

See discussions, stats, and author profiles for this publication at: <https://www.researchgate.net/publication/236598145>

Complete mitochondrial genome of the megamouth shark *Megachasma pelagios* (Chondrichthyes, Megachasmidae)

Article in *Mitochondrial DNA* · April 2013

DOI: 10.3109/19401736.2013.792068 · Source: PubMed

CITATIONS

14

READS

83

5 authors, including:



Chia-Hao Chang

Tunghai University

50 PUBLICATIONS 343 CITATIONS

[SEE PROFILE](#)



Kwang-Tsao Shao

Academia Sinica

327 PUBLICATIONS 3,179 CITATIONS

[SEE PROFILE](#)



Wei Chuan Chiang

Fisheries Research Institute, COA

45 PUBLICATIONS 702 CITATIONS

[SEE PROFILE](#)



Nian-Hong Jang-Liaw

Taipei Zoo

39 PUBLICATIONS 358 CITATIONS

[SEE PROFILE](#)

Some of the authors of this publication are also working on these related projects:



Population Dynamics of Eurasian otter in Kinmen Is. [View project](#)



Post-release fishing mortality in marine species [View project](#)

MITOGENOME ANNOUNCEMENTS

Complete mitochondrial genome of the megamouth shark *Megachasma pelagios* (Chondrichthyes, Megachasmidae)Chia-Hao Chang^{1,2}, Kwang-Tsao Shao², Yeong-Shin Lin¹, Wei-Chuan Chiang³, and Nian-Hong Jang-Liaw⁴¹Department of Biological Science and Technology, National Chiao Tung University, Hsinchu, Taiwan, ²Biodiversity Research Center, Academia Sinica, Taipei, Taiwan, ³Eastern Marine Biology Research Center of Fisheries Research Institute, Taitung, Taiwan, and ⁴Animal Department, Taipei Zoo, Taipei, Taiwan**Abstract**

Here we describe the complete mitochondrial genome sequence of the megamouth shark, *Megachasma pelagios*, which is an extremely rare species of deepwater shark. The circle genome (16,694 bp) consists of 13 protein coding, 22 tRNA, 2 rRNA genes and 1 control region. It has the typical vertebrate mitochondrial gene arrangement.

Keywords

Complete mitochondrial genome, *Megachasma pelagios*, megamouth shark

History

Received 24 March 2013
Accepted 31 March 2013
Published online 30 April 2013

Megamouth shark, *Megachasma pelagios* (Taylor et al., 1983) is one of the most famous fishes in the twentieth century (Berra, 1997). This extremely rare deepwater shark is known distributed in the Indian, Pacific and Atlantic Oceans, including off sea of Hualien and Taitung County, eastern Taiwan (Lee & Shao, 2009). Here we present the complete mitochondrial genome of *M. pelagios* that was deposited in GenBank with the accession number KC702506. The megamouth shark specimen used for this study was caught off Taitung County, eastern Taiwan on 15 October 2012, and partial alcohol-fixed tissue specimen was deposited in the Research Museum of Biodiversity Research Center, Academia Sinica, Taipei, Taiwan, with the specimen number ASIZP0915911. This is the 54th confirmed record of this species since the first catch record in 1976 (FMNH, 2013).

All the experiments were carried out by following the standard laboratory procedures described by Chang et al. (2013b) with eight pairs of primers, which are available from the authors on request. The organization of mitochondrial genome of *M. pelagios* is shown in Table 1, which has the typical vertebrate mitochondrial gene arrangement (Lin et al., 2012; Miya et al., 2003; Saitoh et al., 2006). It was sequenced and determined to be 16,694 bp in size, including 13 typical vertebrate protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes and a control region.

All genes were encoded on the H-strand with the exception of one protein-coding gene (*ND6*) and eight tRNA genes (*tRNA^{Gln}*, *tRNA^{Ala}*, *tRNA^{Asn}*, *tRNA^{Cys}*, *tRNA^{Tyr}*, *tRNA^{Ser(UCN)}*, *tRNA^{Glu}* and *tRNA^{Pro}*). The base composition was counted using MEGA5 (Tamura et al., 2011). The overall base composition in descending order is A (32.23%), T (31.02%), C (23.63%) and G (13.12%) with 36.75% GC content. The AT content is higher than GC content, which is similar to other fishes (e.g. Chang et al., 2013a,b; Jang-Liaw et al., 2013a,b,c; Miya et al., 2003). The positions of RNA genes were predicted by the MITOS (Bernt et al., 2012) and the locations of protein-coding genes were identified by comparing with the homologous genes of goblin shark *Mitsukurina owstoni* (GenBank accession number NC_011825) and star-spotted smooth-hound shark *Mustelus manazo* (NC_000890; Cao et al., 1998). The 22 tRNA genes range from 66 to 75 bp in length and can fold into a typical cloverleaf secondary structure that was estimated by the online software tRNAscan-SE v1.21 (Schattner et al., 2005), except for *tRNA^{Ser(AGY)}*. The two ribosomal RNA genes, *12S rRNA* (955 bp) and *16S rRNA* (1668 bp), located between *tRNA^{Phe}* and *tRNA^{Leu(UUR)}* genes and were separated by the *tRNA^{Val}* gene as seen in other vertebrates (Table 1). *ND5* and *ND6* overlap by 18 nucleotides, whereas they are encoded on the opposing strand. Except for *COI* with a GTG start codon, the remaining 12 protein-coding genes start with an ATG codon. Nine protein-coding genes in megamouth shark mitochondrial genome end with complete stop codons, TAA (*ND1*, *ND2*, *COI*, *ATP8*, *ATP6*, *COIII*, *ND4L* and *ND5*) and TAG (*ND6*). The remaining protein-coding genes end with the incomplete stop codons representing as ‘T’ (*COII*, *ND3*, *ND4* and *Cyt b*). The origin of L-strand replication (*O_L*), in *M. pelagios*, was located between the *tRNA^{Asn}* and *tRNA^{Cys}* genes within a cluster of five tRNA genes (WANCY region, Table 1) as in most vertebrates, which is 33 bp long. *D-loop* is 1071 bp long and no repeat set was found (in total 15,624–16,694; checked by online software ‘‘Tandem Repeats Finder’’; Benson, 1999).

Table 1. Characteristics of the mitochondrial genome of *Megachasma pelagios*.

Gene	Position		Length (bp)	Codon		Intergenic nucleotides*	Strand†
	From	To		Start	Stop		
<i>tRNA^{Phe}</i>	1	66	66			–	H
<i>12S rRNA</i>	67	1021	955			0	H
<i>tRNA^{Val}</i>	1019	1090	72			–3	H
<i>16S rRNA</i>	1091	2758	1668			0	H
<i>tRNA^{Leu(UUR)}</i>	2758	2832	75			–1	H
<i>ND1</i>	2833	3807	975	ATG	TAA	0	H
<i>tRNA^{Ile}</i>	3810	3878	69			2	H
<i>tRNA^{Gln}</i>	3877	3948	72			–2	L
<i>tRNA^{Met}</i>	3949	4017	69			0	H
<i>ND2</i>	4018	5061	1044	ATG	TAA	0	H
<i>tRNA^{Trp}</i>	5061	5131	71			–1	H
<i>tRNA^{Ala}</i>	5133	5201	69			1	L
<i>tRNA^{Asn}</i>	5202	5274	73			0	L
<i>O_L</i>	5275	5307	33			0	–
<i>tRNA^{Cys}</i>	5308	5374	67			0	L
<i>tRNA^{Tyr}</i>	5376	5445	70			1	L
<i>COI</i>	5447	7000	1554	GTG	TAA	1	H
<i>tRNA^{Ser(UCN)}</i>	7002	7072	71			1	L
<i>tRNA^{Asp}</i>	7077	7146	70			4	H
<i>COII</i>	7154	7844	691	ATG	T–	7	H
<i>tRNA^{Lys}</i>	7845	7918	74			0	H
<i>ATP8</i>	7920	8087	168	ATG	TAA	1	H
<i>ATP6</i>	8078	8761	684	ATG	TAA	–10	H
<i>COIII</i>	8761	9546	786	ATG	TAA	–1	H
<i>tRNA^{Gly}</i>	9549	9618	70			2	H
<i>ND3</i>	9619	9967	349	ATG	T–	0	H
<i>tRNA^{Arg}</i>	9968	10,037	70			0	H
<i>ND4L</i>	10,038	10,334	297	ATG	TAA	0	H
<i>ND4</i>	10,328	11,708	1381	ATG	T–	–7	H
<i>tRNA^{His}</i>	11,709	11,777	69			0	H
<i>tRNA^{Ser(AGY)}</i>	11,778	11,844	67			0	H
<i>tRNA^{Leu(CUN)}</i>	11,845	11,916	72			0	H
<i>ND5</i>	11,917	13,755	1839	ATG	TAA	0	H
<i>ND6</i>	13,738	14,262	525	ATG	TAG	–18	L
<i>tRNA^{Glu}</i>	14,263	14,332	70			0	L
<i>Cytb</i>	14,335	15,478	1144	ATG	T–	2	H
<i>tRNA^{Thr}</i>	15,479	15,552	74			0	H
<i>tRNA^{Pro}</i>	15,555	15,623	69			2	L
<i>D-loop</i>	15,624	16,694	1071			0	–

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

†H and L denote heavy and light.

Declaration of interest

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

References

- Benson G. (1999). Tandem repeats finder: A program to analyze DNA sequences. *Nucl Acids Res* 27:573–80.
- Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritsch G, Pütz J, et al. (2013). MITOS: Improved de novo metazoan mitochondrial genome annotation. *Mol Phylogenet Evol*, doi: 10.1016/j.ympev.2012.08.023.
- Berra TM. (1997). Some 20th century fish discoveries. *Environ Biol Fish* 50:1–12.
- Cao Y, Waddell PJ, Okada N, Hasegawa M. (1998). The complete mitochondrial DNA sequence of the shark *Mustelus manazo*: Evaluating rooting contradictions to living bony vertebrates. *Mol Biol Evol* 15:1637–46.
- Chang CH, Lin HY, Jang-Liaw NH, Shao KT, Lin YS, Ho HC. (2013a). The complete mitochondrial genome of the tiger tail seahorse, *Hippocampus comes* (Teleostei, Syngnathidae). *Mitochondrial DNA*, doi: 10.3109/19401736.2012.744983.
- Chang CH, Tsai CL, Jang-Liaw NH. (2013b). Complete mitochondrial genome of the Chinese rasbora *Rasbora steineri* (Teleostei, Cyprinidae). *Mitochondrial DNA*, doi: 10.3109/19401736.2012.744977.
- FMNH (Florida Museum of Natural History). (2013). Ichthyology-Megamouth: Distribution Table of Confirmed Megamouth Shark Sightings. Available at: <http://www.flmnh.ufl.edu/fish/Sharks/Megamouth/tablemega.htm> (Accessed 19 March 2013).
- Jang-Liaw NH, Chang CH, Tsai CL. (2013a). Complete mitogenomes of two *Puntius* in Taiwan: *P. semifasciolatus* and *P. snyderi* (Cypriniformes: Cyprinidae). *Mitochondrial DNA*, doi: 10.3109/19401736.2012.752472.
- Jang-Liaw NH, Tsai CL, Chang CH, Watanabe K. (2013b). Complete mitochondrial genome of the Moltrecht's minnow, *Aphyocypris moltrechtii* (Teleostei, Cyprinidae), in comparison with *A. kikuchii*. *Mitochondrial DNA* 24:117–19.
- Jang-Liaw NH, Tsai CL, Watanabe K. (2013c). Complete mitochondrial genome of the Kikuchi's minnow *Aphyocypris kikuchii* (Teleostei, Cyprinidae). *Mitochondrial DNA* 24:11–13.
- Lee PF, Shao KT. (2009). Two new records of lamniform shark from the waters adjacent to Taiwan. *J Fish Soc Taiwan* 36:303–11.
- Lin CY, Lin WW, Kao HW. (2012). The complete mitochondrial genome of the mackerel icefish, *Champsocephalus gunnari* (Actinopterygii: Channichthyidae), with reference to the evolution of mitochondrial genomes in Antarctic notothenioids. *Zool J Linn Soc* 165:521–33.
- Miya M, Takeshima H, Endo H, Ishiguro NB, Inoue JG, Mukai T, Satoh TP, et al. (2003). Major patterns of higher teleostean phylogenies: A new perspective based on 100 complete mitochondrial DNA sequences. *Mol Phylogenet Evol* 26:121–38.
- Saitoh K, Sado T, Mayden RL, Hanzawa N, Nakamura K, Nishida M, Miya M. (2006). Mitogenomic evolution and interrelationships of the

- Cypriniformes (Actinopterygii: Ostariophysii): The first evidence toward resolution of higher-level relationships of the world's largest freshwater fish clade based on 59 whole mitogenome sequences. *J Mol Evol* 63:826–41.
- Schattner P, Brooks AN, Lowe TM. (2005). The tRNAscan-SE, snoscan and snoGPS web servers for the detection of tRNAs and snoRNAs. *Nucleic Acids Res* 33:W686–9.
- Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. (2011). MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Mol Biol Evol* 28:2731–9.
- Taylor LR, Compagno LJ, Struhsaker PJ. (1983). Megamouth – a new species, genus and family of lamnoid shark (*Megachasma pelagios*, family Megachasmidae) from the Hawaiian Islands. *Proc Calif Acad Sci* 43:87–110.