

## MITOGENOME ANNOUNCEMENT

# The complete mitochondrial genome of the Blue-face angelfish, *Pomacanthus xanthometapon* (Perciformes: Pomacanthidae)

Kang-Ning Shen<sup>1</sup>, Kar-Hoe Loh<sup>2</sup>, Ching-Hung Chen<sup>3,4</sup>, and Chung-Der Hsiao<sup>5</sup><sup>1</sup>Center of Excellence for the Oceans, National Taiwan Ocean University, Keelung, Taiwan, ROC, <sup>2</sup>Institute of Ocean and Earth Sciences, University of Malaya, Kuala Lumpur, Malaysia, <sup>3</sup>WeThink Biotech INC., Taoyuan, Taiwan, ROC, <sup>4</sup>Zgenebio Biotech INC., Taipei, Taiwan, ROC, and <sup>5</sup>Department of Bioscience Technology, Chung Yuan Christian University, Chung-Li, Taiwan, ROC**Abstract**

In this study, the complete mitogenome sequence of the Blue-face angelfish, *Pomacanthus xanthometapon* (Perciformes: Pomacanthidae) has been sequenced by the next-generation sequencing method. The assembled mitogenome consisting of 16,533 bp includes 13 protein coding genes, 22 transfer RNAs, and two ribosomal RNAs genes. The overall base composition of Blue-face angelfish is 28.7% for A, 28.9% for C, 15.9% for G, 26.6% for T and show 84% identities to flame angelfish *Centropyge loriculus*. The complete mitogenome of the Blue-face angelfish provides essential and important DNA molecular data for further phylogeography and evolutionary analysis for marine angelfish phylogeny.

**Keywords**

Blue-face angelfish, mitogenome, next-generation sequencing

**History**

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The Blue-face angelfish, *Pomacanthus xanthometapon* (Bleeker 1853), are widely distributed in Indo-west Pacific, Western Pacific from southern Japan to Australia, ranging west into Indian Ocean to the Maldives, and east to Vanuatu, Coral Sea (Debelius et al., 2003). *Pomacanthus xanthometapon* juveniles have a color pattern of vertical white lines on a blue background that is similar to other juveniles of *Pomacanthus* spp. This species has some regional color morphs. Individuals from the Pacific Ocean have a yellow area around eye and ventral parts. The individuals from the Indian Ocean have more vivid orange color on the same area (Endoh, 2007). Adults live in coral-rich lagoons and along outer reefs in a depth of 5–35 m. This species is shy and usually seen solitary in most places, but it occasionally forms pairs. The establishment of Blue-face angelfish mitogenome is important for further molecular phylogenetic and population studies.

Samples of Blue-face angelfish were collected from Maldives 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 5,605,632 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 53 × coverage (2514 out of 5,605,632 reads, 0.04%). The complete mitochondrial genome of *P. xanthometapon* consisting of 16,533 bp (GenBank: KP218258) includes 13 protein coding genes, 22 transfer RNAs, and two ribosomal RNAs genes (Table 1). The overall base composition of Blue-face angelfish is 28.7% for A, 28.9% for C, 15.9% for G, 26.6% for T and show 84% identities to flame angelfish *Centropyge loriculus*. The protein coding and tRNA genes of *P. xanthometapon* 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 H-strand except ND6. All tRNA genes were encoded on H-strand except 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 ND1 (TTA) and COX1 (GTG). 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 CAG (ND1), ACC (ND2), AAC (CO1), GAC (CO2), GTT (ATP6 and ND6), TCA (CO3), GAA (ND3), TGT (ND4L), GCC (ND4), CTT (ND5), and GAG (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 (958 bp) and 16S rRNA gene (1706 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 *Pomacanthus xanthurus*.

Gene/element	From	To	Length	Start codon	Stop codon	Anticodon	Strand
tRNA-Phe	1	71	71			GAA	H
12S rRNA	72	1029	958				H
tRNA-Val	1030	1101	72			TAC	H
16S rRNA	1102	2807	1706				H
tRNA-Leu (UAA)	2808	2882	75			TAA	H
ND1	2884	3867	984	TTA	CAG		H
tRNA-Ile	3872	3941	70			GAT	H
tRNA-Gln	3941	4011	71			TTG	L
tRNA-Met	4011	4081	71			CAT	H
ND2	4082	5128	1047	ATG	ACC		H
tRNA-Trp	5141	5209	69			TCA	H
tRNA-Ala	5210	5278	69			TGC	L
tRNA-Asn	5280	5352	73			GTT	L
tRNA-Cys	5395	5461	67			GCA	L
tRNA-Tyr	5462	5531	70			GTA	L
CO 1	5533	7083	1551	GTG	AAC		H
tRNA-Ser (UGA)	7085	7155	71			TGA	L
tRNA-Asp	7160	7231	72			GTC	H
CO 2	7239	7929	691	ATG	GAC		H
tRNA-Lys	7930	8004	75			TTT	H
ATP8	8006	8173	168	ATG	TGA		H
ATP6	8164	8846	683	ATG	GTT		H
CO 3	8847	9631	785	ATG	TCA		H
tRNA-Gly	9632	9703	72			TCC	H
ND3	9704	10,052	349	ATG	GAA		H
tRNA-Arg	10,053	10,121	69			TCG	H
ND4L	10,122	10,418	297	ATG	TGT		H
ND4	10,412	11,792	1381	ATG	GCC		H
tRNA-His	11,793	11,861	69			GTG	H
tRNA-Ser (GCU)	11,862	11,929	68			GCT	H
tRNA-Leu (UAG)	11,934	12,006	73			TAG	H
ND5	12,007	13,845	1839	ATG	CTT		H
ND6	13,842	14,363	522	ATG	GTT		L
tRNA-Glu	14,365	14,433	69			TTC	L
Cyt b	14,437	15,573	1137	ATG	GAG		H
tRNA-Thr	15,578	15,649	72			TGT	H
tRNA-Pro	15,649	15,719	71			TGG	L
Control region (D-loop)	15,720	16,533	814				

## Declaration of interest

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

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