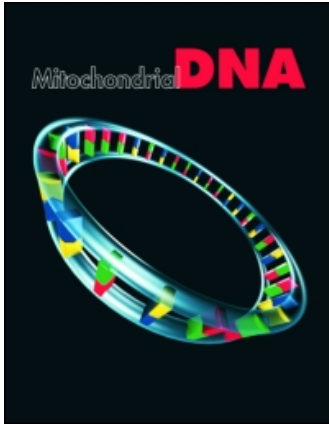


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MITOGENOME ANNOUNCEMENT

Mitochondrial genome of *Boleophthalmus* sp. nov. (Osteichthyes: Gobiidae)

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Abstract

Boleophthalmus is a genus that consists of six valid species and possesses a number of specializations in terms of amphibious life. The complete mtDNA sequence of *Boleophthalmus* sp. nov. (17,113 bp in length) has 13 protein-coding genes, 22 tRNA genes, two rRNA genes (12S and 16S rRNA), and one control region. By comparing the COI sequences, *Boleophthalmus* sp. nov. is closely related of *B. pectinirostris* but exhibits 8.93% genetic distance with *B. pectinirostris* and 13.26% with *B. boddarti*. This finding may fill some gaps remaining on the taxonomy and biodiversity of this taxon and contribute to the understanding of the phylogeographic relationships between the continental coast and Southeast Asia.

Keywords

Boleophthalmus sp. nov., genome, mitochondrion

History

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Subfamily Oxudercinae comprises 10 genera and 41 species. Oxudercine gobiiforms are chiefly distributed in the Indo-Pacific with an extending range of one species endemic to West Africa (Murdy, 1989). Among Oxudercinae, *Boleophthalmus* is a genus that consists of six valid species and possesses a number of specializations in terms of amphibious life (Ishimatsu et al., 1998, 1999; Takita et al., 1999, 2011; Zhang et al., 2000, 2003).

Despite the identification of many unique characteristics and mechanisms in aerial respiration, aerial circulation, and terrestrial locomotion, some gaps remain on the taxonomy and biodiversity of this taxon.

In this study, the complete mitochondrial genomes of *Boleophthalmus* sp. nov. were amplified and sequenced using 14 primer pairs. The base composition of mtDNA included T

Table 1. Characteristics of the *Boleophthalmus* sp. nov. mitochondrial DNA genome.

Gene name	Coding strand	Start position	End position	Intergenic nucleotides	Overlapping nucleotides	Size (bp)	No. of codons	Start codon	Stop codon
tRNA ^{Phe}	H	1	68			68			
12s rRNA	H	69	1015			947			
tRNA ^{Val}	H	1016	1087			72			
16s rRNA	H	1088	2773			1686			
tRNA ^{Leu}	H	2774	2848			75			
<i>ND1</i>	H	2849	3823	3		975	324	ATG	TAA
tRNA ^{Ile}	H	3827	3896		1	70			
tRNA ^{Gln}	L	3896	3966		1	71			
tRNA ^{Met}	H	3966	4034			69			
<i>ND2</i>	H	4035	5081	1		1047	348	ATG	TAA
tRNA ^{Trp}	H	5083	5153	2		71			
tRNA ^{Ala}	L	5156	5224	1		69			
tRNA ^{Asn}	L	5226	5298			73			
Repeat region	L	5299	5333			35			
tRNA ^{Cys}	L	5334	5398			65			
tRNA ^{Tyr}	L	5399	5469	1		71			
<i>COX1</i>	H	5471	7024			1554	517	GTG	TAA
tRNA ^{Ser}	L	7025	7095	3		71			

(continued)

Table 1. Continued.

Gene name	Coding strand	Start position	End position	Intergenic nucleotides	Overlapping nucleotides	Size (bp)	No. of codons	Start codon	Stop codon
tRNA ^{Asp}	H	7099	7170	4		72			
COX2	H	7175	7865			691	230	ATG	T
tRNA ^{Lys}	H	7866	7941	1		76			
ATP8	H	7943	8107		4	165	54	ATG	TAG
ATP6	H	8104	8785			682	227	ATA	T
COX3	H	8786	9569			784	261	ATG	T
tRNA ^{Gly}	H	9570	9641			72			
ND3	H	9642	9990			349	116	ATG	T
tRNA ^{Arg}	H	9991	10,059			69			
ND4L	H	10,060	10,356		7	297	98	ATG	TAA
ND4	H	10,350	11,730			1381	460	ATG	T
tRNA ^{His}	H	11,731	11,799			69			
tRNA ^{Ser}	H	11,800	11,873		3	74			
tRNA ^{Leu}	H	11,871	11,943			73			
ND5	H	11,944	13,782		4	1839	612	ATG	TAA
ND6	L	13,779	14,300			522	173	ATG	TAA
tRNA ^{Glu}	L	14,301	14,369	5		69			
Cytb	H	14,375	15,515			1141	380	ATG	T
tRNA ^{Thr}	H	15,516	15,587			72			
tRNA ^{Pro}	L	15,588	15,657			70			
D-loop	H	15,658	17,113			1456			

(26.1%), C (28.8%), A (29.7%), and G (15.5%), with the percentage of G and C (44.3%) being slightly lower than that of A and T (55.8%). The complete mtDNA sequence of this species (17,113 bp in length; KP277118) had 13 protein-coding genes, 22 tRNA genes, two rRNA genes (12S and 16S rRNA), and one control region (Table 1). In 13 protein-coding genes, only *ND6* lies in the L-strand, the shortest gene was *ATP8* (165 bp), and longest was *ND5* (1839 bp). Eleven of the 13 protein-coding genes used ATG as the start codon, whereas *COX1* and *ATP6* utilized GTG and ATT, respectively (Table 1). Six of the 13 protein-coding genes regard TAA as the stop codon, whereas *ATP8* ends with TAG. Six other genes (*COX2*, *ATP6*, *COX3*, *ND3*, *ND4* and *Cytb*) used T as an incomplete stop codon, which was presumably completed as TAA via post-transcriptional polyadenylation. The 22 tRNA genes range in size from 65 bp in tRNA^{Cys} to 76 bp in tRNA^{Lys}. The lengths of the 12S and 16S rRNA genes were 947 and 1686 bp, respectively. These ribosomal subunit genes were located between the tRNA^{Phe} and tRNA^{Leu} genes and were further separated by the tRNA^{Val} gene. The control region was 1456 bp long. The origin of L-strand replication (OL) was inside a cluster of five tRNA genes (Table 1), which is 35 bp long, as found in most vertebrates.

Several reports indicated that only *Boleophthalmus boddarti* was distributed in Southeast Asia (Murdy, 1989). Recently, *B. boddarti* and *B. pectinirostris* were reportedly sympatric along Malacca Strait (Polgar et al., 2013). However, the present result shows that *Boleophthalmus* sp. nov, which was collected in Brunei and Indonesia, was closely related to *B. pectinirostris* but exhibits 8.93% genetic distance with *B. pectinirostris* and 13.26% with *B. boddarti*. *Boleophthalmus* gobies are the subjects of polygeny or phylogeography studies because of their distribution pattern, endemism, and life strategy (adult and subadult individuals are almost restricted within a narrow coast area). The estimated dating of the phylogenetic splits of the sister species may contribute to the understanding of the phylogeographic relationships between the continental coast and Southeast Asia.

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Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This project was supported by National Program on Key Basic Research Project of China (2011CB943800) and Grants-in-Aid for Scientific Research of Japan (23405033).

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