

MITOGENOME ANNOUNCEMENT

Next generation sequencing yields the complete mitochondrial genome of the Clarion angelfish, *Holacanthus clarionensis* (Perciformes: Pomacanthidae)Kang-Ning Shen¹, Chih-Wei Chang^{2,3}, Kar-Hoe Loh⁴, Ching-Hung Chen^{5,6}, and Chung-Der Hsiao⁷

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Abstract

In this study, the complete mitogenome sequence of the Clarion angelfish, *Holacanthus clarionensis* (Perciformes: Pomacanthidae) has been sequenced by next-generation sequencing method. The length of the assembled mitogenome is 16,615 bp, including 13 protein coding genes, 22 transfer RNAs, and two ribosomal RNAs genes. The overall base composition of Clarion angelfish is 28.3% for A, 29.3% for C, 16.5% for G, 25.9% for T and show 85% identities to flame angelfish *Centropyge loriculus*. The complete mitogenome of the Clarion angelfish provides essential and important DNA molecular data for further phylogeography and evolutionary analysis for marine angelfish phylogeny.

Keywords

Clarion angelfish, mitogenome, next generation sequencing

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Clarion angelfish *Holacanthus clarionensis* is a special species with brilliant orange body color in angelfishes. This species is only distributed in Eastern Pacific, ranging from off Mexico, north to the southern part of the Gulf of California and south to Clipperton Island, inhabiting shallow rocky and coastal reefs at the depth around 30 m. Small juveniles are solitary, while adults are more facultative in single, small group or large schooling in some localities. Juveniles have blue vertical lines on the head and posterior part of the body similar to its relative King angelfish *Holacanthus passer*. However, those blue vertical lines will darken with age and eventually fade away. The establishment of Clarion angelfish mitogenome is usefulness for further phylogenetic research of marine angelfishes.

Sample of Clarion angelfish was imported from Mexico and their genomic DNA was extracted from muscle by using Genomic DNA Purification Kit (GeneMark, Taichung, Taiwan). About 2 µg high-quality genomic DNA was subjected to build up genomic library and pair-end sequencing (2 × 300 bp) by MiSeq (Illumina, San Diego, CA) to generate 2,910,692 raw reads. We perform de novo assembly by using commercial software (Geneious V8, Auckland, New Zealand) to produce a single, circular form of complete mitogenome with about an average 31 × coverage (1493 out of 2,910,692 reads, 0.05%). The complete mitochondrial genome of Clarion angelfish was 16,615 bp in size (GenBank: KP218260) and its overall base composition is 28.3% for A, 29.3% for C, 16.5% for G, 25.9% for T and show 85% identities to

flame angelfish *Centropyge loriculus*. The complete mitogenome of Clarion angelfish includes 13 protein-coding genes, 22 transfer RNA genes, and two ribosomal RNA genes (Table 1).

The protein coding and tRNA genes of *H. clarionensis* mitogenome were predicted by using DOGMA (Wyman et al., 2004), ARWEN (Laslett & Canback, 2008), and MitoAnnotator (Iwasaki et al., 2013) tools. All protein coding genes were encoded on the H-strand with exception of protein-coding genes of ND6. All protein coding genes were encoded on the H-strand with exception of protein-coding genes of ND6. All tRNA genes were encoded on the H-strand with exception of *tRNA-Gln*, *tRNA-Ala*, *tRNA-Asn*, *tRNA-Cys*, *tRNA-Tyr*, *tRNA-Ser* (UGA) *tRNA-Glu*, and *tRNA-Pro*. All the 13 mitochondrial protein-coding genes share the start codon ATG, except for COX1 (GTG start codon). It also important to note that only one of the 13 protein-coding genes is inferred to terminate with TGA termination codon (ATP8), while others are terminated with codons of ATG (ND1), ACC (ND2), ATT (CO1), GAC (CO2), GTC (ATP6), TCA (CO3), GAA (ND3), TGT (ND4L), GCC (ND4), TTA (ND5), GTT (ND6), and TCT (CYTB). The longest one is ND5 gene (1839 bp) in all protein coding genes, whereas the shortest is ATP8 gene (168 bp). The two ribosomal RNA genes, 12S rRNA gene (956 bp) and 16S rRNA gene (1700 bp), are located between *tRNA-Phe* and *tRNA-Leu* (UAA) and separated by *tRNA-Val*. We expect that the present result would elucidate the further phylogenetic approach among different species of marine angelfish.

Table 1. Genes and other regions in the mitochondrial genome of *Holacanthus clarionensis*.

Gene/element	From	To	length	Start codon	Stop codon	Anticodon	Strand
<i>tRNA-Phe</i>	1	68	68			GAA	H
<i>12S rRNA</i>	69	1024	956				H
<i>tRNA-Val</i>	1025	1096	72			TAC	H
<i>16S rRNA</i>	1097	2796	1700				H
<i>tRNA-Leu (UAA)</i>	2797	2871	75			TAA	H
<i>ND1</i>	2872	3846	975	ATG	ATG		H
<i>tRNA-Ile</i>	3852	3921	70			GAT	H
<i>tRNA-Gln</i>	3921	3991	71			TTG	L
<i>tRNA-Met</i>	3991	4060	70			CAT	H
<i>ND2</i>	4061	5107	1047	ATG	ACC		H
<i>tRNA-Trp</i>	5134	5207	74			TCA	H
<i>tRNA-Ala</i>	5208	5276	69			TGC	L
<i>tRNA-Asn</i>	5278	5350	73			GTT	L
<i>tRNA-Cys</i>	5390	5458	69			GCA	L
<i>tRNA-Tyr</i>	5459	5528	70			GTA	L
<i>CO 1</i>	5530	7080	1551	GTG	AAT		H
<i>tRNA-Ser (UGA)</i>	7083	7153	71			TGA	L
<i>tRNA-Asp</i>	7158	7229	72			GTC	H
<i>CO 2</i>	7237	7927	691	ATG	GAC		H
<i>tRNA-Lys</i>	7928	8002	75			TTT	H
<i>ATP8</i>	8004	8171	168	ATG	TGA		H
<i>ATP6</i>	8162	8844	683	ATG	GTC		H
<i>CO 3</i>	8845	9629	785	ATG	TCA		H
<i>tRNA-Gly</i>	9630	9701	72			TCC	H
<i>ND3</i>	9702	10,050	349	ATG	GAA		H
<i>tRNA-Arg</i>	10,051	10,119	69			TCG	H
<i>ND4L</i>	10,120	10,416	297	ATG	TGT		H
<i>ND4</i>	10,410	11,790	1381	ATG	GCC		H
<i>tRNA-His</i>	11,791	11,860	70			GTG	H
<i>tRNA-Ser (GCU)</i>	11,861	11,927	67			GCT	H
<i>tRNA-Leu (UAG)</i>	11,931	12,003	73			TAG	H
<i>ND5</i>	12,004	13,842	1839	ATG	TTA		H
<i>ND6</i>	13,839	14,360	522	ATG	GTT		L
<i>tRNA-Glu</i>	14,361	14,429	69			TTC	L
<i>Cyt b</i>	14,435	15,575	1141	ATG	TCT		H
<i>tRNA-Thr</i>	15,576	15,647	72			TGT	H
<i>tRNA-Pro</i>	15,647	15,717	71			TGG	L
Control region (D-loop)	15,718	16,615	898				

Declaration of interest

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

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