



Mitochondrial DNA Part A

DNA Mapping, Sequencing, and Analysis


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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of the gilthead seabream *Sparus aurata* L. (Sparidae)

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Abstract

The complete mitochondrial genome of the gilthead seabream *Sparus aurata* Linnaeus 1758, one of the world's most important mariculture species, was sequenced using next generation sequencing technology. The genome sequence is comprised of 16,652 bp exhibiting the canonical vertebrate mitochondria gene order. Regions of gene overlap, tRNA length, as well as start and stop codon were similar to those observed in other Sparidae. Phylogenetic reconstructions based on mitochondrial protein coding genes corroborate the view that Sparidae is paraphyletic and includes Centracanthidae.

Keywords

Centracanthidae, mitogenomics, next-generation sequencing, perciformes, phylogeny

History

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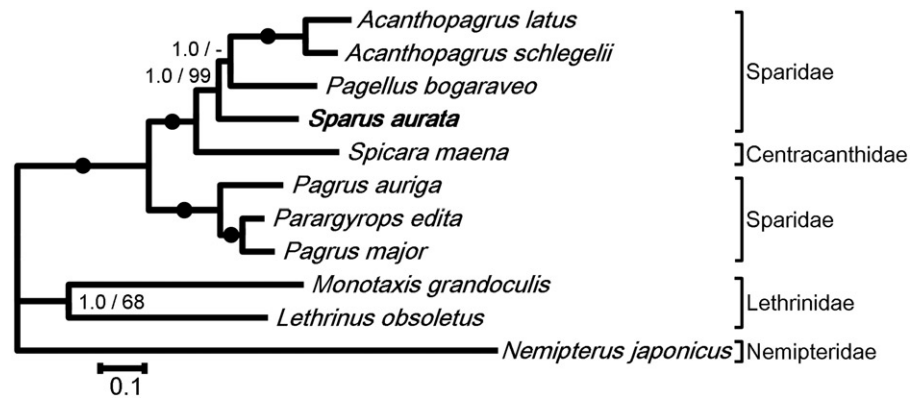
The gilthead seabream *Sparus aurata* Linnaeus, 1758, is native of the Mediterranean Sea and north-east Atlantic Ocean. Among the porgies (Sparidae), it is the most highly esteemed species, and since the nineties it has become one of the world's most important marine aquaculture species, with production exceeding 150,000 tonnes in 2013 (FAO, 2013). Here, we report the complete mitochondrial genome (mitogenome) of *S. aurata* and reconstruct Sparidae relationships. The sequence was deposited in the EMBL-EBI European Nucleotide Archive under accession number LK022698.

A specimen of aquaculture origin was obtained from the Jaffa fish market (Israel) in July 2013. DNA extraction was performed, from muscle tissue, using the DNeasy Blood & Tissue Kit (Qiagen) following standard protocol. Total gDNA sequencing was performed by the Technion Genome Center (Haifa, Israel). A total of ~95,000,000 paired reads (150 bp) were obtained with Illumina MiSeq sequencer. To assemble the complete mitochondrial sequence we followed the approach of Rubinstein et al. (2013) which found that transcriptome assembler performed better than genomic assembler to reconstruct mitochondrial

contigs. The assembly was performed using Trinity r20131110 (Haas et al., 2013) under default parameters. A Blast search was conducted to identify the mitogenome contig. The mean coverage of the mitogenome was computed with the software Geneious Pro version 6.1.7 and was estimated to be 1040 (SD=95). The annotation was performed with MitoAnnotator (Iwasaki et al., 2013). Phylogenetic relationships among Sparidae were investigated using protein-coding genes encoded on the H-strand whilst discarding regions that overlap between genes. A maximum likelihood (ML) analysis was performed with RaxML v8 (Stamatakis, 2014) with 100 starting trees and 500 bootstrap replicates. In addition, a Bayesian analysis was conducted with MrBayes 3.2.2 (Ronquist et al., 2012) using 10,000,000 generations under default settings. In both analyses, sequences were partitioned according to codon position and unlinked GTR+ Γ +I models were chosen for each partition. We verified that the convergence of the Bayesian analysis was achieved before the burnin threshold.

The mitogenome of *S. aurata* is 16,652 bp in length and possesses the canonical vertebrate gene arrangement. The mitogenome consists of 26.8% A 27.3% T 28.8% C and 17.1% G, which is similar to the mitogenome composition of other members of the Sparidae (Shi et al., 2012; Xia et al., 2008). Regions of gene overlap, tRNA length, as well as start and stop codon are also similar to those observed in other sparids (Jang et al., 2014; Ponce et al., 2008; Shi et al., 2012; Xia et al., 2008). Phylogenetic trees constructed using ML and Bayesian inferences corroborate the view that the Sparidae are paraphyletic with Centracanthidae being more closely related to the genera *Acanthopagrus*, *Pagellus* and *Sparus* than to *Pagrus* and *Parargyrops* (Chiba et al., 2009; Santini et al., 2014); similarly, our trees agree with the parafyly of *Pagrus* (Santini et al., 2014; Xia et al., 2008; Figure 1).

Figure 1. Phylogeny of Sparidae inferred from the concatenation of the DNA sequences of 12 mitochondrial protein coding genes. Bayesian consensus tree obtained using the GTR+ Γ +I model. Bayesian posterior probabilities (PP)/ML bootstrap (BP) support values are indicated above the corresponding node. “-” indicates that the corresponding node is absent from the ML tree. Solid circles indicate branches with maximal support values (PP = 1.0 and BP = 100).



Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This work was supported by the Israel Science Foundation (Grant No. 663/10 to D.H.).

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