

Short Communication: Effectiveness of nuclear gene in species and subspecies determination of captive orangutans

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Manuscript received: 28 May 2020. Revision accepted: 21 July 2020.

Abstract. *Abdul-Manan MN, Mohd-Ridwan AR, Aifat NR, Osman NA, Abdul-Latiff MA, Dharmalingam S, Md-Zain BM. 2020. Short Communication: Effectiveness of nuclear gene in species and subspecies determination of captive orangutans. Biodiversitas 21: 3665-3669.* Genetic identification of captive orangutans is of paramount importance in providing a correct identity that is essential for captive management. Thus, the utility of nuclear DNA sequences was tested in this study to identify the genetic identity of captive orangutans at Bukit Merah Orang Utan Island. Out of 24 DNA samples that were successfully extracted, only 10 orangutan samples were successfully sequenced for the von Willebrand factor (vWF) gene. From the results, this gene was able to separate the genus *Pongo* at the species level. Distance and character analyses indicated that a clear separation between *P. pygmaeus* and *P. abelii* at the species level. However, the degree of separation at species level was indicated in tree topology with moderate bootstrap values. At the subspecies level of *P. pygmaeus*, this gene was unable to show a clear separation between three Bornean subspecies. All the subspecies were formed clade together with each other. The vMF gene is a good nuclear gene for the study of phylogenetic relationships of orangutans in captivity at the species level, but the genetic identification at subspecies level in the genus level remains unclear. We suggest that future studies should involve multiple independent nuclear markers to increase the probability of getting reliable results.

Keywords: Captive orangutan, nuclear DNA, von Willebrand Factor (vMF) gene, phylogenetic, *Pongo*

INTRODUCTION

The orangutans, genus *Pongo*, are the merely available Hominidae (great apes) that exist in Asia on Borneo and Sumatra Island (Loken et al. 2013; Kamaluddin et al. 2019). This genus consists of three different species (Nater et al. 2017), namely, Bornean orangutan (*Pongo pygmaeus*), Sumatran orangutan (*Pongo abelii*), and Tapanuli orangutan (*Pongo tapanuliensis*). Roos et al. (2014) classified the Bornean orangutan into three subspecies, namely, *P. p. pygmaeus* (Sarawak and Northwest Borneo), *P. p. wurmbii* (Southwest and Central Borneo), and *P. p. morio* (Sabah and Northeast Borneo). These subspecies of orangutans were classified based on morphology and genetic study of orangutans by primatologists (Warren et al. 2001; Zhang et al. 2001). The Bornean orangutan is presently red-listed as critically endangered under the IUCN (Ancrenaz et al. 2016). Most of the remaining orangutans live outside the protected area (Meijaard and Wich 2007). Over the years, logging, poaching, habitat loss and illegal trades are the major threats to natural populations of orangutans (Freund et al. 2016; Hardus et al. 2012).

There are five primate families found in Malaysia namely Lorisiidae, Tarsiidae, Cercopithecidae, Hylobatidae and Hominidae (Md-Zain et al. 2010). Previous molecular systematic studies on Malaysian primates were more focused on the Cercopithecidae, Tarsiidae, and Lorisiidae families rather than Hominidae (Md-Zain et al. 2010, 2019; Abdul-Latiff et al. 2019). These previous phylogenetic studies were all based on mitochondrial DNA (mtDNA) markers. All these studies resolved the taxonomy and systematics of Malaysian primates at species and subspecies level using mtDNA markers. In addition, Warren et al. (2001) had also employed mtDNA to identify the distribution of Bornean orangutan. Zhang et al. (2001) utilized microsatellites and mitochondrial DNA sequences to study the genetic divergence of orangutans in Borneo and Sumatra. Zhi et al. (1996) tried to differentiate orangutan subspecies among natural populations using genetic materials, specifically mitochondrial 16S ribosomal RNA sequences, minisatellite loci, and mtDNA restriction fragment length polymorphisms. The findings of this study revealed that Sumatran and Bornean orangutans are largely dissimilar in terms of phylogenetic and genetic distance. However, among isolated populations of Bornean