

MITOGENOME ANNOUNCEMENT

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

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ABSTRACT

The complete mitochondrial genome of the Ukrainian nine-spined stickleback *Pungitius platygaster* was obtained using massive parallel sequencing of genomic DNA. The mitogenome sequence was 16 570 bp long, and the gene order and contents were identical to those of other sequenced *Pungitius* mitogenomes. In a phylogenetic analysis, the mitogenome of *P. platygaster* clustered with other *Pungitius* mitogenomes, yet being clearly distinct from those of *P. pungitius*, *P. sinensis* and *P. kaibarae*.

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Caspian nine-spined stickleback; Gasterosteidae; genome; mtDNA; *Pungitius platygaster*

The Ukrainian nine-spined stickleback *P. platygaster* is morphologically one of the most easily identifiable sticklebacks in the genus *Pungitius* (Keivany & Nelson 2000). Hence, most taxonomic treatments recognize it as a valid species, rather than a subspecies of *P. pungitius* (Wootton 1984; Keivany & Nelson 2000; Mattern 2007). However, in contrast to most other species in this genus, the genetics of this species is

poorly studied. To the best of our knowledge, the only genetic studies of this species involved phylogenetic analysis of mitochondrial DNA (mtDNA) fragments by Geiger et al. (2014) and Wang et al. (2015). Access to the complete mitogenome of this species might be helpful in piecing together the evolutionary affinities and biogeographic history of this species which (together with *P. hellenicus*) has an enigmatic southern

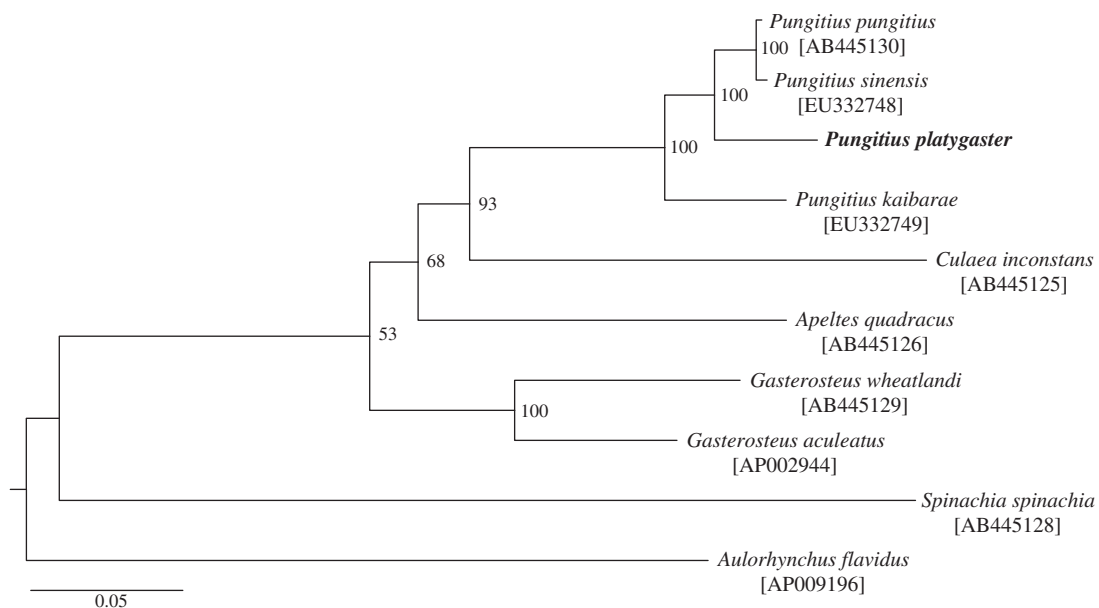


Figure 1. A maximum likelihood tree inferred from 37 mitochondrial genes among nine Gasterosteidae and an outgroup species. Bootstrap support is indicated at nodes. GenBank accession numbers are indicated in brackets.

distribution at the Black Sea, Sea of Azov, Aral Sea and Caspian Sea basins. All other members of the genus have much more northern distribution ranges (Wootton 1976, 1984).

We sequenced the genomic DNA of *P. platygaster* collected from the River Loudias drainage in Greece (40°50'N, 22°18'E) on the Illumina HiSeq2000 platform with 100 paired-end strategy. A total of 11.8 million reads were aligned against the *P. sinensis* mitogenome (Hwang et al. 2012a) with bwa-0.5.10 (Li & Durbin 2009). Mean sequence coverage across the genome was 27.58 reads per base pair and 100% of the reference genome had one-fold coverage (72.61% of the bases had ≥ 20 -fold coverage). The consensus sequence of the *P. platygaster* mitochondrial genome was exported with samtools 1.2 (Li et al. 2009) and manually checked. The complete mitochondrial genome of *P. platygaster* is 16 570 bp (GenBank Accession No. KT989570), consisting of 13 protein-coding genes, 22 transfer RNA (tRNA) genes, two ribosomal RNA (rRNA) genes and a control region. The order and direction of these genes were identical to those of other Gasterosteidae fishes (Miya et al. 2001; Kawahara et al. 2009; Hwang et al. 2012a, 2012b). Of the 13 protein-coding genes, four (*ND2*, *COII*, *ND4* and *Cytb*) showed an incomplete stop codon. The base composition of the entire mitochondrial genome was 27.8% for A, 26.6% for T, 17.2% for G and 28.4% for C. The phylogenetic position of *P. platygaster* in Gasterosteidae fishes was investigated based on a maximum likelihood tree constructed with the 37 genes (15 583 bp in total) using RAxML v.8.0 under the GTR + GAMMA model (37 gene partitions and 100 thorough bootstrap replicates; Stamatakis 2014). *P. platygaster* was phylogenetically positioned with other *Pungitius* species (i.e., *P. pungitius*, *P. sinensis* and *P. kaibarae*), but showed clear albeit shallow divergence from them (Figure 1). Nucleotide identity in the 37 gene regions of *P. platygaster* was 95.7%, 95.6% and 93.0% in comparison with those of *P. pungitius* (GenBank Accession No. AB445130; Kawahara et al. 2009), *P. sinensis* (EU332748; Hwang et al. 2012a) and *P. kaibarae* (EU332749; Hwang et al. 2012b), respectively.

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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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