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MITOGENOME ANNOUNCEMENT

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The complete mitochondrial genome of Malayan Gaur (*Bos gaurus hubbacki*) from Peninsular Malaysia

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ABSTRACT

Here, we present the first complete mitochondrial genome of Malayan Gaur (*Bos gaurus hubbacki*) inferred using next-generation sequencing. The mitogenome is 16,367 bp in length with the structural organization of a typical bovine mitochondrial arrangement comprising 13 protein-coding genes, 21 tRNAs, and 2 rRNAs. No internal stop codon was found in the protein-coding genes. Phylogenetic tree analysis revealed that Malayan gaur is more closely related to Burmese banteng instead of gaur.

Introduction

Traditionally three subspecies have been recognized based on coloration and size (Duckworth et al. 2016): *Bos gaurus gaurus*; *B. g. readei*; and *B. g. hubbacki*. However, only two subspecies are recognized by the International Union for Conservation of Nature (IUCN) which were based on the measurements of skulls and horns (Groves and Grubb 2011; Duckworth et al. 2016). These two subspecies are *B. g. gaurus* which can be found in India, Nepal, and Bhutan; and *B. g. laosiensis* found in Myanmar, southern China, Laos, Vietnam, Cambodia, Thailand, and Peninsular Malaysia). Nonetheless, this dual classification is still inconclusive as the morphological measurements are based only on a few skull samples, and there is no supporting genetic analysis (Hassanin 2014).

In the past, wild gaur can be found in significant numbers in the states of Pahang, Perak, Kelantan, and Terengganu (Conry 1989). Nonetheless, due to poaching and habitat destruction, recently it is estimated that only around 270–300 individuals of wild gaur still exist in Peninsular Malaysia (DWNP 2012). Here, we present the first complete mitochondrial genome of *B. gaurus* isolate from Peninsular Malaysia with 16,367 bp in length. The full mitogenome reported here have the structural organization of a typical bovine mitochondrial arrangement comprising of 13 protein-coding genes, 21 tRNAs, and 2 rRNAs. No internal stop codon was found in the protein-coding genes. This annotated mitogenome has been deposited in GenBank under accession number MK770201.

Genomic DNA isolation and mitogenome sequencing

Tissue sample of a deceased male Malayan gaur with studbook number S0029 from Sungkai Wildlife Conservation Centre (Latitude: 4.034714 | Longitude: 101.369063) was used for extraction and analysis to generate the data presented here. The tissue samples are catalogued as WGRB-BGH40 and deposited in the Wildlife Genetic Resource Bank (WGRB) at National Wildlife Forensic Laboratory, Department of Wildlife and National Parks Peninsular Malaysia. Genomic DNA (gDNA) was used to generate sequences library of paired-end, 250-bp reads. It generated 2,541,912 of short-read sequences (SRS) totaling 635,478,000 bases of DNA.

Assembly and gene annotation

The raw SRS were screened using FastQC (Andrews 2010) and trimmed using BBduk (Bushnell 2015). Trimmed SRS were then assembled using repeated referenced mapping and *de novo* assembly. Repeated reference mapping was performed by employing end-to-end mapping and local

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