Complete mitochondrial genome of *Rusa unicolor cambojensis* (Artiodactyla: Cervidae)

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**ABSTRACT**

*Rusa unicolor* has been listed as a vulnerable species by the International Union for Conservation of Nature and Natural Resources because of human activities. In recent years, population numbers have decreased due to heavy hunting and habitat loss, and little genetic data on this species exists; thus, our knowledge of range distribution and population size remains limited. In the current study, the complete *R. u. cambojensis* mitochondrial genome was sequenced using polymerase chain reaction followed by direct sequencing. The complete mitochondrial genome was determined to be circular and contain 16,557 bp, including 13 protein-coding genes, 2 rRNA genes, 22 tRNA genes, and 1 control region, the gene composition and order were similar to those of most other vertebrates reported to date. Most mitochondrial genes, except for ND6 and eight tRNAs, were encoded on the heavy strand. The overall base composition of the heavy strand was 33.6% A, 28.9% T, 24.2% C, and 13.3% G, with a strong AT bias of 62.5%. There were 13 regions of gene overlap totaling 96 bp and 12 intergenic spacer regions totaling 70 bp. The phylogenetic analyses (maximum likelihood and Bayesian inference) of *R. unicolor* based on the mitochondrial genome four subspecies of *R. unicolor* were clustered into a well-supported single clade, and *R. u. cambojensis* was most closely related to *R. u. dejeani*. This study will assist in the exploration of the evolutionary history and taxonomic status of the sambar, as well as its protection as a genetic resource.

**Keywords**

Mitogenome; phylogenetics; *Rusa unicolor cambojensis*

**Article history**

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non-coding control region (D-loop). The overall base composition of the heavy strand was 33.6% A, 28.9% T, 24.2% C, and 13.3% G, with a strong AT bias of 62.5%.

Phylogenies of the mitogenome were constructed using maximum likelihood, implemented in PHYML 3.0 (Guindon et al. 2010). Bayesian inference was implemented in MRBAYES 3.2.1 (Ronquist et al. 2012). Based on the complete genomes (Figure 1), four subspecies of *R. unicolor* were clustered in a well-supported single clade, with *R. unicolor* swinhoei as its sister species. Intraspecific phylogenetics demonstrated that *R. u. cambojensis* was more closely related to *R. u. dejeani* than to *R. u. swinhoei* and *R. u. hainana*, which are respectively endemic to the islands of Taiwan and Hainan. The *R. u. cambojensis* mitogenome will be useful for its identification and conservation, as well as for evolutionary research on *R. unicolor*.

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**Disclosure statement**

The authors declare no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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**Data availability statement**

The datasets supporting the results of this article are available in GenBank of the NCBI at (https://www.ncbi.nlm.nih.gov/) under accession number MK941883.

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