatics work. Takahito Shikano is thanked for his help with preparation of this manuscript and Jacquelin DeFaveri for useful suggestion on earlier version of it. The sequencing was conducted at Finnish Institute for Molecular Medicine.

Declaration of interest

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

Funding information

This study was supported by grants (108601 & 118673) from the Academy of Finland.

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