The complete mitochondrial genome of the apple snail *Pomacea maculate* (Gastropoda: Ampullariidae)

Huirong Yang, Jia-En Zhang, Zhixin Deng, Hao Luo, Jing Guo, Chunxia Zhang, Yuanyuan Wu, Mingzhu Luo and Benliang Zhao

*Contact* Jia-En Zhang

**ABSTRACT**

We present the complete mitochondrial genome of *Pomacea maculate* in this study. The mitochondrial genome is 15,512 bp in length, containing 13 protein-coding genes, 2 rRNA genes, 22 tRNA genes. Overall nucleotide compositions of the light strand are 41.13% of A, 30.81% of T, 15.25% of C and 12.81% of G. Its gene arrangement and distribution are different from the typical vertebrates. The absence of D-loop is consistent with the Gastropoda, but at least one lengthy non-coding region is essential regulatory element for the initiation of transcription and replication. Phylogenetic tree is constructed by the maximum-likelihood method based on the complete mitochondrial genomes of 15 species of Caenogastropoda, using *Helix aspersa* as outgroup to assess their actual phylogenetic relationship and evolution. The result provides fundamental data for resolving phylogenetic and genetic problems related to effective management strategies.

**ARTICLE HISTORY**

Received 19 July 2018
Accepted 10 August 2018

**KEYWORDS**

Ampullariidae; *Pomacea maculate*; mitochondrial genome

---

*Pomacea maculate* (formerly *P. insularum*) (Perry, 1810), was introduced to Asia from Brazil and Argentina independently (Hayes et al. 2008). Subsequently, Lv et al. (2013) reported that *P. maculate*, was established in China. *Pomacea maculate* is one of two most common and highly invasive apple snail species as *P. canaliculata* (Lamarck, 1822) currently (Hayes et al. 2012), which strips vegetation, reproduces at tremendous rates, and have reduced rice production and caused ecosystem issues in Asia (Pimentel et al. 2005; Zedler and Kercher 2005; Burlakova et al. 2009). Some studies confirmed a much lower haplotype diversity of *P. maculate* in populations of China than that in their native countries Argentina and Brazil with a statistic ratio of 3:34 (Hayes et al. 2008; Lv et al. 2013; Yang et al. 2018). Furthermore, just a single lineage of *P. maculate* from Brazil was introduced into and established in China.

We sequenced its complete mitogenome to analyze phylogenetic relationship and evolutionary history for broadening the understanding of their population diversity, invasion processes and implementing effective management strategies. The specimen was sampled from Ningxi Teaching and Research Farm of South China Agricultural University in Guangzhou (E 113°29’, N 23°5’), and stored in the specimen museum of SCAU (accession number: 201502118).

The complete mitochondrial genome of *P. maculate* (Genbank accession number KY008699) is 15,512 bp in length, containing 13 protein-coding genes, 2 ribosomal RNA genes (rrns and rrnl), 22 transfer RNA genes (tRNA), which are encoded on the heavy strand except 8 tRNA genes (Met, Tyr, Cys, Trp, Gln, Gly, Glu and Thr) on the light strand. 22 tRNA genes vary from 64 to 75 bp in length, and all fold into the typical cloverleaf secondary structure. Among 13 protein-coding genes (total 11,238 bp) encoding 3,733 amino acids, the maximum is ND5 with 1,710 bp, and the minimum is ATP8 with only 159 bp. Rns and rrl genes are 934 and 1331 bp, respectively, located between the tRNA^Glu^ and tRNA^Leu^ genes and separated by the tRNA^Val^ gene. Overall nucleotide compositions of the light strand in descending order are 41.13% of A, 30.81% of T, 15.25% of C and 12.81% of G. Gene arrangement and distribution are different from the typical vertebrates (Yang, Sun, Zhao, et al. 2016; Yang, Sun, Zhao, Yang, et al. 2016; Yang, Zhao, Sun, Chen, et al. 2016; Yang, Zhao, Sun, Xie, et al. 2016; Yang, Zhao, Sun, Xie, et al. 2016; Yang, Zhao, Sun, Yang, et al. 2016). The absence of D-loop is consistent with the Gastropoda (Yang, Zhang, Deng, et al. 2016; Yang, Zhang, Guo, et al. 2016; Yang, Zhang, Luo, et al. 2016; Guo et al. 2017). The absence of D-loop is consistent with the Gastropoda (Yang, Zhang, Deng, et al. 2016; Yang, Zhang, Guo, et al. 2016; Yang, Zhang, Luo, et al. 2016; Guo et al. 2017), but at least one lengthy non-coding region is essential regulatory element for the initiation of transcription and replication (Wolstenholme 1992). There are 24 intergenic spacers (total 547 bp) varying from 3 to 141 bp in length, the largest...
of which is 141 bp between tRNA-Phe and NC III gene, and 2 gene overlaps (total 13 bp).

Phylogenetic tree is constructed by the maximum-likelihood method based on the complete mitogenomes of 15 species of Caenogastropoda, using *Helix aspersa* as outgroup. The published sequences in GenBank adopted are *Neptunea arthritica* (KU246047), *Volotharpa perryi* (KT382829), *Varicinassa varicifera* (KM603509), *Babylonia areolata* (HQ416443), *Babylonia lutos* (KF897830), *Terebra dimidata* (NC_013239), *Conus consors* (KF887950), *Conus tulipa* (K006970), *Bellamya quadrate* (NC_031850), *Cipangopaludina cathayensis* (NC_025577), *Pomacea maculata* (NC_027503), *Pomacea maculate* (KY008699), *Pomacea canaliculara* (NC_024586), *Pomacea bridgesii* (KY008698), *Marisa comuanieta* (NC_025334), *Helix aspersa* (NC_021747).

![Phylogenetic tree](image)

**Figure 1.** Phylogenetic tree generated by the maximum-likelihood method based on the complete mitochondrial genomes of 15 species of Caenogastropoda, using *Helix aspersa* as outgroup. The published sequences in GenBank adopted are *Neptunea arthritica* (KU246047), *Volotharpa perryi* (KT382829), *Varicinassa varicifera* (KM603509), *Babylonia areolata* (HQ416443), *Babylonia lutos* (KF897830), *Terebra dimidata* (NC_013239), *Conus consors* (KF887950), *Conus tulipa* (K006970), *Bellamya quadrate* (NC_031850), *Cipangopaludina cathayensis* (NC_025577), *Pomacea maculata* (NC_027503), *Pomacea maculate* (KY008699), *Pomacea canaliculara* (NC_024586), *Pomacea bridgesii* (KY008698), *Marisa comuanieta* (NC_025334), *Helix aspersa* (NC_021747).

**Disclosure statement**

No potential conflict of interest was reported by the authors.

**Funding**

This work is supported by the National Natural Science Foundation of China [No. U1131006, No. 30770403, No. 30900187, No. 31502144], Natural Science Foundation of Guangdong Province [No. 2015A030313409] Guangdong Science and Technology Program [No. 2007B02079007, No. 2015B090903077], Foundation for High-level Talents in Higher Education of Guangdong Province.

**References**

Burlakova LE, Karatayev AY, Padilla DK, Cartwright LD, Hollas DN. 2009. Wetland restoration and invasive species: apple snail (*Pomacea insularum*) feeding on native and invasive aquatic plants. *Restor Ecol.* 17(3):433–440.

Guo J, Yang HR, Zhang CX, Xue HY, Xia Y, Zhang JE. 2017. Complete mitochondrial genome of the apple snail *Pomacea diffusa* (Gastropoda, Ampullariidae) with phylogenetic consideration. *Mitochondrial DNA B.* 2(2):865–867.

Hayes KA, Cowie RH, Thiengo SC, Strong EE. 2012. Comparing apples with apples: clarifying the identities of two highly invasive neotropical Ampullariidae (Caenogastropoda). *Zool J Linn Soc-Lond.* 166(4):723–753.

Hayes KA, Joshi RC, Thiengo SC, Cowie RH. 2008. Out of South America: multiple origins of non-native apple snails in Asia. *Divers Distrib.* 14(4):701–712.

Lv S, Zhang Y, Liu HX, Hu L, Liu Q, Wei FR, Guo YH, Steinmann P, Hu W, Zhou XN, Utzinger J 2013. Phylogenetic evidence for multiple and secondary introductions of invasive snails: *Pomacea* species in the People’s Republic of China. *Diversity Distrib.* 19(2):147–156.

Pimentel D, Zuniga R, Morrison D. 2005. Update on the environmental and economic costs associated with alien-invasive species in the United States. *Ecol Econ.* 52(3):273–288.
Wolstenholme DR. 1992. Animal mitochondrial DNA: structure and evolution. Int Rev Cytol. 141:173–216.
Yang HR, Sun JJ, Zhao HH, Chen YB, Yang ZT, Li GF, Liu L. 2016. The complete mitochondrial genome of the *Clarias fuscus* (Siluriformes, Claridae). Mitochondrial DNA A. 27(2):1255–1256.
Yang HR, Sun JJ, Zhao HH, Yang ZT, Xiao SB, Li GF, Liu L. 2016. The complete mitochondrial genome of *Nibea coibor* (Perciformes, Sciaenidae). Mitochondrial DNA A. 27(2):1530–1522.
Yang Y, Xie Z, Peng C, Wang J, Li S, Zhang Y, Zhang H, Lin H. 2016. The complete mitochondrial genome of the orange-spotted grouper *Epinephelus coioides* (Perciformes, Serranidae). Mitochondrial DNA A. 27(3):1674–1676.
Yang HR, Zhang JE, Deng ZX, Luo H, Guo J, He SM, Luo MZ, Zhao BL. 2016. The complete mitochondrial genome of the golden apple snail *Pomacea canaliculata* (Gastropoda: Ampullariidae). Mitochondrial DNA B. 1(1):45–47.
Yang HR, Zhang JE, Guo J, Deng ZX, Luo H, Luo MZ, Zhao BL. 2016. The complete mitochondrial genome of the giant African snail *Achatina fulica* (Mollusca: Achatinidae). Mitochondrial DNA A. 27(3):1622–1624.
Yang HR, Zhang JE, Luo H, Luo MZ, Guo J, Deng ZX, Zhao BL. 2016. The complete mitochondrial genome of the mudsnail *Cipangopaludina cathayensis* (Gastropoda: Viviparidae). Mitochondrial DNA A. 27(3):1892–1894.
Yang HR, Zhao HH, Sun JJ, Chen YB, Liu LJ, Zhang Y, Liu L. 2016. The complete mitochondrial genome of the *Hemibarbus medius* (Cypriniformes, Cypriniidae). Mitochondrial DNA A. 27(2):1070–1072.
Yang HR, Zhao HH, Sun JJ, Xie ZZ, Yang ZT, Liu L. 2016. The complete mitochondrial genome of the *Culter recurviceps* (Teleostei, Cyprinidae). Mitochondrial DNA A. 27(1):762–763.
Yang HR, Zhao HH, Sun JJ, Yang ZT, Xiao SB, Li GF, Liu L. 2016. The complete mitochondrial genome of the amoy croaker *Argyrosomus amoyensis* (Perciformes, Sciaenidae). Mitochondrial DNA A. 27(2):1530–1532.
Yang HR, Zhao HH, Sun JJ, Zhang Y, Yang ZT, Liu L. 2016. The complete mitochondrial genome of the *Hemibagrus wyckioides* (Siluriformes, Bagridae). Mitochondrial DNA A. 27(1):766–768.
Yang HR, Zhao HH, Xie ZZ, Sun JJ, Yang ZT, Liu L. 2016. The complete mitochondrial genome of the *Hemibagrus guttatus* (Teleostei, Bagridae). Mitochondrial DNA A. 27(1):679–681.
Yang QQ, Liu SW, He C, Yu XP. 2018. Distribution and the origin of invasive apple snails, *Pomacea canaliculata* and *P. maculata* (Gastropoda: Ampullariidae) in China. Sci Rep. 8:1185.
Zedler JB, Kercher S. 2005. Wetland resources: status, trends, ecosystem services, and restorability. Annu Rev. Environ. Resour. 30:39–74.