

## MITOGENOME ANNOUNCEMENT

**The complete mitochondrial genome of Wanieso lizardfish  
*Saurida wanieso* Shindo & Yamada, 1972 (Aulopiformes: Synodontidae)**Han-Yang Lin<sup>1</sup>, Chia-Hao Chang<sup>1,2,3</sup>, Hsuan-Ching Ho<sup>4,5</sup>, and Kwang-Tsao Shao<sup>1</sup><sup>1</sup>Biodiversity Research Center, Academia Sinica, Taipei, Taiwan, <sup>2</sup>Department of Biological Science and Technology, National Chiao Tung University, Hsinchu, Taiwan, <sup>3</sup>Department of Biology, St. Louis University, MO, USA, <sup>4</sup>National Museum of Marine Biology & Aquarium, Pingtung, Taiwan, and <sup>5</sup>Institute of Marine Biodiversity and Evolutionary Biology, National Donghwa University, Pingtung, Taiwan**Abstract**

The complete mitochondrial genome of the Wanieso lizardfish (*Saurida wanieso*) was determined by using a PCR-based method. The total length of mitochondrial DNA is 16,552 base pairs including 13 protein-coding genes, 2 ribosomal RNA, 22 transfer RNA genes, 1 replication origin region and 1 control region as other *Saurida* spp. and bony fish. Base composition of the genome is A (25.7%), T (25.2%), C (31.5%), and G (17.6%) with an A + T-rich hallmark as that of other vertebrate mitochondrial genomes.

**Keywords**

Complete mitochondrial genome, *Saurida wanieso*, Wanieso lizardfish

**History**

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The Wanieso lizardfish *Saurida wanieso* Shindo and Yamada, 1972 (Shindo & Yamada, 1972a,b) belongs to the order Aulopiformes, is a demersal fish which usually inhabits at sandy bottoms in shallow water and is distributed majorly around the Yellow sea, middle and southern East China Sea and South China Sea (Yamada et al., 2009). The genus comprises 21 species currently and 7 species occur in Taiwanese waters. With the commercial fishery importance in Taiwan, large number of *Saurida* were trawled and made into the fish floss, fish cakes or fish balls. Of them, *Saurida wanieso* can be distinguished from other congeners by having a combination of following characters: Dorsal-fin rays 10–12, anal-fin rays 10–12, pectoral-fin rays 14–15, lateral-line scales 54–56 and a dusky lower margin on caudal fin (Nakabo, 2013). In this study, we sequenced the complete mitochondrial genome of the Wanieso lizardfish (GenBank accession number KP027408). The voucher specimen used for this study was trawled from off Yilan county, northeastern Taiwan, and was deposited in the Research Museum of Biodiversity Research Center, Academia Sinica, Taipei, with the specimen number ASIZP0075079.

The complete mitochondrial genome of Wanieso lizardfish is sequenced to be 16,552 base pairs in length and shares high similarity on gene content and structure with most vertebrates, such as *Hippocampus trimaculatus* (Chang et al., 2013), *Aphyocypris kikuchii* (Jang-Liaw et al., 2013) and its congeners,

like *S. undosquamis* (Zhao et al., 2014) and *S. microlepis* (Wang et al., 2014).

The complete genome consisted of 2 rRNA genes (12s rRNA and 16s rRNA), 22 tRNA genes, 13 protein-coding genes and 2 non-coding region (L-strand replication origin and D-loop) (Table 1). The positions of RNA genes were predicted by the MITOS (Bernt et al., 2013) and the locations of protein-coding genes were recognized by comparing with the homologous genes of other *Saurida* spp. Same with *S. undosquamis* and *S. microlepis*, most mitochondrial genes of Wanieso lizardfish are encoded on the H-strand, except for *ND6* and eight tRNA (Gln, Ala, Asn, Cys, Tyr, Ser-UCN, Glu and Pro) genes that are encoded on the L-strand (Wang et al., 2014; Zhao et al., 2014).

The overall base composition of the entire genome is as follows: A (25.7%), T (25.2%), C (31.5%), and G (17.6%), that revealed an A + T (50.9%)-rich hallmark as that of other vertebrate mitochondrial genomes. Among the mitochondrial protein-coding genes, the *ND5* was the longest, while the *ATP8* was the shortest. The usage of the start codon was mainly ATG in the most of the mitochondrial protein-coding genes, besides the *COI* gene employing the GTG; the usage of the stop one was either complete or incomplete. The control region was 919 base pairs in size and had no repeats inspected by the program “TANDEM REPEATS FINDER” (Benson, 1999).

Table 1. Characters of the *Saurida wanieso* mitochondrial genome.

Gene	Position		Length (bp)	Codon		Intergenic nucleotides	Strand†
	From	To		Start	Stop		
<i>tRNA<sup>Phe</sup></i>	1	68	68			–	H
12S rRNA	69	1013	945			0	H
<i>tRNA<sup>Val</sup></i>	1013	1084	72			–1	H
16S rRNA	1085	2756	1672			0	H
<i>tRNA<sup>Leu(UUR)</sup></i>	2757	2830	74			0	H
<i>ND1</i>	2831	3805	975	ATG	TAG	0	H
<i>tRNA<sup>Ile</sup></i>	3809	3880	72			3	H
<i>tRNA<sup>Gln</sup></i>	3880	3950	71			–1	L
<i>tRNA<sup>Met</sup></i>	3950	4019	70			–1	H
<i>ND2</i>	4020	5066	1047	ATG	TAA	0	H
<i>tRNA<sup>Trp</sup></i>	5066	5136	71			–1	H
<i>tRNA<sup>Ala</sup></i>	5137	5205	69			0	L
<i>tRNA<sup>Asn</sup></i>	5207	5279	73			1	L
<i>O<sub>L</sub></i>	5280	5312	33			0	–
<i>tRNA<sup>Cys</sup></i>	5313	5377	65			0	L
<i>tRNA<sup>Tyr</sup></i>	5378	5447	70			0	L
<i>COI</i>	5449	6999	1551	GTG	TAA	1	H
<i>tRNA<sup>Ser(UCN)</sup></i>	7000	7070	71			0	L
<i>tRNA<sup>Asp</sup></i>	7074	7144	71			3	H
<i>COII</i>	7158	7848	691	ATG	T	13	H
<i>tRNA<sup>Lys</sup></i>	7849	7920	72			0	H
<i>ATP8</i>	7922	8089	168	ATG	TAA	1	H
<i>ATP6</i>	8080	8762	683	ATG	TA	–10	H
<i>COIII</i>	8763	9547	785	ATG	TA	0	H
<i>tRNA<sup>Gly</sup></i>	9548	9618	71			0	H
<i>ND3</i>	9619	9967	349	ATG	T	0	H
<i>tRNA<sup>Arg</sup></i>	9968	10,036	69			0	H
<i>ND4L</i>	10,037	10,333	297	ATG	TAA	0	H
<i>ND4</i>	10,327	11,707	1381	ATG	T	–7	H
<i>tRNA<sup>His</sup></i>	11,708	11,778	71			0	H
<i>tRNA<sup>Ser(AGY)</sup></i>	11,779	11,847	69			0	H
<i>tRNA<sup>Leu(CUN)</sup></i>	11,849	11,921	73			1	H
<i>ND5</i>	11,922	13,760	1839	ATG	TAG	0	H
<i>ND6</i>	13,756	14,277	522	ATG	TAA	–5	L
<i>tRNA<sup>Glu</sup></i>	14,279	14,347	69			1	L
<i>Cytb</i>	14,352	15,492	1141	ATG	T	4	H
<i>tRNA<sup>Thr</sup></i>	15,493	15,564	72			0	H
<i>tRNA<sup>Pro</sup></i>	15,564	15,633	70			–1	L
<i>D-loop</i>	15,634	16,552	919			0	H

Numbers correspond to the nucleotides separating different genes. Negative numbers indicate overlapping nucleotides between contiguous genes.

†H and L respectively denote heavy and light strands.

## Declaration of interest

The authors report no conflicts of interest. The authors along are responsible for the content and writing of the paper.

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