Mitochondrial DNA

http://informahealthcare.com/mdn
ISSN: 1940-1736 (print), 1940-1744 (electronic)

Mitochondrial DNA, Early Online: 1–2
 DOI: 10.3109/19401736.2015.1022735

informa
healthcare

MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the *Macaca mulatta brevicaudus*

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Abstract

The complete mitochondrial sequence of the *Macaca mulatta brevicaudus* has been determined by mapping the raw data to previously published mitochondrial assemblies of the corresponding species. The total sequence length is 16,561 bp, consisting of 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes, and one D-loop control region. The base composition of the mtDNA genome is 31.77% A, 25.14% T, 30.33% C, and 12.76% G, with an AT content of 56.90%. The arrangement of genes in *M. m. brevicaudus* is identical to that of *M. mulatta*. All genes are encoded on the heavy strand with the exception of ND6 and eight tRNA genes. The mitochondrial genome of *M. m. brevicaudus* presented here will contribute to a better understanding of the population genetics, help to protect its genetic diversity and resolve phylogenetic relationships within the family.

Keywords

Complete mitochondrial genome, *Macaca mulatta brevicaudus*, Hainan island macaca

History

Received 25 January 2015
Revised 16 February 2015
Accepted 21 February 2015
Published online 12 May 2015

The *Macaca mulatta brevicaudus* (*M. m. brevicaudus*) is the southernmost subspecies of *Macaca mulatta* in China, belonging to genus *Macaca* (Colobinae: Cercopithecidae). This species is endemic to Hainan Island (Elliot, 1912), and categorized as critically endangered (CR) in the IUCN Red List of Threatened Species (IUCN, 2013).

In this study, the complete mitochondrial genome sequence of the *M. m. brevicaudus* has been reported for the first time. Muscle samples of *M. m. bravicaudus* were collected from deceased individuals found in the wild of Hainan Island and stored in 95% ethanol. Genomic DNA was extracted with the help of the DNeasy Blood & issue Kit (Qiagen, Valencia, CA) according to the instructions of the manufacturer. We assembled its mitochondrial genome (mtDNA) with paired-end reads with length between 94 and 114 bp. We captured reads from the mitochondrial genome by mapping the raw data to previously published mitochondrial assemblies of the corresponding species. The mapping was carried out using mrFAST (Alkan et al., 2009) with paired-end mode and 6% of divergence. We removed low-quality reads when at least one of both paired-ends had a median Phred quality score lower than 32. The mtDNA sequence was annotated in comparison with the complete mitochondrial genomes of *M. mulatta* (Liedigk et al., 2014). The accession numbers of the GenBank for *M. m. brevicaudus* mtDNA is KP641672. The complete mtDNA sequence (16,561 bp in length) consists of 13 protein coding genes, 22 tRNA genes, two rRNA genes, and one D-loop control region. All genes are encoded on the heavy strand with the exception of ND6 and eight tRNA genes (*tRNA-Gln*, *tRNA-Ala*, *tRNA-Asn*, *tRNA-Cys*, *tRNA-Tyr*, *tRNA-Ser*, *tRNA-Glu*, and *tRNA-Pro*). For 10 of the 13 protein-coding genes, the start codon is ATG, while ND2 and ND3 utilize ATT and ND5 utilizes ATA. With regard to stop codons, six genes (*COX1*, *COX2*, *ATP6*, *ATP8*, *ND4L*, and *ND5*) use TAA, ND6 uses AGG, and six genes (*ND1*, *ND2*, *ND3*, *ND4*, *COX3*, and *CYTB*) have an incomplete stop codon T, which were presumably completed as TAA by posttranscriptional polyadenylation (Anderson et al., 1981). The 12S and 16S ribosomal RNA genes are 951 bp and 1564 bp long, respectively. The *tRNA* genes are various from 59 bp to 75 bp. In our study, the D-loop control region of the *M. nigra* mtDNA is 1083 bp long and is located between the *tRNA-Pro* and *tRNA-Phe* genes. We did not find repeat sequences in the D-loop control region. The mitochondrial genome have been proved to be very useful for phylogenetic relationships at several taxonomic levels, mainly because of its maternal inheritance, its small size, an accelerated rate of mutation compared with that of the nuclear DNA, and little or no recombination (Ballard & Whitlock, 2004; Brown et al., 1979). In this study, we also built a neighbor-joining (NJ) tree of *M. m. brevicaudus* with other nine closely related *Macaca* mitogenome sequences to inform their phylogenetic relationship (Figure 1). The phylogenetic tree was constructed with MEGA 5 (MEGA Inc., Englewood, NJ) using the neighbor-joining (NJ) method (Tamura et al., 2011). The other nine closely related *Macaca* mitogenome sequences used in this phylogenetic tree were downloaded from the GeneBank (*Macaca mulatta lasiotus*: KF830702.1, *Macaca mulatta*: NC_005943.1, *Macaca arctoides*: NC_025201.1, *Macaca fascicularis*: NC_012670.1, *Macaca assamensis*: NC_023795.1, *Macaca thibetana*: NC_011519.1, *Macaca tonkeana*: NC_025222.1; *Macaca Silenus*: NC_025221.1, *Macaca sylvanus*: NC_002764.1).

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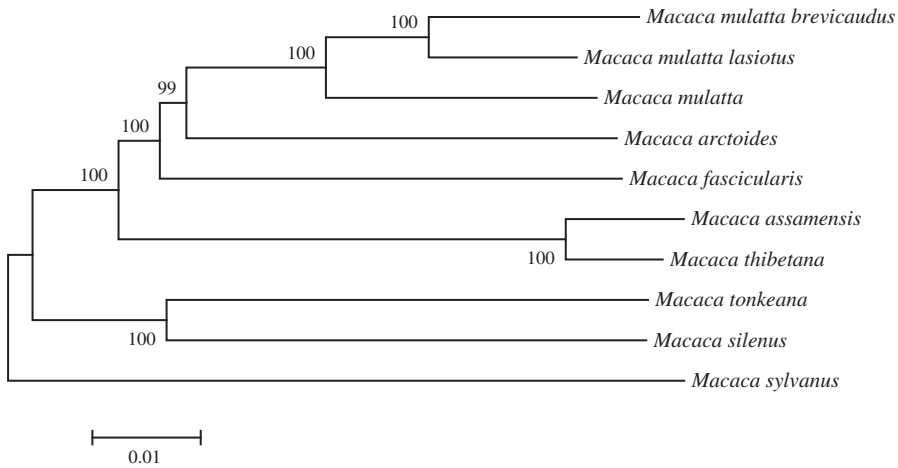

Figure 1. The phylogenetic tree of 10 closely related *Macaca* constructed with mitogenome sequences.

Our result was mostly consistent with previous studies (Perelman et al., 2011; Tosi et al., 2003). We expect these results will provide relevant information for *M. m. brevicaudus* comparative studies in the future.

Acknowledgements

We thank helpful corrections and comments regarding this manuscript.

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This project was supported by Natural Science Foundation of China (No. 31471989).

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