Complete mitochondrial genome of the distinct red-eared slider (Trachemys scripta ssp., Testudines: Emydidae) in Korea

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Abstract

The complete mitochondrial (mt) genome of Trachemys scripta ssp. in Korea was sequenced and characterized. The mt genome is constituted of 37 genes (13 protein-coding genes, 22 transfer RNA genes and 2 ribosomal RNA genes) and a control region. Phylogenetic analysis based on the complete mt genome showed that the unidentified turtle had the mt genome closely related to that of T. s. elegans, though it had distinct morphology compared to T. s. elegans. This study can provide information for biogeographical studies and management plan for invasive species.

ARTICLE HISTORY

Received 10 December 2020
Accepted 2 March 2021

KEYWORDS

Trachemys scripta ssp.; invasive species; mitochondrial genome; phylogenetic analysis

The red-eared slider (Trachemys scripta) is native to the United States and is the most common and abundant turtle on Earth (Parham et al. 2020). As the popularity of the turtles and their exports to other countries increased, so did the frequency of intentional releases to other ecosystems (Parham et al. 2013; Koo et al. 2019). International Union for Conservation of Nature (IUCN) designated this turtle as the invasive species (http://www.iucn.org). The invasive species can lead to hybridization with native species, causing genetic contamination of native species (Koo et al. 2020; Parham et al. 2020). An unidentified turtle was found in Gwangju, Korea. It had no red line on both sides of its head, no yellow lines on carapace, and no black spot, but irregular patterns on the plastron, which was different from general morphology of the red-eared slider (Buhlmann et al. 2008). Therefore, we sequenced the complete mt genome of the unknown turtle. Consequently, it had the mt genome of T. s. elegans, which is referred to as T. s. elegans. This can contribute to understanding the effect of the invasive species, especially T. scripta.

The T. scripta ssp. specimen was collected from Gwangju (35°10’28.11”N; 126°54’35.9”E), Korea, and the total genomic DNA was extracted from the tail using the DNeasy Blood & Tissue kit (Qiagen, Valencia, CA) according to the manufacturer’s protocol. The extracted DNA sample was deposited at the Museum of Wildlife, located in Research Center of Ecomimetics, Chonnam National University, Korea (Specimen accession number: 2020-RCE-TSSSP001; shcol2002@chonnam.ac.kr). The mt genome was analyzed by primer walking method (Supplementary table 1) and sequenced using Applied Biosystems 3730XL DNA Analyzer (Bionics, Seoul, Korea). The reads were aligned and the complete sequence was annotated by comparing GenBank data (FJ392294, KM216748, and KM216749).

The complete mt genome of T. s. ssp. is 16,807 bp in length deposited in GenBank (Accession number: MW122291), and contains 13 protein-coding genes, 22 transfer RNA (tRNA) genes, 2 ribosomal RNA (rRNA) genes, and a putative long non-coding control region. 12 protein-coding genes, 14 tRNA genes, and 2 rRNA genes are encoded in heavy strand, whereas 1 protein-coding gene (NADH dehydrogenase subunit 6) and 8 tRNA genes in light strand. The nucleotide composition of the T. s. ssp. mt genome (A = 34.3%, T = 27.0%, C = 25.9%, and G = 12.9%) is identical with that of T. scripta Canada (A = 34.3%, T = 27.0%, C = 25.9%, and G = 12.9%), and almost identical to that of T. s. scripta China (A = 34.2%, T = 27.0%, C = 25.9%, and G = 12.9%). The sequence comparisons of T. s. ssp. with T. scripta Canada or T. s. elegans China indicated 99.8 or 99.7% sequence identity, respectively. However, the sequence identity between T. s. ssp. and T. s. scripta China is 99.3%. Furthermore, T. scripta Canada (Accession number: FJ392294) is referred to as red-eared slider (T. s. elegans) in GenBank.
data, even though there is no subspecies name. These data indicate that T. s. ssp. is closer to T. s. elegans than T. s. scripta.

To investigate the phylogenetic position of T. s. ssp., the complete mt genome sequences of 13 species in Testudines were extracted from GenBank and the phylogenetic tree was constructed using MEGA X software (Figure 1) (Kumar et al. 2018). The sequences were aligned using MUSCLE algorithm and tree building was performed using the maximum likelihood method and Tamura-Nei model with 1000 bootstrap replicates (Tamura and Nei 1993; Edgar 2004). It was found that every T. scripta species is clearly clustered in monophyletic manner and separated completely with other species. And like a sequence identity data, T. s. ssp. is in closer position with T. s. elegans and T. scripta (equal to T. s. elegans) than T. s. scripta. This analysis implies that T. s. ssp. which are different from general morphology (T. s. elegans) exist, though the reason is unknown. These data provide important molecular data for further biogeographical studies and can be utilized meaningfully to control ecological disturbance by T. s. elegans which is an invasive species in many countries including Korea.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

**Funding**

This work was supported by Korea Environmental Industry and Technology Institute (KEITI) through the Project for the Development of Biological Diversity Threats Outbreak Management Technology [RE201807039], funded by Korea Ministry of Environment (MOE).

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**Data availability statement**

The data that support the findings of this study are openly available in NCBI at [https://www.ncbi.nlm.nih.gov/nuccore/MW122291](https://www.ncbi.nlm.nih.gov/nuccore/MW122291), reference number MW122291.

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