Taylor & Francis
Taylor & Francis Group

MITOGENOME ANNOUNCEMENT

🔓 OPEN ACCESS

The complete mitochondrial genome of horn-nosed boxfish (*Ostracion rhinorhynchos*)

Yu Huang[a], Xiaomeng Zhao[a], Zhiqiang Ruan[a], Min Wang[a,b], Junmin Xu[a,b] and Qiong Shi[a,b]

[a]Shenzhen Key Lab of Marine Genomics, Guangdong Provincial Key Lab of Molecular Breeding in Marine Economic Animals, BGI, Shenzhen, China; [b]BGI-Zhenjiang Institute of Hydrobiology, Zhenjiang, China

ABSTRACT

The horn-nosed boxfish, *Ostracion rhinorhynchos* (Tetraodontiformes: Ostraciidae) is a toxic marine species inhabiting tropical coral reefs. In this study, we first reported its whole mitochondrial genome sequence. The complete mitochondrial genome, 16 483 bp with an AT ratio of 56.8%, is composed of 13 protein-coding genes, 22 transfer RNAs, 2 ribosomal RNAs and an 826-bp D-loop control region. The molecular-based phylogenetic tree indicated that *O. rhinorhynchos* has close affinities with fishes from family Ostraciidae as expected.

First described in 1851 (Bleeker 1851), *Ostracion rhinorhynchos*, commonly known as horn-nosed boxfish because of its box-like carapace and large protuberance on the snout, is a toxic marine genus belonging to Ostraciidae in Tetraodontiformes of which most species dwell in and around tropical coral reefs. Ostraciidae contains about 23 extant species in 6 extant genera, but mitochondrial genomes of only two species (*Ostracion immaculatus* and *Lactoria diaphana*) have been sequenced. In this study, we first reported the whole

mitochondrial genome sequence of *O. rhinorhynchos* (GenBank accession number KU308378).

One adult horn-nosed boxfish was collected from Sanya, China. Whole genomic DNA was extracted from its muscle with Puregene Tissue Core Kit A (Qiagen, Germantown, MD, USA) and sequenced by Illumina Hiseq4000 (BGI, Shenzhen, China). Raw data containing adaptor contamination (with >15 bp matched to the adaptor sequence), polyNs (>5 bp Ns) or >1% error rate (>10 bp bases with quality score <20) were filtered

Table 1. Mitochondrial genome characteristics of the *Ostracion rhinorhynchos*.

Gene name	Position		Size (bp)	Intergenic nucleotides[a]	Coding strand	Identity with Ostraciidae species (%)	
	Start	End				*Ostracion immaculatus*	*Lactoria diaphana*
tRNA-Phe	1	68	68	0	H	/	/
s-rRNA	69	1011	943	6	H	/	/
tRNA-Val	1018	1089	72	0	H	/	/
l-rRNA	1090	2771	1682	2	H	/	/
tRNA-Leu	2774	2847	74	0	H	/	/
ND1	2848	3819	972	7	H	91.87	84.36
tRNA-Ile	3827	3897	71	−1	H	/	/
tRNA-Gln	3897	3967	71	−1	L	/	/
tRNA-Met	3967	4035	69	0	H	/	/
ND2	4036	5079	1044	2	H	92.24	83.33
tRNA-Trp	5082	5153	72	0	H	/	/
tRNA-Ala	5154	5222	69	1	L	/	/
tRNA-Asn	5224	5296	73	37	L	/	/
tRNA-Cys	5334	5400	67	0	L	/	/
tRNA-Tyr	5401	5471	71	1	L	/	/
COX1	5473	7020	1548	4	H	95.28	87.34
tRNA-Ser	7025	7095	71	3	L	/	/
tRNA-Asp	7099	7169	71	7	H	/	/
COX2	7177	7866	690	1	H	96.52	89.57
tRNA-Lys	7868	7942	75	1	H	/	/
ATP8	7944	8108	165	−7	H	93.94	93.94

(*continued*)

CONTACT Qiong Shi ✉ shiqiong@genomics.cn 💬 Shenzhen Key Lab of Marine Genomics, Guangdong Provincial Key Lab of Molecular Breeding in Marine Economic Animals, BGI, Bldg 11 Room 618, Beishan Industrial Zone, Shenzhen 518083, China

Table 1. Continued

| Gene name | Position | | | | | Identity with Ostraciidae species (%) | |
	Start	End	Size (bp)	Intergenic nucleotides[a]	Coding strand	Ostracion immaculatus	Lactoria diaphana
ATP6	8102	8782	681	2	H	95.15	86.93
COX3	8785	9567	783	2	H	95.79	88.89
tRNA-Gly	9570	9641	72	0	H	/	/
ND3	9642	9989	348	1	H	92.24	81.9
tRNA-Arg	9991	10 060	70	0	H	/	/
ND4L	10 061	10 354	294	−4	H	97.28	87.41
ND4	10 351	11 730	1380	1	H	93.81	84.75
tRNA-His	11 732	11 800	69	0	H	/	/
tRNA-Ser	11 801	11 868	68	4	H	/	/
tRNA-Leu	11 873	11 945	73	0	H	/	/
ND5	11 946	13 781	1836	2	H	93.03	85.19
ND6	13 784	14 302	519	0	L	91.71	84.39
tRNA-Glu	14 303	14 371	69	4	L	/	/
CYTB	14 376	15 515	1140	1	H	92.89	84.7
tRNA-Thr	15 517	15 588	72	−1	H	/	/
tRNA-Pro	15 588	15 657	70	0	L	/	/
D-loop	15 658	16 483	826	0		/	/

[a]Positive numbers indicate the number of nucleotides found in intergenic spacers between different genes. Negative numbers indicate overlapping nucleotides between adjacent genes.
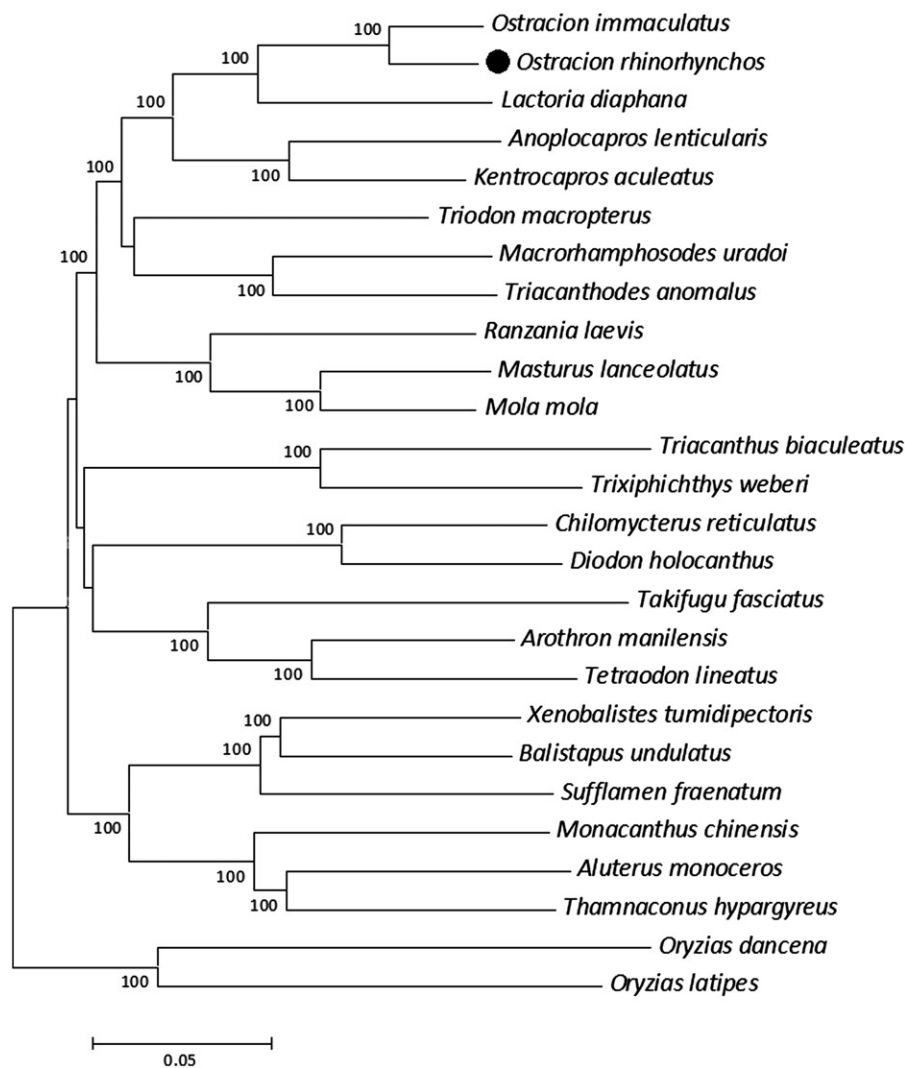

Figure 1. Phylogenetic tree based on *Ostracion rhinorhynchos* together with other 25 reported species. GenBank accession numbers of mitochondrial genome sequences are listed as follows: *Aluterus monoceros*: NC_027268.1; *Anoplocapros lenticularis*: NC_011319.1; *Arothron manilensis*: NC_015371.1; *Balistapus undulatus*: NC_011946.1; *Chilomycterus reticulatus*: NC_011331.1; *Diodon holocanthus*: NC_009866.1; *Kentrocapros aculeatus*: NC_009864.1; *Lactoria diaphana*: NC_011330.1; *Macrorhamphosodes uradoi*: NC_009860.1; *Masturus lanceolatus*: NC_005837.1; *Mola mola*: NC_005836.1; *Monacanthus chinensis*: NC_011925.1; *Oryzias dancena*: NC_012976.1; *Oryzias latipes*: NC_004387.1; *Ostracion immaculatus*: NC_009865.1; *Ranzania laevis*: NC_007887.1; *Sufflamen fraenatum*: NC_004416.1; *Takifugu fasciatus*: NC_013087.1; *Tetraodon lineatus*: NC_028551.1; *Thamnaconus hypargyreus*: NC_027070.1; *Triacanthodes anomalus*: NC_009861.1; *Triacanthus biaculeatus*: NC_009863.1; *Triodon macropterus*: NC_009859.1; *Trixiphichthys weberi*: NC_009862.1; *Xenobalistes tumidipectoris*: NC_011321.1.

out with a Perl script (Zhou et al. 2013; Tang et al. 2014). Clean reads were subsequently assembled with SOAPdenovo-Trans (Xie et al. 2014) and annotated with DOGMA (Wyman et al. 2004). tRNA genes were further identified using tRNAscan-SE 1.21 (http://lowelab.ucsc.edu/tRNAscan-SE).

The complete mitochondrial genome of *O. rhinorhynchos* is 16 483 bp in length. The overall base composition is 29.7% A, 27.1% T, 27.7% C and 15.4% G, with an AT bias of 56.8%, in common with other vertebrate mitochondrial genomes and slightly higher than that in reported *O. immaculatus* (Yamanoue et al. 2007). This circular molecule contains 13 protein-coding genes, 22 transfer RNA gens, 2 ribosomal RNA genes (12S rRNA and 16S rRNA) and an 826-bp D-loop control region (Table 1). ND6 is the only protein coding gene coded by L-strand while 14 out of 22 tRNAs are coded by H-strand. The 13 protein coding genes were aligned to two reported Ostraciidae fishes (*O. immaculatus* and *L. diaphana*) with Blastall (Mount 2007) and the result shows that, except for ATP8 which presents the same identity (93.94%), other 12 genes all have higher identity in *O. immaculatus* than those in *L. diaphana*, confirming that *O. rhinorhynchos* and *O. immaculatus* which are in the same genus have relatively closer phylogenetic relationship (Table 1).

Several studies have confirmed the phylogenetic position of Tetraodontiformes fishes as a monophyletic group within the higher teleosts (Holcroft 2004; Yamanoue et al. 2007). However, within this order, the genetic relationship is not clear (Yamanoue et al. 2007; Santini et al. 2013). Taking *Oryzias latipes* and *Oryzias dancena* in order Beloniformes as outgroups, we constructed a neighbour-joining tree using MEGA6 (Tamura et al. 2013), based on the complete mitochondrial genomes of *O. rhinorhynchos* together with other 23 reported affinis species in order Tetraodontiformes (Figure 1). As expected, *O. rhinorhynchos* has closer affinities with other Ostraciidae species. The achieved mitochondrial genome of *O. rhinorhynchos* will be useful for verification of the evolutionary relationship within Tetraodontiformes.

Acknowledgements

Disclosure statement

Funding information

References

Bleeker P. 1851. Bijdrage tot de kennis der Balistini en Ostraciones van den Indischen Archipel. Verb Bat Gen. 24:1–38.

Holcroft NI. 2004. A molecular test of alternative hypotheses of tetraodontiform (Acanthomorpha: Tetraodontiformes) sister group relationships using data from the RAG1 gene. Mol Phylogenet Evol. 32:749–760.

Mount DW. 2007. Using the basic local alignment search tool (BLAST). CSH Protoc. 1(2007):pdb.top17.

Santini F, Sorenson L, Marcroft T, Dornburg A, Alfaro ME. 2013. A multilocus molecular phylogeny of boxfishes (Aracanidae, Ostraciidae; Tetraodontiformes). Mol Phylogenet Evol. 66:153–160.

Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. 2013. MEGA6: molecular evolutionary genetics analysis version 6.0. Mol Biol Evol. 30: 2725–2729.

Tang M, Tan M, Meng G, Yang S, Su X, Liu S, Song W, Li Y, Wu Q, Zhang A, et al. 2014. Multiplex sequencing of pooled mitochondrial genomes – a crucial step toward biodiversity analysis using mito-metagenomics. Nucleic Acids Res. 42:e166.

Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organellar genomes with DOGMA. Bioinformatics 20:3252–3255.

Xie Y, Wu G, Tang J, Luo R, Patterson J, Liu S, Huang W, He G, Gu S, Li S, et al. 2014. SOAPdenovo-Trans: de novo transcriptome assembly with short RNA-Seq reads. Bioinformatics 30:1660–1666.

Yamanoue Y, Miya M, Matsuura K, Yagishita N, Mabuchi K, Sakai H, Katoh M, Nishida M. 2007. Phylogenetic position of tetraodontiform fishes within the higher teleosts: Bayesian inferences based on 44 whole mitochondrial genome sequences. Mol Phylogenet Evol. 45:89–101.

Zhou X, Li Y, Liu S, Yang Q, Su X, Zhou L, Tang M, Fu R, Li J, Huang Q. 2013. Ultra-deep sequencing enables high-fidelity recovery of biodiversity for bulk arthropod samples without PCR amplification. GigaScience 2:4.