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The complete mitochondrial genome of the Picasso panda clownfish(Perciformes:Pomacentridae)

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Abstract:

In this study, we determined the complete mitochondrial genome of the Picasso panda clownfish for the first time. The length of the whole mitogenome is 16,652 bp long and contained 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA genes, 2 non-coding regions and 1 control region(D-lop). The mitochondrial genome of the Picasso panda clownfish consisted of A = 29.19%, T = 25.49%, G = 15.93% and C = 29.40% (AT-skew = 0.067 and GC-skew = −0.297). Molecular phylogenetic analysis suggested that *Amphiprion ocellaris*, *Amphiprion percula*, *Premnas biaculeatus* and the Picasso panda clownfish clustered in one branch of the phylogenetic tree. Picasso panda clownfishand and *A. ocellaris* are most closely related.

Keywords: Mitochondrial genome; Pomacentridae; Picasso panda clownfish; Phylogeny

Marine species are becoming increasingly popular in the aquarium market (Andrews 1990,

Hoff 1996). There are more than 30 kinds of clownfish in the world and Clownfish are the most popular species of fish in the marine aquarium trade (Marcionetti A et al.,2018; Hoff 1996). Picasso panda clownfish is a kind of seawater ornamental fish loved by the majority of consumers. In this study, the complete mitochondrial sequence of Picasso panda clownfish was determined and analyzed for the first time. The results provided important basic information for germplasm identification and genetic identification of Picasso panda clownfish.

The Picasso panda clownfish were collected from Yida aquariums in Xiamen(24°27′3.75″N，118°09′47.71″E), Fujian Province, China in May 2021. The specimen was deposited at the Culture Collection of Fish at Fisheries Research Institute of Fujian （Libin He and 670170442@qq.com） under the voucher number XMXCY2021518. DNA samples were stored −20 °C until extraction. Total genomic DNA was extracted using the Magnetic Universal Genomic DNA Kit according to the manufacturer's protocol. Adapter-modified DNA fragments were PCR-amplified using PE PCR primers. Libraries were sequenced using an Illumina NovaSeq6000 at Origingene-Shanghai, China, with 10.68 Gb of 2×150-bp paired-ends,which was constructed with two indexes using VAHTS Universal Plus DNA Library Prep Kit for IIIumina(vazyme,ND617). The phylogenetic trees were drawn using iTOL v5.0 (https://itol.embl.de).

The complete mitogenome (16,652bp) of the Picasso panda clownfish (GenBank accession number: OK326863), and the overall base composition of the genome was A = 29.19%, T = 25.49%, G = 15.93% and C = 29.40% (AT-skew = 0.067 and GC-skew = −0.297).The AT content (54.68%) was higher than the GC content (45.32%). The mitochondrial genome of the Picasso pand clownfish contained 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA genes, 2 non-coding regions and 1 control region(D-lop). Among all 37 identified genes, the NAD6、trnQ、trnA、trnN、trnC、trnY、trnS2、trnE and trnP were located on the light-strand (L-strand), and the remaining twenty-eight genes were encoded on the heavy-strand (H-strand), which were similar to those of other vertebrates (Lv et al. 2018; Sun and Xu 2018).

MAFFT (Katoh et al., 2002) was used to aligned the sequences of 13 mitochondrial protein-coding genes and 2 ribosomal RNA genes. The maximum-likelihood method was used to infer the phylogenetic relationship with 1000 bootstrap replicates in RaxML. Bayesian inference (BI)analysis, using Mrbayes v3.2 (Ronquist et al., 2012) and

the Markov Chain Monte Carlo (MCMC), was run for 1 × 108 generations, and samples were recorded every 1000 generations. The results showed that *A. percula*, Picasso panda clownfish，*A. ocellaris,* and *Premnas biaculeatus* clustered in one branch of the phylogenetic tree(Fig.1). Picasso panda clownfishand and *A. ocellaris* are most closely related, and they may have similar genetic background.

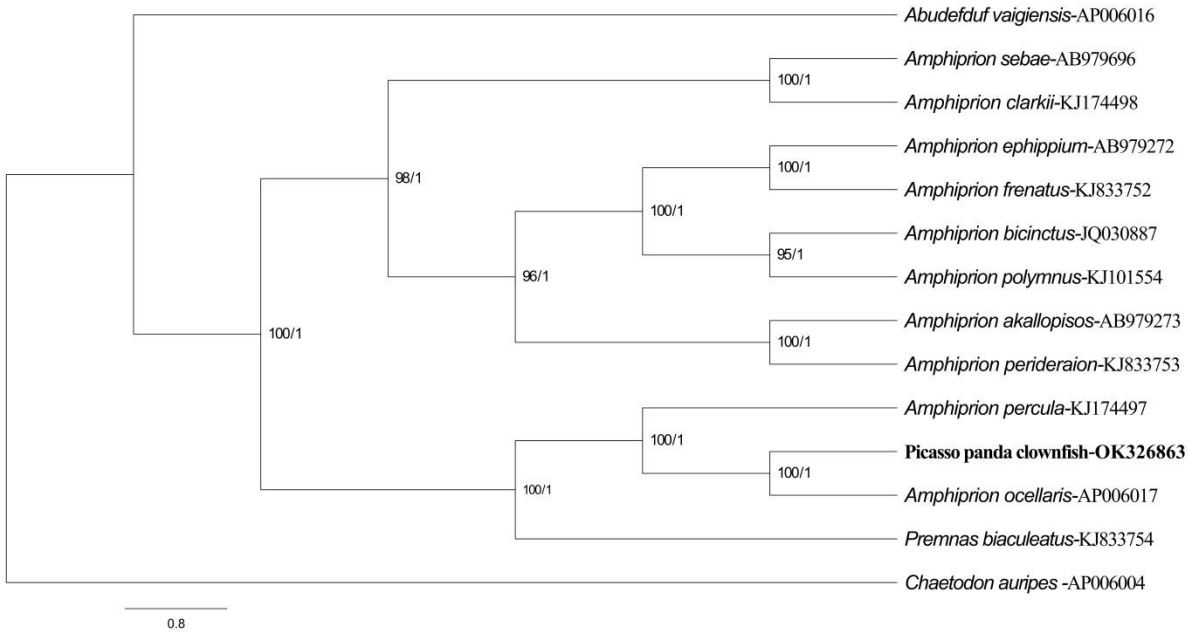

Fig. 1 The maximum-likelihood method (ML) and Bayesian inference (BI) analyses based on nucleotide sequences of 13 mitochondrial protein-coding genes and 2 ribosomal RNA genes.

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Authors's contributions

HE Li-bin conceived and designed the study; HE Li-bin and LUO Hui-yu collected the data; HE Li-bin performed the RNA-Seq analysis. HE Li-bin and ZHENG Le-yun wrote the manuscript. All authors read, edited, and approved the final manuscript for submission.

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Data availability statement (DAS)

The data that support the findings of this study are openly available in GenBank database at ［ https://www.ncbi.nlm.nih.gov ］ (https://www.ncbi.nlm.nih.gov) under the accession no.OK326863. The associated BioProject, SRA, and BioSample numbers are PRJNA818441, SRR18460539, and SAMN26857680 respectively.

References

[1] Andrews C. (1990). The ornamental fish trade and fish conservation. Journal of Fish Biology 37: 53-59.

[2] Hoff F.H. Jr. (1996) Conditioning, spawning and rearing of fish with emphasis on marine clownfish. Aquaculture Consultants Inc. Dade City,212pp.

[3] Katoh K, Misawa K, Kuma K, Miyata T.. (2002). MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Res. 30(14):3059－3066.

[4] Marcionetti A, Rossier V, Bertrand J A M, Litsios G,Salamin N.(2018). First draft genome of an iconic clownfish species (Amphiprion frenatus). Molecular Ecology Resources 18(5):1092-1101.

[5] Ronquist F, Teslenko M, vander Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. (2012). MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61: 539－542.

[6] Lv YY, Li YP, Ruan ZQ, Bian C, You XX, Yang JX, Jiang WS, Shi Q. 2018. The complete mitochondrial genome of Glyptothorax macromaculatus provides a well-resolved molecular phylogeny of the Chinese sisorid catfishes. Genes. 9(6):282.

[7] Sun YN, Xu TJ. 2018. Complete mitochondrial genome of Caranx equula (Perciformes, Carangidae): genome characterization and phylogenetic analysis. Mitochondrial DNA B Resour. 3(2):786－787.