

MITOGENOME ANNOUNCEMENT

**The complete mitochondrial genome of *Pomacea canaliculata* (Gastropoda: Ampullariidae)**

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**Abstract**

The mitochondrial genome of *Pomacea canaliculata* (Gastropoda: Ampullariidae) is the first complete mtDNA sequence reported in the genus *Pomacea*. The total length of mtDNA is 15,707 bp, which containing 13 protein-coding genes, 2 ribosomal RNAs, 22 transfer RNAs, and a 359 bp non-coding region. The A+T content of the overall base composition of H-strand is 71.7% (T: 41%, C: 12.7%, A: 30.7%, G: 15.6%). ATP6, ATP8, CO1, CO2, ND1-3, ND5, ND6, ND4L and *Cyt b* genes begin with ATG as start codon, CO3 and ND4 begin with ATA. ATP8, CO2-3, ND4L, ND2-6 and *Cyt b* genes are terminated with TAA as stop codon, ATP6, ND1, and CO1 end with TAG. A long non-coding region is found and a 23 bp repeat unit repeat 11 times in this region.

**Keywords**

Ampullariidae, mitogenome, *Pomacea canaliculata*

**History**

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*Pomacea* spp. are a group of freshwater gastropod, which were introduced into East and Southeast Asia from South America as food in 1980s (Halwart, 1994). However, most of species in this genus, including the golden apple snail (*P. canaliculata*), are now regarded as invasive alien species in Asian countries (Carlsson et al., 2004; Hayes et al., 2008). It is well known that invasive species may cause decrease of biodiversity after habitat loss (Lowe et al., 2000). For example, the rapid spread of

*P. canaliculata* in China has caused ecological problems, such as reducing biodiversity and altering ecosystem processes, as well as great economic losses in southern provinces, China. Additionally, this species is recognized as one of the 100 worst invasive alien species in the world (Lowe et al., 2000). However, at present, genetic information of *Pomacea* spp. are largely unknown (Hayes et al., 2008; Rawlings et al., 2007), which is critical to understanding of dispersal mode and

Table 1. Organization and location in the mtDNA of golden apple snail.

Gene/region	Start position	Stop position	Spacer (+) Overlap(-)	Size (bp)	Start codon	Stop codon	Strand
CO1	1	1536	27	1536	ATG	TAG	H
CO2	1564	2250	17	687	ATG	TAA	H
tRNA <sup>Asp</sup>	2268	2335	0	68			H
ATP8	2336	2494	12	159	ATG	TAA	H
ATP6	2507	3205	28	699	ATG	TAG	H
tRNA <sup>Met</sup>	3234	3298	35	65			L
tRNA <sup>Tyr</sup>	3334	3400	8	67			L
tRNA <sup>Cys</sup>	3409	3473	5	65			L
tRNA <sup>Trp</sup>	3479	3543	11	65			L
tRNA <sup>Gln</sup>	3555	3618	9	64			L
tRNA <sup>Gly</sup>	3628	3694	25	67			L
tRNA <sup>Glu</sup>	3720	3783	0	64			L
srRNA	3784	4712	0	929			H
tRNA <sup>Val</sup>	4713	4780	0	68			H
lrRNA	4781	6114	0	1334			H
tRNA <sup>Leu</sup>	6115	6181	-1	67			H
tRNA <sup>Leu</sup>	6181	6248	0	68			H

(continued)

Table 1. Continued

Gene/region	Start position	Stop position	Spacer (+) Overlap(–)	Size (bp)	Start codon	Stop codon	Strand
ND1	6249	7208	–11	960	ATG	TAG	H
tRNA <sup>Pro</sup>	7198	7265	0	68			H
ND6	7266	7760	18	495	ATG	TAA	H
Cyt b	7779	8918	9	1140	ATG	TAA	H
tRNA <sup>Ser</sup>	8928	8993	20	66			H
tRNA <sup>Thr</sup>	9014	9081	9	68			L
ND4L	9091	9387	20	297	ATG	TAA	H
ND4	9408	10,748	3	1341	ATA	TAA	H
tRNA <sup>His</sup>	10,752	10,816	0	65			H
ND5	10,817	12,526	0	1710	ATG	TAA	H
tRNA <sup>Phe</sup>	12,527	12,595	0	69			H
Nocoding region	12,596	12,954	0	359			H
CO3	12,955	13,734	48	780	ATA	TAA	H
tRNA <sup>Lys</sup>	13,783	13,849	18	67			H
tRNA <sup>Ala</sup>	13,868	13,935	29	68			H
tRNA <sup>Arg</sup>	13,965	14,033	2	69			H
tRNA <sup>Asn</sup>	14,036	14,104	21	69			H
tRNA <sup>Ile</sup>	14,126	14,195	0	70			H
ND3	14,196	14,549	22	354	ATG	TAA	H
tRNA <sup>Ser</sup>	14,572	14,641	–1	70			H
ND2	14,641	15,702	5	1062	ATG	TAA	H

population structure of these species. Additionally, the scarce of useful molecular marker also made the taxonomy and identification within the genus unstable, which is solely based on the unclear morphological criteria. Here, we firstly presented the complete mitochondrial genome of *P. canaliculata*.

Several primers were used to amplify and sequence different gene segments (COI, 12S, 16S) of mtDNA (Rawlings et al., 2007). Species-specific primers were designed for amplify long segments of the mtDNA. The organization of mitochondrial genome is shown in Table 1. The complete mtDNA was 15,707 bp in length and contains 13 protein-coding genes, 2 ribosomal RNAs, 22 transfer RNAs, and a long non-coding region with 359 bp in length. The A+T content of the overall base composition of H-strand was 71.7% (T: 41%, C: 12.7%, A: 30.7%, G: 15.6%). ATP6, ATP8, CO1, CO2, ND1-3, ND5, ND6, ND4L and *Cyt b* genes began with ATG as start codon, CO3 and ND4 began with ATA. ATP8, CO2-3, ND4L, ND2-6 and *Cyt b* genes were terminated with TAA as stop codon, ATP6, ND1 and CO1 ended with TAG. Within the mitochondrial genome of *P. canaliculata*, there were three reading frame overlaps (tRNA-*Leu1* and tRNA-*Leu2* share one nucleotide; ND1 and tRNA-*Pro* share eleven nucleotides; tRNA-*Ser* and ND2 share one nucleotide). The non-coding regions include a long non-coding region and twenty-three intergenic spacers (range from 2 to 48 bp). The long non-coding region is 359 bp in length, and the A+T content of this region is 79.4% (A: 49.9%, C: 6.1%, G: 14.5%, T: 29.5%). A 23-bp repeat unit (AGATATAAAGAACTAAGAGATA) repeats 11 times in this region.

### Nucleotide sequence accession number

The complete genome sequence of *P. canaliculata* has been assigned GenBank accession number KJ739609.

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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 research was supported by grants from the Natural Science Foundation of China (NSFC) project (grant no. 31100274) and the Natural Science Foundation of Jiangsu Province (grant no. BK20131087).

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