## MOLECULAR PHYLOGENY OF THE OLD WORLD PORCUPINES (FAMILY HYSTRICIDAE) USING MITOCHONDRIAL CYTOCHROME *B* GENE

## JEFFRINE JAPNING ROVIE-RYAN<sup>1</sup>\*, FAISAL ALI ANWARALI KHAN<sup>2</sup>, ZAINAL ZAHARI ZAINUDDIN<sup>3</sup>, ABDUL HAMID AHMAD<sup>4</sup>, MILLAWATI GANI<sup>1</sup>, AHMAD MASHUR JULAIHI<sup>1</sup> AND SALMAN SAABAN<sup>1</sup>

<sup>1</sup>National Wildlife Forensic Laboratory, Ex-Situ Conservation Division, Department of Wildlife and National Parks Peninsular Malaysia, 56100 Kuala Lumpur, Malaysia. <sup>2</sup>Department of Zoology, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 93400 Kota Samarahan, Sarawak, Malaysia. <sup>3</sup>Borneo Rhino Alliance, 88400 Kota Kinabalu, Sabah, Malaysia. <sup>4</sup>Institute for Tropical Biology and Conservation, Universiti Malaysia Sabah, 88400 Kota Kinabalu, Sabah, Malaysia.

\*Corresponding author: jeffrine@wildlife.gov.my

Abstract: The Old World porcupines (Family Hystricidae) are generally large terrestrial rodents. The major threats to their survival includes over-hunting primarily due to high demand for their meat that is thought to be of high medicinal value. This threat is further impacted by mass habitat destruction where forest is converted into agricultural land or human settlements. Despite their large and unique appearance, little is known with regards to their intrafamilial phylogenetic relationships. This is hampered by the limited DNA sequences that are available on public databases for species identification and comparison. In this study, the phylogenetic relationships among eight out of eleven extant species of Hystricidae were examined using a partial cytochrome b gene of the mitochondrial DNA. The first reference record of DNA sequence for all four species of porcupines in Malaysia (Atherurus macrourus, Hystrix brachyura, Thecurus crassispinis, and Trichys fasciculata) were made available in GenBank database. These reference sequences are crucial for species identification in a forensic case framework. The phylogeny supported the monophyly of the family Hystricidae. Except for *Thecurus*, the genera within Hystricidae: Atherurus, Hystrix, and Trichys formed distinct groups supporting their genus status with Trichys forming the basal group. Based on the positioning of Thecurus crassispinis within the Hystrix species group in the phylogeny tree, we suggested that Thecurus crassispinis to be systematically classified as Hystrix crassispinis. Within the genus Hystrix, further studies are needed to elucidate the relationships by including the remaining three species within the genus (Hystrix javanica, Hystrix pumila, and Hystrix sumatrae). Furthermore within Hystrix brachyura, additional studies are needed to investigate the regional populations structuring within their range countries in Southeast Asia to assist in the sustainable management and conservation of the species.

Keywords: Hystricidae, reference DNA sequence data, *Thecurus crassispinis*, phylogenetic relationship, mitochondrial cytochrome *b*, sustainability.

## Introduction

The Old World porcupines (Hystricidae) belongs to the infraorder Phiomorpha, which is distinct from the infraorder Caviomorpha found native to the American continent. Hystricidae consists of eleven extant species from possibly four genera (*Hystrix, Atherurus, Thecurus* and *Trichys*). Eight species are Asiatic in origin while the remaining three can be found in Africa and the Mediterranean (Figure 1). Members within this family are generally large terrestrial

rodents characterized by their unique spines covering their whole body.

In Malaysia four species exist, namely Atherurus macrourus (brush-tailed porcupine), Hystrix brachyura (Malayan porcupine), Thecurus crassispinis (thick-spined porcupine), and Trichys fasciculata (long-tailed porcupine) (Wilson & Reeder, 2005; IUCN, 2016; Phillipps & Phillipps, 2016) (Figure 2). A. macrourus are nocturnal rat-like species and have long slender body and almost the entire body are covered by