


Complete mitochondrial genome of a Toque Macaque (*Macaca sinica*)

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ABSTRACT

The Toque macaque (*Macaca sinica*) is the only macaque species on Sri Lanka and endemic to the island. The newly generated mitochondrial genome (Genbank accession number MG870385), obtained from a captive individual, has a length of 16,525 bp and exhibits the typical structure of mammalian mitochondrial genomes. Phylogenetically, the Toque macaque is nested within the *Macaca sinica* species group and represents a sister lineage to a *M. assamensis*/*M. thibetana* clade. The new data help to further illuminate and better understand the complex phylogeny of macaques.

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The Toque macaque (*Macaca sinica*) is one of 23 macaque species and occurs only on Sri Lanka (Zinner et al. 2013; Roos et al. 2014). Based on the structure of male external genitalia, the species was lumped, together with *M. assamensis*, *M. thibetana* and *M. radiata*, into the *Macaca sinica* species group (Fooden 1976). The species group further contains *M. munzala* and *M. leucogenys*, two species that were newly described in recent years (Sinha et al. 2005; Li et al. 2015). In a study by Tosi et al. (2003), this species group classification was verified with genetic data, but to date only five partial sequences of the mitochondrial genome of *M. sinica* are available in Genbank, thus calling for additional sequence data of the species.

Consequently, I report here on the sequencing of a mitochondrial genome of a Toque macaque generated from a faecal sample that was collected from a male individual kept at Berlin Zoo, Germany. Total genomic DNA was extracted with the QIAamp DNA Stool Mini Kit following the standard protocol provided by the company (Qiagen, Valencia, CA). The complete mitochondrial genome was PCR amplified, Sanger-sequenced and assembled following methods described in Liedigk et al. (2014, 2015).

The mitochondrial genome has an A+T content of 56.46% and contains 13 protein-coding genes, 22 transfer

RNAs, two ribosomal RNAs and the control region in the order typically found in mammals (Anderson et al. 1981).

To trace the phylogenetic position of the Toque macaque, I generated a maximum-likelihood tree using an alignment comprising of 15 macaques and a *Papio hamadryas* used to root the tree. Sequences were aligned with Muscle 3.8.31 (Edgar 2010) in SeaView 4.5.4 (Gouy et al. 2010), and indels and poorly aligned positions were removed with Gblocks 0.91b (Castresana 2000). Tree reconstruction was performed with IQ-TREE 1.5.2 (Nguyen et al. 2015) using the optimal substitution model (TIM2+I+G) as determined by ModelFinder (Chernomor et al. 2016; Kalyaanamoorthy et al. 2017) and 10,000 ultrafast bootstrap replicates (Minh et al. 2013). In the phylogenetic tree (Figure 1), the Toque macaque is nested within the *M. sinica* species group and forms a strongly supported (100% bootstrap) sister lineage to a clade consisting of *M. assamensis* and *M. thibetana*. These results are in agreement with Tosi et al. (2003) who used a ca. 1.5 kb fragment of the mitochondrial genome, but complete mitochondrial genome data provide stronger node support. The mitochondrial genome of a Toque macaque is an important addition to further illuminate and better understand the complex evolutionary history of macaques.

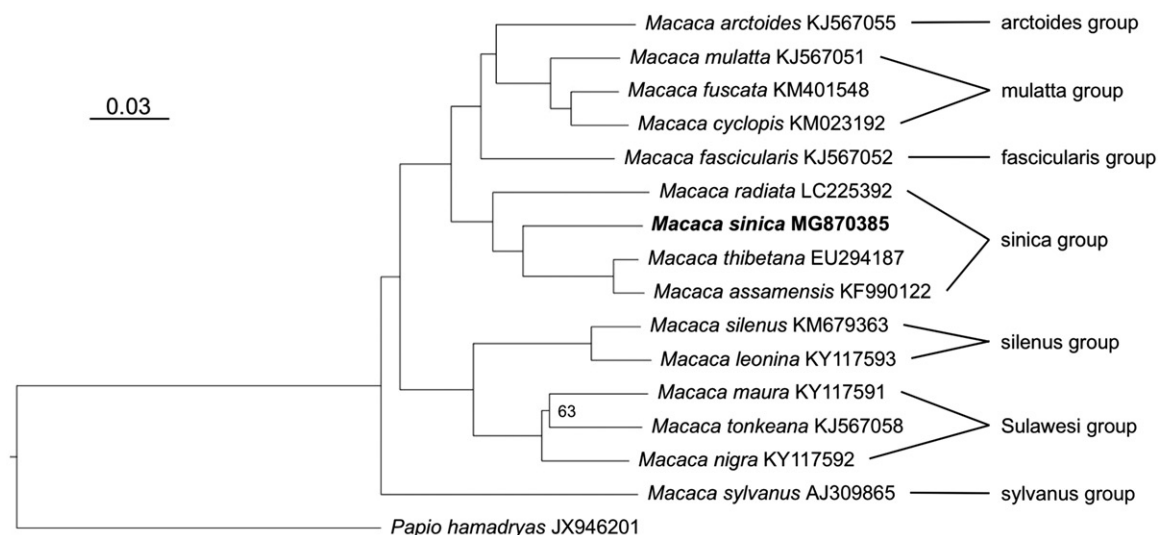


Figure 1. Maximum-likelihood tree displaying phylogenetic relationships among macaques. The Toque macaque, highlighted in bold, is nested within the *M. sinica* species group and is closest related to *M. assamensis* and *M. thibetana*. Node support is generally high with 100% bootstrap support (not shown); only the phylogenetic relationship among the three Sulawesi macaques gained lower bootstrap support (63%). The bar refers to substitutions per site. Genbank accession numbers are given after species names. To the right, macaque species groups are indicated.

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Disclosure statement

The author reports no conflicts of interest. The author alone is responsible for the content and writing of the paper.

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