Complete mitochondrial genome of the Cyclemys pulchristriata (Chelonia: Geoemydidae)

Jun Li, Yuanhua Lu, Jiawei Zan and Liuwang Nie

CONTACT Liuwang Nie lwnie@mail.ahnu.edu.cn

ABSTRACT

In this study, we obtained complete mitochondrial genome sequence of Cyclemys pulchristriata. The mitochondrial genome reaches a length of 16,527 bp, containing 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA genes and 1 control region. All protein-coding genes initiate with ATG as start codon, except for CO1 started with GTG. Most protein-coding genes ended by TAA as stop codon. Interestingly, there is an extra nucleotide A insertion in ND3 gene in C. pulchristriata. This study provides information on the genetic resources of C. pulchristriata that will contribute to protect this species.

Cyclemys pulchristriata distributed in the area of central Vietnam and eastern Kampuchea (Couture 1990). The species in Cyclemys are similar in size and form. It can distinguished from other congeneric species in the details of dorsal and abdomen (Fritz et al. 2008). As the species with a small population quantity, clarifying the specific genetic information, is an important requirement to formulate effective protective measures. C. pulchristriata mitochondrial genome sequence has not been reported.

In this, we sequenced and characterized the complete mitochondrial genome of C. pulchristriata. A sample was collected at Shanghai Zoo and stored in the Provincial Key Lab of the Conservation and Exploitation Research of Biological Resources in Anhui Normal University. Total genomic DNA was extracted from muscle samples by the standard phenol-chloroform method (Kan et al. 2010). Mitochondrial genome was amplified with 16 primers using PCR and then sequenced. These primers were designed by Oligo 7.0 based on the complete mitochondrial genome of C. atripons (GenBank: EF067858). BioEdit 7.2.3 was used to assist artificial sequence splicing after sequencing (Zhou et al. 2015). The mitochondrial genome sequence of C. pulchristriata was submitted to GenBank for accession number NC_026027.

All protein-coding genes initiate with ATG as start codon, except for CO1 started with GTG. Most protein-coding genes ended by TAA as stop codon. The lengths of 125 ribosomal RNA and 16S ribosomal RNA are 965 bp and 1597 bp, respectively. The length of control region is 1149 bp, ranging from 15,513 to 16,527 bp. Interestingly, there is an extra nucleotide A insertion in ND3 gene in C. pulchristriata. The phylogenetic trees of C. pulchristriata were determined by the nucleotide sequence of the 13 PCGs using neighbour-joining (NJ)/maximum parsimony (MP)/maximum-likelihood (ML) analyses (Figure 1). A total of 26 complete mitochondrial genomes were sampled for phylogenetic analysis. Mega 6.06 was used for NJ analyses and PAUP 4.0 beta 10 was used for MP analyses (Swofford 2002). The NJ analyses were conducted using 1000 bootstrap and MP analyses were performed with 1000 bootstrap values. ML analysis was performed in RAxML GUI v 1.3.1 under GTRGAMMAX model, which was implemented in 1000 bootstrap values (Lan et al. 2015). There are 24 species from the Geoemydidae, which contain Batagur, Cuora, Cyclemys, Heosemys, Mauremys, Notochelys and Sacalia, using Notochelys platynota and Testudo kleinmanni as outgroup.

According to clusters of the phylogenetic trees, the evolutionary relationships between C. atripons and C. pulchristriata are most close. This conclusion is consistent with previously reported results (Stuart and Fritz 2008). Cyclemys initially clustered with the Notochelys, followed by clustering with the Heosemys. Twenty-four representative turtles of Geoemydidae were divided into seven families. This study...
provides information on the genetic resources of *C. pulchristriata* will contribute to protect this species.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

**Funding**

This research received the support of the National Natural Science Foundation of China (NSFC, No. 31372198 and 30970351).

**Reference**

Couture G. 1990. Effects of the mixing of the W boson with a t-b-bar bound state at an e+e- collider[J]. Phys Rev D Part Fields. 41:2776–2781.

Fritz U, Guicking D, Auer M, Sommer R, M, Hundsdorfer A. 2008. Diversity of the Southeast Asian leaf turtle genus Cyclemys: how many leaves on its tree of life? Zool Script. 37:367–390.

Kan XZ, Li XF, Zhang LQ, Chen L, Qian CJ, Zhang XW, Wang L. 2010. Characterization of the complete mitochondrial genome of the Rock pigeon, *Columbia livia* (Columbiformes: Columbidae). Genet Mol Res. 9:1234

Lan J, Chen J, Ping W, Ren Q, Jian Y, Qian C, Hua X, Guo Z, Lei Z, Yang J. 2015. The mitochondrial genomes of *Aquila fasciata* and *Buteo lagoensis* (Aves, Accipitriformes): Sequence, Structure and Phylogenetic Analyses. PLoS One. 10:200–204.

Stuart BL, Fritz U. 2008. Historical DNA from museum type specimens clarifies diversity of Asian leaf turtles (*Cyclemys*). Biol J Linnean Soc. 94:131–141.

Swofford D. 2002. PAUP: Phylogenetic Analysis Using Parsimony (*and Other Methods*) Sunderland, Mccarthy.

Zhou H, Jiang Y, Nie L, Yin H, Li H, Dong X, Zhao F, Zhang H, Pu Y, Huang Z. 2015. The Historical Speciation of Mauremys Sensu Lato: Ancestral Area Reconstruction and Interspecific Gene Flow Level Assessment Provide New Insights. PLoS One. 10:e0144711.