

## GENETIC IDENTIFICATION OF CRITICALLY ENDANGERED ORANGUTANS IN CAPTIVITY

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**Abstract:** A large number of the orangutans' genetic status in captivity is unknown to its exact, thus complicates the translocation process to their true natural habitat. A study was carried out to identify 37 captive orangutans in Peninsular Malaysia at the species and subspecies level using mitochondrial DNA (mtDNA) displacement loop (D-loop) region DNA sequences. Orangutan genetic samples were provided by the Bukit Merah Orang Utan Island (BMOUI), Zoo Negara, Zoo Taiping and the A' Famosa. Total genomic DNA was extracted from both fecal and blood samples. Polymerase chain reaction (PCR) was performed using specific primers for the orang utan. Data analyses were carried out using distance and character based approaches, namely the neighbor joining (NJ), maximum parsimony (MP), and Bayesian techniques. About 8 individuals were identified as *Pongo pygmaeus pygmaeus*, 20 as *P. p. morio*, 5 as *P. p. wurmbii*, and 4 as *P. abelii*. All samples were successfully identified with high probabilities. The results obtained in this study contributes to improve the understanding of captive orangutans' genetic identification, and indirectly, a guide to the authorities in developing plans for the management in captivity and conservation of primates in Malaysia using molecular data.

Keywords: Orangutan, *Pongo*, mitochondrial DNA, genetic identification, captive

### Introduction

Orangutans, genus *Pongo* are the only great apes found in Asia, and they are only found on the Borneo and Sumatra islands (Brandon-Jones *et al.*, 2004). Taxonomically, orangutans on both islands were initially considered to represent two different subspecies, *Pongo pygmaeus pygmaeus* and *P. p. abelii* (Jalil *et al.*, 2008); although the behavioral and morphological features of these groups are almost the same, they are quite distinct in term of molecular genetics (Ryder & Chemnick, 1993). However, recent data have established the orangutan taxonomy as representing three different species, namely the Bornean orangutan, *P. pygmaeus*, the Sumatran orangutan, *Pongo abelii* and the Tapanuli orangutan, *Pongo tapanuliensis* based on morphometric, behavioral and genomic analyses (Nater *et al.*, 2017). Further taxonomic classification of Bornean orangutans had

suggests the existence of three subspecies. The first three groups *P. p. pygmaeus* in Sarawak and Northwest Kalimantan, *P. p. morio* in Sabah and east Kalimantan, and *P. p. wurmbii* in southwest and central Kalimantan (Warren *et al.*, 2001).

Orangutans are classified as critically endangered species based on the IUCN Redlist 2017. Over the years, natural populations of orangutans have been declining due to factors such as hunting, habitat loss and illegal trades (Robinson & Bennet, 2000). Several ex situ institutions have been developed to overcome the declining trend of orangutan populations in the wild. In fact, translocation and rehabilitation efforts, such as the establishment of rehabilitation centers at Bohorok in north Sumatra (Indonesia), Sepilok in Sabah (Malaysia), Batang Ai and Semenggoh in Sarawak (Malaysia), and Tanjung Puting in central Kalimantan (Indonesia), are being implemented by various stakeholders