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Data Article

Sequence variation data of the mitochondrial DNA D-loop region of the captive Malayan Gaur (*Bos gaurus hubbacki*)

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ABSTRACT

This article contains data of the sequence variation in the mitochondrial DNA D-loop region of the Malayan gaur (*Bos gaurus hubbacki*), locally known as the seladang, from two captive centers. Thirty fecal samples of Malayan gaur were collected from Jenderak Selatan Wildlife Conservation Center (Pahang) and the Sungkai Wildlife Reserve (Perak) for DNA extraction and amplification with polymerase chain reactions. DNA sequences were then analyzed using neighbor joining (NJ) and maximum parsimony (MP) methods. Based on the 652 base pairs obtained, we found seven variable characters with a value of 1%. The genetic distance between the two captive centers was 0.001. Haplotype analyses detected only four haplotypes between these two captive centers. Both NJ and MP trees demonstrate that all individuals in the Jenderak and Sungkai captive centers are in the same clade. Genetic variation of the Malayan gaur in these centers is considered low, possibly because individuals share the same common parent. This sequence variation data are of paramount importance for designing a proper breeding and management program of the Malayan gaur in the future.

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